



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 135509

TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Tuesday, October 19, 2004

Case Serial Number: 09/695451

From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526

david.schreiber@uspto.gov

Search Notes

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: D. Schreiber

Searcher Phone #: 272-2526

Searcher Location: Rm 101 A61

Date Searcher Picked Up: _____

Date Completed: 10/17

Searcher Prep & Review Time 20

Clerical Prep Time: _____

Online Time: 183

Type of Search

NA Sequence (#) 30

AA Sequence (#) _____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems CompuGen

WWW/Internet _____

Other (specify) _____

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 65²⁰.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:17:38 ; Search time 0.001 Seconds
(without alignments)
0.352 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tgcaggagaaacagacaccg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 8 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : rst1-727.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	6.4	29.1	8	1	CF921494
					ACCESSION:CF921494

ALIGNMENTS

RESULT 1
CF921494/c
LOCUS
DEFINITION CF921494 8 bp mRNA linear EST 05-NOV-2003
gmthRw3-10_B07.1.061 Soybean root hair subtracted cDNA library
gmthRw3 Glycine max cDNA, mRNA sequence.
CF921494
ACCESSION CF921494.1 GI:38192288
VERSION
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 8)
REFERENCE Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
AUTHORS Expressed sequence tags from soybean root hair subtractive cDNA
TITLE library
JOURNAL Unpublished (2003)
COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7.

FEATURES source

Location/Qualifiers
1..8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmthRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."

Query Match 29.1%; Score 6.4; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 734 AGAARACAG 741

Db 8 AARACAG 1

Search completed: October 18, 2004, 14:17:39

Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:09:43 ; Search time 0.001 Seconds
(without alignments)
135.608 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tgcaggagaacagacacg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 276 seqs, 3082 residues

Total number of hits satisfying chosen parameters: 552

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 276 summaries

Database : rni1-727.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	15.4	70.0	18	1	US-08-485-942A-45
C 3	15.4	70.0	18	1	US-08-488-214A-45
C 4	15.4	70.0	18	1	US-08-488-208A-45
C 5	15.4	70.0	18	1	US-08-483-211A-45
C 6	15.4	70.0	18	1	US-08-488-223A-45
C 7	15.4	70.0	18	1	US-08-438-431A-45
C 8	13.8	62.7	18	1	US-08-577-081A-67
C 9	13.8	62.7	18	1	US-08-488-225A-45
C 10	12.4	56.4	18	1	US-08-465-095-6
C 11	12.4	56.4	18	1	US-08-179-656A-6
C 12	12.4	56.4	18	1	PCT-US94-00300-6
C 13	12.4	56.4	18	1	US-08-288-140-28
C 14	12.2	55.5	18	1	US-08-422-978-4649
C 15	11.8	53.6	18	1	US-08-912-129A-42
C 16	11.4	51.8	17	1	US-08-329-350-40
C 17	11.4	51.8	17	1	US-08-584-040-5499
C 18	11.4	51.8	17	1	US-08-371-772B-2330
C 19	11.2	50.9	17	1	US-08-584-040-6036
C 20	11.2	50.9	17	1	US-08-371-772B-2873
C 21	11	50.0	15	1	5182195-60
C 22	10.8	49.1	15	1	US-08-291-932A-10
C 23	10.4	47.3	12	1	US-08-242-664-12
C 24	10.4	47.3	12	1	US-08-484-138-12
C 25	10.4	47.3	12	1	PCT-US95-06379-12
C 26	10.4	47.3	14	1	US-08-639-080-4
C 27	10.4	47.3	14	1	US-08-535-249-125
C 28	10.4	47.3	14	1	US-08-874-601-18
C 29	10.4	47.3	15	1	US-08-291-932A-11
C 30	10.4	47.3	15	1	US-08-363-240A-654
C 31	10.4	47.3	15	1	US-08-081-646-132
C 32	10.4	47.3	15	1	US-08-081-646-867
C 33	10.4	47.3	16	1	US-08-137-024-4

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Sequence 15, Appl	15	45.5	10	US-09-081-646-456	1
Sequence 43, Appl	14	44.5	9	US-08-303-004-13	1
Sequence 11, Appl	14	44.5	9	US-08-442-513A-11	1
Sequence 16, Appl	14	44.5	9	US-08-442-513A-16	1
Sequence 186, Appl	14	44.5	9	US-08-173-489C-186	1
Sequence 126, Appl	14	44.5	9	US-08-173-489C-198	1
Sequence 11, Appl	15	44.5	9	US-09-049-190-11	1
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Sequence 60, Appl	15	44.5	9	US-09-531-000-60	1
Sequence 9, Appl	12	42.7	9	US-08-560-313A-9	1
Sequence 13, Appl	12	42.7	9	US-08-611-155B-13	1
Sequence 15, Appl	12	42.7	9	US-08-916-120A-15	1
Sequence 14, Appl	12	42.7	9	US-08-507-032-14	1
Sequence 162, Appl	12	42.7	9	US-09-281-418-162	1
Sequence 73, Appl	12	42.7	9	US-09-513-783A-73	1
Sequence 9, Appl	12	42.7	9	US-08-809-513A-9	1
Sequence 4, Appl	13	42.7	9	US-08-809-513A-4	1
Sequence 59, Appl	13	42.7	9	US-09-874-601-59	1
Sequence 35, Appl	14	41.8	9	US-08-535-249-35	1
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108	7.8	35.5	12	1	US-09-475-947A-59	Sequence 59, Appl	181	6.8	30.9	10	1	US-08-388-353-186	Sequence 186, App
109	7.8	35.5	12	1	US-09-475-947A-329	Sequence 329, App	182	6.8	30.9	10	1	US-08-388-353-187	Sequence 187, App
110	7.4	33.6	9	1	US-08-687-916-11	Sequence 11, Appl	183	6.8	30.9	10	1	US-08-980-357-48	Sequence 48, Appl
111	7.4	33.6	9	1	US-09-138-614-11	Sequence 11, Appl	184	6.8	30.9	10	1	US-08-488-551B-73	Sequence 73, Appl
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114	7.4	33.6	10	1	US-08-808-474A-3	Sequence 3, Appl	187	6.8	30.9	10	1	US-08-488-551B-187	Sequence 187, App
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117	7.4	33.6	10	1	US-08-522-384-35	Sequence 35, Appl	190	6.8	30.9	10	1	US-08-724-466B-26	Sequence 26, Appl
118	7.4	33.6	10	1	US-08-522-384-36	Sequence 36, Appl	191	6.8	30.9	10	1	US-08-522-384-121	Sequence 121, App
119	7.4	33.6	10	1	US-08-522-384-93	Sequence 93, Appl	192	6.8	30.9	10	1	US-08-711-417C-148	Sequence 148, App
120	7.4	33.6	10	1	US-08-849-567A-41	Sequence 41, Appl	193	6.8	30.9	10	1	US-08-088-661F-20	Sequence 20, Appl
121	7.4	33.6	10	1	US-08-475-947A-135	Sequence 135, App	194	6.8	30.9	10	1	US-08-088-661F-30	Sequence 30, Appl
122	7.4	33.6	10	1	US-09-508-753B-36	Sequence 36, Appl	195	6.8	30.9	10	1	US-08-245-041-129	Sequence 129, App
123	7.4	33.6	10	1	PCT-US94-08023-32	Sequence 32, Appl	196	6.8	30.9	10	1	US-08-882-184D-26	Sequence 26, Appl
124	7.4	33.6	11	1	US-08-237-233-3	Sequence 3, Appl	197	6.8	30.9	10	1	US-08-150-156A-5	Sequence 5, Appl
125	7.4	33.6	11	1	US-08-435-350-92	Sequence 92, Appl	198	6.8	30.9	10	1	US-08-150-156A-6	Sequence 6, Appl
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129	7.4	33.6	11	1	US-08-196-523-23	Sequence 23, Appl	202	6.8	30.9	10	1	US-08-618-834C-45	Sequence 45, Appl
130	7.4	33.6	11	1	US-08-930-828A-25	Sequence 25, Appl	203	6.8	30.9	10	1	US-08-108-591B-8	Sequence 8, Appl
131	7.4	33.6	11	1	US-08-722-015A-4	Sequence 4, Appl	204	6.8	30.9	10	1	US-08-108-591B-9	Sequence 9, Appl
132	7.4	33.6	11	1	US-09-249-155A-86	Sequence 86, Appl	205	6.8	30.9	10	1	US-08-108-591B-12	Sequence 12, Appl
133	7.4	33.6	11	1	US-09-249-155A-124	Sequence 124, App	206	6.8	30.9	10	1	US-08-108-591B-15	Sequence 15, Appl
134	7.4	33.6	11	1	5214136-10	Patent No. 5214136	207	6.8	30.9	10	1	US-08-108-591B-28	Sequence 28, Appl
135	7.4	31.8	8	1	US-08-376-362A-3	Sequence 3, Appl	208	6.8	30.9	10	1	US-08-685-114B-56	Sequence 56, Appl
136	7.4	31.8	8	1	US-08-859-954-30	Sequence 30, Appl	209	6.8	30.9	10	1	US-08-154-750A-14	Sequence 14, Appl
137	7.4	31.8	8	1	US-08-859-954-541	Sequence 541, App	210	6.8	30.9	10	1	US-09-154-750A-54	Sequence 54, Appl
138	7.4	31.8	10	1	US-09-985-799-19	Sequence 19, Appl	211	6.8	30.9	10	1	US-09-394-457C-7	Sequence 7, Appl
139	7.4	31.8	10	1	US-07-739-642-13	Sequence 13, Appl	212	6.8	30.9	10	1	US-08-275-951-61	Sequence 61, Appl
140	7.4	31.8	10	1	US-07-739-643-13	Sequence 13, Appl	213	6.8	30.9	10	1	US-09-709-596A-7	Sequence 7, Appl
141	7.4	31.8	10	1	US-07-739-642-13	Sequence 13, Appl	214	6.8	30.9	10	1	US-09-485-853-8	Sequence 8, Appl
142	7.4	31.8	10	1	US-08-548-199-14	Sequence 14, Appl	215	6.8	30.9	10	1	US-09-475-947A-106	Sequence 106, App
143	7.4	31.8	10	1	US-08-440-787A-66	Sequence 66, Appl	216	6.8	30.9	10	1	US-09-475-947A-122	Sequence 122, App
144	7.4	31.8	10	1	US-08-440-787A-70	Sequence 70, Appl	217	6.8	30.9	10	1	US-09-914-259-101	Sequence 101, App
145	7.4	31.8	10	1	US-08-594-031-19	Sequence 19, Appl	218	6.8	30.9	10	1	US-09-916-228-7	Sequence 7, Appl
146	7.4	31.8	10	1	US-08-388-353-481	Sequence 481, App	219	6.8	30.9	10	1	US-09-655-104A-7	Sequence 7, Appl
147	7.4	31.8	10	1	US-08-488-551B-481	Sequence 481, App	220	6.8	30.9	10	1	US-08-301-037-7	Sequence 7, Appl
148	7.4	31.8	10	1	US-08-522-384-13	Sequence 13, Appl	221	6.8	30.9	10	1	US-08-466-539-7	Sequence 7, Appl
149	7.4	31.8	10	1	US-09-054-832-3	Sequence 3, Appl	222	6.8	30.9	10	1	US-09-394-455-53	Sequence 53, Appl
150	7.4	31.8	10	1	US-09-640-953-3	Sequence 3, Appl	223	6.8	30.9	10	1	US-09-508-753B-37	Sequence 37, Appl
151	7.4	31.8	10	1	US-08-867-915-21	Sequence 21, Appl	224	6.8	30.9	10	1	US-09-508-753B-51	Sequence 51, Appl
152	7.4	31.8	10	1	US-09-508-753B-135	Sequence 135, App	225	6.8	30.9	10	1	US-09-508-753B-76	Sequence 76, Appl
153	7.4	31.8	10	1	US-09-508-753B-319	Sequence 319, App	226	6.8	30.9	10	1	US-09-508-753B-79	Sequence 79, Appl
154	7.4	31.8	10	1	US-09-769-482-29	Sequence 29, App	227	6.8	30.9	10	1	US-09-508-753B-82	Sequence 82, Appl
155	7.4	31.8	10	1	US-09-083-235A-52	Sequence 52, App	228	6.8	30.9	10	1	US-09-508-753B-126	Sequence 126, App
156	7.4	31.8	10	1	US-09-083-235A-56	Sequence 56, App	229	6.8	30.9	10	1	US-09-508-753B-131	Sequence 131, App
157	6.8	30.9	10	1	US-07-681-703B-55	Sequence 55, Appl	230	6.8	30.9	10	1	US-09-508-753B-133	Sequence 133, App
158	6.8	30.9	10	1	US-08-049-883A-32	Sequence 32, Appl	231	6.8	30.9	10	1	US-09-508-753B-157	Sequence 157, App
159	6.8	30.9	10	1	US-07-949-541A-13	Sequence 13, Appl	232	6.8	30.9	10	1	US-09-508-753B-160	Sequence 160, App
160	6.8	30.9	10	1	US-08-396-479B-16	Sequence 16, Appl	233	6.8	30.9	10	1	US-10-042-111-42	Sequence 42, Appl
161	6.8	30.9	10	1	US-08-088-558-4	Sequence 4, Appl	234	6.8	30.9	10	1	US-10-042-111-43	Sequence 43, Appl
162	6.8	30.9	10	1	US-08-818-623-16	Sequence 16, Appl	235	6.8	30.9	10	1	US-09-394-467-7	Sequence 7, Appl
163	6.8	30.9	10	1	US-08-686-116A-49	Sequence 49, Appl	236	6.8	30.9	10	1	US-10-104-81-7	Sequence 7, Appl
164	6.8	30.9	10	1	US-08-685-484-49	Sequence 49, Appl	237	6.8	30.9	10	1	US-09-989-789-1332	Sequence 1332, App
165	6.8	30.9	10	1	US-08-847-108-49	Sequence 49, Appl	238	6.8	30.9	10	1	US-09-989-789-1333	Sequence 1333, App
166	6.8	30.9	10	1	US-08-847-108-49	Sequence 49, Appl	239	6.8	30.9	10	1	US-09-989-789-1334	Sequence 1334, App
167	6.8	30.9	10	1	US-08-686-113A-56	Sequence 56, Appl	240	6.8	30.9	10	1	US-09-989-789-1335	Sequence 1335, App
168	6.8	30.9	10	1	US-08-847-095A-49	Sequence 49, Appl	241	6.8	30.9	10	1	US-09-337-304-56	Sequence 56, Appl
169	6.8	30.9	10	1	US-08-465-590-148	Sequence 148, App	242	6.8	30.9	10	1	US-09-855-159A-7	Sequence 7, Appl
170	6.8	30.9	10	1	US-08-808-474A-4	Sequence 4, Appl	243	6.8	30.9	10	1	US-09-723-909-148	Sequence 148, App
171	6.8	30.9	10	1	US-08-173-489C-67	Sequence 67, Appl	244	6.8	30.9	10	1	US-08-466-639-7	Sequence 7, Appl
172	6.8	30.9	10	1	US-08-173-489C-72	Sequence 72, Appl	245	6.8	30.9	10	1	US-08-466-639-7	Sequence 7, Appl
173	6.8	30.9	10	1	US-08-173-489C-151	Sequence 151, App	246	6.8	30.9	10	1	PCT-US91-03680-75	Sequence 75, Appl
174	6.8	30.9	10	1	US-08-173-489C-175	Sequence 175, App	247	6.4	29.1	8	1	US-07-739-642-14	Sequence 14, App
175	6.8	30.9	10	1	US-08-173-489C-205	Sequence 205, App	248	6.4	29.1	8	1	US-07-739-643-14	Sequence 14, App
176	6.8	30.9	10	1	US-08-286-819A-48	Sequence 48, App	249	6.4	29.1	8	1	US-07-739-142-14	Sequence 14, App
177	6.8	30.9	10	1	US-08-545-253A-5	Sequence 5, Appl	250	6.4	29.1	8	1	US-08-465-590-117	Sequence 117, App
178	6.8	30.9	10	1	US-08-471-507A-4	Sequence 4, Appl	251	6.4	29.1	8	1	US-08-859-954-38	Sequence 38, Appl
179	6.8	30.9	10	1	US-08-388-353-73	Sequence 73, Appl	252	6.4	29.1	8	1	US-08-859-954-205	Sequence 205, App

253 6.4 29.1 8 1 US-08-859-954-375 Sequence 375, App
254 6.4 29.1 8 1 US-08-711-417C-117 Sequence 117, App
255 6.4 29.1 8 1 US-09-723-909-117 Sequence 117, App
256 6.4 29.1 8 1 PCT-US93-08743-117 Sequence 117, App
257 6.4 29.1 9 1 US-08-088-658-5 Sequence 5, Appl
258 6.4 29.1 9 1 US-08-410-779B-28 Sequence 28, Appl
259 6.4 29.1 9 1 US-08-465-590-126 Sequence 126, App
260 6.4 29.1 9 1 US-08-605-163-7 Sequence 7, Appl
261 6.4 29.1 9 1 US-08-605-163-18 Sequence 18, Appl
262 6.4 29.1 9 1 US-08-471-907A-5 Sequence 5, Appl
263 6.4 29.1 9 1 US-08-461-607-21 Sequence 21, Appl
264 6.4 29.1 9 1 US-08-711-417C-126 Sequence 126, App
265 6.4 29.1 9 1 US-09-363-600-21 Sequence 21, Appl
266 6.4 29.1 9 1 US-09-163-485-23 Sequence 23, Appl
267 6.4 29.1 9 1 US-09-327-138C-13 Sequence 13, Appl
268 6.4 29.1 9 1 US-09-989-789-530 Sequence 530, App
269 6.4 29.1 9 1 US-09-989-789-2021 Sequence 2021, App
270 6.4 29.1 9 1 US-09-989-789-2022 Sequence 2022, App
271 6.4 29.1 9 1 US-09-989-789-2401 Sequence 2401, App
272 6.4 29.1 9 1 US-09-989-789-2402 Sequence 2402, App
273 6.4 29.1 9 1 US-09-989-789-2403 Sequence 2403, App
274 6.4 29.1 9 1 US-09-723-909-126 Sequence 126, App
275 6.4 29.1 9 1 PCT-US93-08743-126 Sequence 126, App
276 6.4 29.1 9 1 PCT-US95-04477-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-106-038A-47/c
; Sequence 47, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Coweert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106.038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-47

Query Match 77.3%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 732 GGAGAAACAGAACACCG 748
DB 18 GGAGAAACAGAACACCG 2
RESULT 2
US-08-485-942A-45/c
; Sequence 45, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE;
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; TITLE OF INVENTION: AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: sequence tagged-site specific PCR primer sws2359
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-485-942A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAACAC 746
DB 18 CAGGAGAAACAGAACAC 2

RESULT 3

US-08-488-214A-45/c

; Sequence 45, Application US/08488214A

; Patent No. 6124439

; GENERAL INFORMATION:

; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,

; TITLE OF INVENTION: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE

; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING

; NUMBER OF SEQUENCES: 99 (AS AMENDED)

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,214A

; FILING DATE: JUNE 7, 1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: August 17, 1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: August 17, 1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: sequence tagged-site specific PCR primer sWS2359

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; US-08-488-214A-45

Query Match

Best Local Similarity 70.0%; Score 15.4; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAACACACAC 746

| | | | | | | | | | | | | | | |

Db 18 CAGGAGAACACACAC 2

RESULT 4

US-08-488-208A-45/c

; Sequence 45, Application US/08488208A

; Patent No. 6124448

; GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

; TITLE OF INVENTION: USES THEREOF

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,208A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/485,943

; FILING DATE: June 7, 1995

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. 6124448ember 30, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (primer)

; DESCRIPTION: sequence tagged-site specific PCR primer sWS2359

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Human

; US-08-488-208A-45

Query Match

Best Local Similarity 70.0%; Score 15.4; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAACACACAC 746

| | | | | | | | | | | | | | | |

Db 18 CAGGAGAACACACAC 2

RESULT 5

US-08-483-211A-45/c

; Sequence 45, Application US/08483211A

; Patent No. 6309853

; GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TO NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
USE THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,211A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: August 17, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Human
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-483-211A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAACAC 746
DB 18 CAGGAGAAACAGAACAC 2

RESULT 6
US-08-488-223A-45/c
Sequence 45, Application US/08488223A
Patent No. 6350730
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC

ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,223A
FILING DATE: 07-JUN-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6350730ember 30, 1994
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Human
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-488-223A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAACAC 746
DB 18 CAGGAGAAACAGAACAC 2

RESULT 7
US-08-438-431A-45/c
Sequence 45, Application US/08438431A
Patent No. 6429290
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,431A
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6429290ember 30, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer SMS2359
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
US-08-438-431A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGACAC 746
Db 18 CAGGAGAAACACACAC 2

RESULT 8
US-08-488-225A-45/c
; Sequence 45, Application US/08488225A
; Patent No. 6471956
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,225A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/483,211
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6471956ember 30, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; DESCRIPTION: sequence tagged-site specific PCR primer
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-488-225A-45

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 6.6;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGACAC 746
Db 18 CAGGAGAAACACACAC 2

RESULT 9
US-08-577-081A-67
; Sequence 67, Application US/08577081A
; Patent No. 6030775
; GENERAL INFORMATION:
; APPLICANT: Yang, Soo Young
; APPLICANT: Cereb, Nezh
; TITLE OF INVENTION: Methods and Reagents for Typing HLA
; TITLE OF INVENTION: Class I Genes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street Suite 309
; CITY: Yorktown
; STATE: NY
; COUNTRY: US
; ZIP: 10598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,081A
; FILING DATE:
; CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-095-6

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGACCA 745
Db 16 GCAGAACAGACCA 3

RESULT 11
US-08-179-656A-6/c
Sequence 6, Application US/08179656A
Patent No. 6673893
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Iida, Naoka
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,656A
FILING DATE: 07-JAN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-179-656A-6

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGACCA 745
Db 16 GCAGAACAGACCA 3

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK-P-001-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:

OTHER INFORMATION: hybridization probe GE2-183 for typing of
OTHER INFORMATION: HLA Class I genes
US-08-577-081A-67

Query Match 62.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGACACC 747
Db 2 AGGAGACACGGACACC 18

RESULT 10
US-08-465-095-6/c
Sequence 6, Application US/08465095
Patent No. 5849534
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Iida, Naoka
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,095
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,656
FILING DATE: 07-JAN-1994
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2

```
Db      16 GCAGAAACAGAAC 3

RESULT 12
PCT-US94-00300-6/c
; Sequence 6, Application PC/TUS9400300
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Lida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00300
; FILING DATE: 07-JAN-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: G21-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US94-00300-6

Query Match      56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      732 GCAGAAACAGAAC 3
Db      16 GCAGAAACAGAAC 3

RESULT 13
US-09-268-140-28/c
; Sequence 28, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28

Db      16 GCAGAAACAGAAC 3

Query Match      56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      732 GCAGAAACAGAAC 3
Db      16 GCAGAAACAGAAC 3

RESULT 14
US-09-422-978-4649/c
; Sequence 4649, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4649
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
; US-09-422-978-4649

Query Match      55.5%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 25;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      731 AGGAGAAACAGAACACC 747
Db      17 AGGAGAAACAGAGGAAC 1

RESULT 15
US-08-912-129A-42
; Sequence 42, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANADRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITEK, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEWARE, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
```

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912.129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dancakers, Andreas M.
REGISTRATION NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109 US.01
TELEPHONE: 847-937-9803
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-912-129A-42

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 29;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
Db 3 CAGCAGGACAGAAC 17
|||||

RESULT 16
US-09-329-350-40
Sequence 40, Application US/09329350
Patent No. 6184019
GENERAL INFORMATION:
APPLICANT: Miettinen-Oinonen, Arja
APPLICANT: Londenborough, John
APPLICANT: Vehmaanper, Jari
APPLICANT: Haakana, Heli
APPLICANT: M ntyl, Arja
APPLICANT: Lantto, Raija
APPLICANT: Elovainio, Minna
APPLICANT: Joutsenoki, Vesa
APPLICANT: Falohelmo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,350
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/841,636
FILING DATE: 30-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,335
FILING DATE: 17-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,926
FILING DATE: 04-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,840
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/732,181
FILING DATE: 16-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00550
FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Shea Jr., Timothy
REGISTRATION NUMBER: 41,306
REFERENCE/DOCKET NUMBER: 1716.0510006/MAC/TJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-329-350-40

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 32;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGACACCG 748
Db 4 GAAACAGACACCG 17
|||||

RESULT 17
US-08-584-040-5499
Sequence 5499, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

```

; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5499:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5499

```

```

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 733 GAGAAACAGAACAA 745
Db 2 GAGAAAUAGAACAA 14

```

```

RESULT 18
US-09-371-772B-2390
; Sequence 2390, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Favco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2390
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2390

```

```

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 733 GAGAAACAGAACAA 745
Db 2 GAGAAAUAGAACAA 14

```

```

RESULT 19
US-08-584-040-6036/c
; Sequence 6036, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Favco, Pamela
; APPLICANT: McSwiggen, James

```

```

; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6036:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-6036

```

```

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 728 GCCAGGAGAAACAGAA 743
Db 16 GCCAGGAGACACGTAA 1

```

```

RESULT 20
US-09-371-772B-2873/c
; Sequence 2873, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Favco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08

```



```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2873

Query Match
Best Local Similarity 50.9%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 726 GCACGAGAAACAGAA 743
DB 16 GCACGAGACAGTAA 1

RESULT 21
5182195-60
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIIKO;YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:60.
; LENGTH: 15
5182195-60

Query Match
Best Local Similarity 50.0%; Score 11; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GCAGAAACAGA 742
DB 2 GCAGAAACAGA 12

RESULT 22
US-08-291-932A-10/c
; Sequence 10, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; INCLUDING application

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2873

Query Match
Best Local Similarity 50.9%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 726 GCACGAGAAACAGAA 743
DB 16 GCACGAGACAGTAA 1

RESULT 21
5182195-60
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIIKO;YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:60.
; LENGTH: 15
5182195-60

Query Match
Best Local Similarity 50.0%; Score 11; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GCAGAAACAGA 742
DB 2 GCAGAAACAGA 12

RESULT 22
US-08-291-932A-10/c
; Sequence 10, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; INCLUDING application

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```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-7729-2873

Query Match
Best Local Similarity 50.9%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 726 GCACGAGAAACAGAA 743
DB 16 GCACGAGACAGTAA 1

RESULT 21
5182195-60
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIIKO;YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:60.
; LENGTH: 15
5182195-60

Query Match
Best Local Similarity 50.0%; Score 11; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GCAGAAACAGA 742
DB 2 GCAGAAACAGA 12

RESULT 22
US-08-291-932A-10/c
; Sequence 10, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; INCLUDING application

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2873
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-7729-2873

Query Match
Best Local Similarity 50.9%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 726 GCACGAGAAACAGAA 743
DB 16 GCACGAGACAGTAA 1

RESULT 21
5182195-60
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIIKO;YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:60.
; LENGTH: 15
5182195-60

Query Match
Best Local Similarity 50.0%; Score 11; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GCAGAAACAGA 742
DB 2 GCAGAAACAGA 12

RESULT 22
US-08-291-932A-10/c
; Sequence 10, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; INCLUDING application

```

```
Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
DB 1 AGGAGAAACAGA 12

RESULT 24
US-08-484-138-12
; Sequence 12, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,138
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-484-138-12

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
DB 1 AGGAGAAACAGA 12

RESULT 25
PCT-US95-06379-12
; Sequence 12, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
```

```
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-12

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
DB 1 AGGAGAAACAGA 12

RESULT 26
US-08-639-080-4
; Sequence 4, Application US/08639080
; Patent No. 5843661
; GENERAL INFORMATION:
; APPLICANT: Rothmund, Paul W.K.
; TITLE OF INVENTION: METHOD FOR CONSTRUCTING UNIVERSAL DNA
; TITLE OF INVENTION: BASED MOLECULAR TURING MACHINE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Ste 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,080
FILING DATE: April 24, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Harris, Scott C.
REGISTRATION NUMBER: 32,030
REFERENCE/DOCKET NUMBER: 06618/129001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
```

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: oligonucleotide
US-08-639-080-4

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAAACAGAACAC 746
|||||
Db 2 GAAACAGTACAC 13

RESULT 27
US-08-535-249-125
; Sequence 125, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Retmar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-125

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
|||||
Db 14 AGCAGAAACAGA 3

Db 1 AGGAGAACGACA 12

RESULT 28
US-09-874-601-18/c
; Sequence 18, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-18

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
|||||
Db 14 AGCAGAAACAGA 3

RESULT 29
US-08-291-932A-11/c
; Sequence 11, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 810
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994

CLASSIFICATION: 514
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-291-932A-11

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGGAACACAGA 742
Db 13 AGGGAACACAGA 2

RESULT 30
US-08-363-240A-654/c
Sequence 654, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 654:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-654

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACACAGAA 743
Db 12 GGAGAACACAGAA 1

RESULT 31
US-09-081-646-132
Sequence 132, Application US/09081646
Patent No. 6333152
GENERAL INFORMATION:
APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
APPLICANT: Zhou, Lin
APPLICANT: Zhang, Wei
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
Cancer Cells
FILE REFERENCE: 01107.74664
CURRENT APPLICATION NUMBER: US/09/081,646
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: 60/047,352
EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 871
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 132
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-09-081-646-132

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAGAA 738
Db 3 TGCCAGGAGAGAA 14

RESULT 32
US-09-081-646-867
Sequence 867, Application US/09081646
Patent No. 6333152
GENERAL INFORMATION:
APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
APPLICANT: Zhou, Lin
APPLICANT: Zhang, Wei
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
Cancer Cells
FILE REFERENCE: 01107.74664
CURRENT APPLICATION NUMBER: US/09/081,646
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: 60/047,352
EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 871
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 867
LENGTH: 15
TYPE: DNA

; ORGANISM: Homo sapiens
US-09-081-646-867

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAA 738
Db 3 TGCCAGGAGGAA 14

RESULT 33
US-08-137-024-4
; Sequence 4, Application US/08137024
; Patent No. 6005167
; GENERAL INFORMATION:
; APPLICANT: VAN TUNEN, Adrianus, J.
; APPLICANT: VAN DER MEER, Ingrid M.
; APPLICANT: MOL, Josephus N.M.
; TITLE OF INVENTION: MALE-STERILE PLANTS, METHODS
; TITLE OF INVENTION: FOR OBTAINING MALE STERILE
; TITLE OF INVENTION: PLANTS AND RECOMBINANT DNA FOR
; TITLE OF INVENTION: USE THEREIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Pary
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50 inch, DS, DD 720
; MEDIUM TYPE: KD/720Ko
; COMPUTER: IBM PC Compatible 286 SX 12 Mhz
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,024
; FILING DATE: 14-OCT-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL92/00075
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91200910
; FILING DATE: 16-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford, J.
; REGISTRATION NUMBER: 30086
; REFERENCE/DOCKET NUMBER: U-9373
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Petunia hybrida
US-08-137-024-4

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 4 AGGAGAAACAGA 15

RESULT 34
US-08-646-695-15
; Sequence 15, Application US/08646695
; Patent No. 6168943
; GENERAL INFORMATION:
; APPLICANT: Rose, John K.
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,695
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA
US-08-646-695-15

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
Db 2 CAGGAGAAAC 11

RESULT 35
PCT-US96-06053-15
; Sequence 15, Application PC/TUS9606053
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06053
; FILING DATE: 01-MAY-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-009-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA
; PCT-US96-06053-15

```

```

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 730 CAGGAGAAAC 739
Db 2 CAGGAGAAAC 11

```

```

RESULT 36
US-09-081-646-456
; Sequence 456, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 456
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-456

```

```

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 732 GGAGAAACAG 741
Db 5 GGAGAAACAG 14

```

```

RESULT 37
US-08-303-004-13
; Sequence 13, Application US/08303004
; Patent No. 5556955
; GENERAL INFORMATION:
; APPLICANT: Vergnaud, Gilles
; TITLE OF INVENTION: Process for Detection of New Polymor-

```

```

; TITLE OF INVENTION: phic Loci in an ADN Sequence, Nucleotide Sequences Forming
; TITLE OF INVENTION: Hybridisation Probes and Their Biological Applications
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ollif & Berridge
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,004
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/931,311B
; FILING DATE: 19920818
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-303-004-13

```

```

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 733 GGAGAAACAGCA 745
Db 1 GGAGAAACAGCA 13

```

```

RESULT 38
US-08-442-513A-11/c
; Sequence 11, Application US/08442513A
; Patent No. 5646031
; GENERAL INFORMATION:
; APPLICANT: DeYoung, Mary Beth
; APPLICANT: Siwkowski, Andrew M.
; APPLICANT: Hampel, Arnold E.
; TITLE OF INVENTION: METHOD FOR DERIVING RIBOZYMES FROM
; NUCLEOTIDE SEQUENCES AND RIBOZYMES DERIVED THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5646031thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/442,513A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohn, Kenneth I.
;; REGISTRATION NUMBER: 30,995
;; REFERENCE/DOCKET NUMBER: 2384.00014
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (810) 539-5050
;; TELEFAX: (810) 539-5055
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Ribozyme substrate"
US-08-442-513A-11

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACCG 748
Db 14 AACAGAACTCG 2

;; RESULT 39
;; US-08-442-513A-16/c
;; Sequence 16, Application US/08442513A
;; Patent No. 5646031
;; GENERAL INFORMATION:
;; APPLICANT: DeYoung, Mary Beth
;; APPLICANT: Siwkowski, Andrew M.
;; APPLICANT: Hampel, Arnold E.
;; TITLE OF INVENTION: METHOD FOR DERIVING RIBOZYMES FROM
;; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND RIBOZYMES DERIVED THEREOF
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kohn & Associates
;; STREET: 30500 No. 5646031thwestern Hwy., Suite 410
;; CITY: Farmington Hills
;; STATE: Michigan
;; COUNTRY: US
;; ZIP: 48334
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/442,513A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohn, Kenneth I.
;; REGISTRATION NUMBER: 30,995
;; REFERENCE/DOCKET NUMBER: 2384.00014
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (810) 539-5050
;; TELEFAX: (810) 539-5055
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Ribozyme substrate"
US-08-442-513A-16

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACCG 748
Db 14 AACAGAACTCG 2

;; RESULT 40
;; US-08-173-489C-186/c
;; Sequence 186, Application US/08173489C
;; Patent No. 5861244
;; GENERAL INFORMATION:
;; APPLICANT: WANG, C. -G.
;; APPLICANT: HEPBURN, A. G.
;; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
;; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
;; NUMBER OF SEQUENCES: 365
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
;; STREET: 510 EAST 73RD STREET,
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
;; COMPUTER: IBM PC/XT/AT
;; OPERATING SYSTEM: MS-DOS version 6.2
;; SOFTWARE: Wordperfect Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/173,489C
;; FILING DATE: 22 DEC 1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/968,436
;; FILING DATE: 29 OCT 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Handelman, Joseph H.
;; REGISTRATION NUMBER: 26,179
;; REFERENCE/DOCKET NUMBER: U9518-6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (attorney) (212) 708-1880
;; TELEFAX: (attorney) (212) 246-8959
;; INFORMATION FOR SEQ ID NO: 186:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: third strand derived from Hepatitis B
;; DESCRIPTION: isolate adw2 sequence region in Seq ID No. 5861244185
;; HYPOTHETICAL: yes
;; ANTI-SENSE: no
;; PUBLICATION INFORMATION:
;; RELEVANT RESIDUES IN SEQ ID NO: 186 :FROM 1 TO 14
US-08-173-489C-186

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 13 AGGAGAAACAGAA 1

;; RESULT 41
;; US-08-173-489C-198/c
;; Sequence 198, Application US/08173489C

Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESS: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IEM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelmann, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244197
HYPOTHETICAL: yes
ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 198 :FROM 1 TO 14
US-08-173-489C-198
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAACAGAA 743
Db 13 AGGAGACAGCA 1
RESULT 42
US-08-535-249-126
Sequence 126, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESS: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.

CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-126
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 728 GCACGAGAACCA 740
Db 2 GCAGGAGAGCA 14
RESULT 43
US-09-049-190-11/C
Sequence 11, Application US/09049190
Patent No. 6190866
GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,190
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2560
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone

FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine
OTHER INFORMATION: backbone
US-09-049-190-11
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGAA 743
DB 15 AGGAGAAAGAGTA 3
RESULT 44
US-08-932-140C-11/c
Sequence 11, Application US/08932140C
Patent No. 6300319
GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6300319is LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,140C
FILING DATE: September 16, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2560
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone

```
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-
OTHER INFORMATION: lysine-glycine backbone
US-08-932-140C-11
```

Query Match

44.5%; Score 9.8; DB 1; Length 15;

```
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAA 743
Db 15 AGGAGAAAGAGTA 3

RESULT 45
US-09-081-646-460/c
; Sequence 460, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 460
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-460
```

```
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 728 GCGAGAGAAACA 740
Db 15 GCGAGAGAAACA 3
```

```
RESULT 46
US-09-531-000-60
; Sequence 60, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Marion D.
; APPLICANT: FRESCO, Jacques R.
; TITLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
; FILE REFERENCE: 2448-103
; CURRENT APPLICATION NUMBER: US/09/531,000
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/23765
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/064,997
; PRIOR FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target
; OTHER INFORMATION: sequences
US-09-531-000-60
```

```
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 731 AGGAGAAACAGAA 743
Db 15 AGGAGAAAGAGTA 3
```

```
Db          2 AGGTGAAAAGAA 14

RESULT 47
US-08-560-313A-9/c
; Sequence 9, Application US/08560313A
; Patent No. 5763175
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Simultaneous Sequencing of Tagged Polynucleotides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Power Macintosh
; OPERATING SYSTEM: Macintosh OS ver. 7.5.2
; SOFTWARE: Microsoft Word, vers. 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,313A
; FILING DATE: 17-NOV-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: estlus
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-560-313A-9

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          728 GCCAGGAGAAA 738
Db          12 GCCAGGAGAGA 2

RESULT 48
US-08-611-155B-13/c
; Sequence 13, Application US/08611155B
; Patent No. 5780231
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: DNA Extension and Analysis with Rolling Primers
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          728 GCCAGGAGAAA 738
Db          12 GCCAGGAGAGA 2

RESULT 49
US-08-916-120A-15/c
; Sequence 15, Application US/08916120A
; Patent No. 5962228
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: DNA Extension and Analysis with Rolling Primers
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word, vers. 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,120A
; FILING DATE: 22-AUG-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/611,155
; FILING DATE: 05-MAR-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 811-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-120A-15
```

```

; TITLE OF INVENTION: acment, Method of Assaying Microorganisms, Method of Analyzing Microorganisms
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 162
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-281-418-162

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 2 AGGAGAAACGG 12

RESULT 52
US-09-513-783A-73
; Sequence 73, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase-8
; OTHER INFORMATION: substrate recognition sequence
; US-09-513-783A-73

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
Db 1 GTAGAAACAGA 11

RESULT 53
US-08-809-513A-9/c
; Sequence 9, Application US/0809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York

; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA Fragment
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 162
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-281-418-162

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
Db 12 GCCAGGAGAGA 2

RESULT 50
US-08-507-032-14
; Sequence 14, Application US/08507032
; Patent No. 5989810
; GENERAL INFORMATION:
; APPLICANT: Flanagan, William A.
; APPLICANT: Crabtree, Gerald R.
; TITLE OF INVENTION: Screening Methods for Immunosuppressive
; TITLE OF INVENTION: Agents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,032
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,944
; FILING DATE:
; APPLICATION NUMBER: US 07/749,385
; FILING DATE: 22-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-507-032-14

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACA 740
Db 1 CAGGAGAAAAA 11

RESULT 51
US-09-281-418-162
; Sequence 162, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA Fragment
```

```
/ COUNTRY: USA
/ ZIP: 10591-5144
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
/ COMPUTER: Gateway Pentium II
/ OPERATING SYSTEM: Windows 98
/ SOFTWARE: Word 97
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/809,513A
/ FILING DATE: 24-MAR-1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03663
/ FILING DATE: 18-SEP-1995
/ APPLICATION NUMBER: EP 94115505.3
/ FILING DATE: 30-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kurt G. Briscoe
/ REGISTRATION NUMBER: 33,141
/ REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
/ TELEPHONE: (914) 332-1700
/ TELEFAX: (914) 332-1844
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: RNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Influenza virus, vRNA 3' sequence
/ INDIVIDUAL ISOLATE: pHL1104 vRNA Promoter Element
/ US-08-809-513A-9

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAAACAG 2

RESULT 54
US-08-809-513A-4/c
; Sequence 4, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
/ COMPUTER: Gateway Pentium II
/ OPERATING SYSTEM: Windows 98
/ SOFTWARE: Word 97
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/809,513A
/ FILING DATE: 24-MAR-1997
/ CLASSIFICATION: 424
```

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03663
/ FILING DATE: 18-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94115505.3
/ FILING DATE: 30-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kurt G. Briscoe
/ REGISTRATION NUMBER: 33,141
/ REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
/ TELEPHONE: (914) 332-1700
/ TELEFAX: (914) 332-1844
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: RNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Influenza virus, vRNA 3' sequence
/ INDIVIDUAL ISOLATE: pHL1104 vRNA Promoter Element
/ US-08-809-513A-4

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 13 AGTAGAAACAG 3

RESULT 55
US-09-874-601-59/c
; Sequence 59, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
/ US-09-874-601-59

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 13 AGTAGAAACAG 3
```

```
Db      11 AGCAGAAACAG 1
RESULT 56
US-08-535-249-35
; Sequence 35, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-35
Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAAACAG 743
Db      1 CATGAGAGCAG 14
RESULT 57
US-09-508-753B-21/c
; Sequence 21, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-21
Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 738
Db      9 CAGGAGAA 1
RESULT 58
US-09-508-753B-30
; Sequence 30, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-30
Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      733 GAGAAACAG 741
Db      1 GAGAAACAG 9
RESULT 59
US-09-508-753B-64/c
; Sequence 64, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
```

```
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 64
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-64

Query Match      40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 10 GAGAAACAG 2

RESULT 60
US-09-513-783A-61
; Sequence 61, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-3
US-09-513-783A-61

Query Match      40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 61
US-09-513-783A-75
; Sequence 75, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-8
```

```
; OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-75

Query Match      40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 62
US-09-513-783A-75
; Patent No. 5395927
; APPLICANT: BOCK, AUGUST;BINDER, FLORIAN;MULLER, FRANK
; TITLE OF INVENTION: DNA-FRAGMENT HAVING THE CYCLODEXTRIN
; GLYCOSYLTRANSFERASE GENE
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/450,126
; FILING DATE: 27-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 923,128
; FILING DATE: 24-OCT-1986
; SEQ ID NO:3;
; LENGTH: 13
;
5395927-3

Query Match      40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 3 GAAACAGAA 11

RESULT 63
US-09-332-319-5/c
; Sequence 5, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Ljstori, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-5

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
Db 12 AAAGAGAGAAC 1

RESULT 64
US-09-332-319-6
; Sequence 6, Application US/09332319
; Patent No. 6171821
```

```

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-6

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGAGAGACA 745
DB      1 AAAAAGAGACA 12

RESULT 65
US-09-332-319-10/c
; Sequence 10, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(1)
; OTHER INFORMATION: Wild-type polypyrimidine tract.
US-09-332-319-10

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGAGAGACA 745
DB      12 AAAAAGAGACA 1

RESULT 66
US-09-580-923-28/c
; Sequence 28, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wills, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
;
; TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-28

Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAAACAGA 742
DB      12 AGCAAAAAAAGA 1

RESULT 67
US-08-465-293A-8/c
; Sequence 8, Application US/08465293A
; Patent No. 5789651
; GENERAL INFORMATION:
; APPLICANT: Woychik, Richard P.
; TITLE OF INVENTION: Isolation and Characterization of
; TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 555 13th Street, N.W., Suite #480 West
; CITY: Washington
; STATE: District of Columbia
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,293A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,385
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Edward A. Pennington
; REGISTRATION NUMBER: 32,588
; REFERENCE/POCKET NUMBER: 2240-7054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 857-7887
; TELEFAX: (202) 857-7929
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse

```


STRAIN: Wild
TISSUE TYPE: Adult kidney and testis
IMMEDIATE SOURCE:
CLONE: Wild-type cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: transition point of exon 1 from exon 2 in
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: and the development of tumor in a wide variety of tissues.
US-08-463-293A-8

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACA 745
Db 13 AGAAGCAGCACA 2

RESULT 68
US-08-463-387A-8/c
Sequence 8, Application US/08463387A
Patent No. 5843652
GENERAL INFORMATION:
APPLICANT: Woychik, Richard P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
CITY: Washington
STATE: District of Columbia
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,387A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,385
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Edward A. Pennington
REGISTRATION NUMBER: 32,588
REFERENCE/DOCKET NUMBER: 2240-7054
TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: Wild
TISSUE TYPE: Adult kidney and testis
IMMEDIATE SOURCE:
CLONE: Wild-type cDNA clones

POSITION IN GENOME:
CHROMOSOME/SEGMENT: transition point of exon 1 from exon 2 in
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: and the development of tumor in a wide variety of tissues.
US-08-463-387A-8

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACA 745
Db 13 AGAAGCAGCACA 2

RESULT 69
US-09-102-977-9/c
Sequence 9, Application US/09102977
Patent No. 6080550
GENERAL INFORMATION:
APPLICANT: Woychik, Richard P.
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,977
FILING DATE: 22-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/899,134
FILING DATE: 23-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,732
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ORNL:014--1
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-102-977-9

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACA 745
Db 13 AGAAGCAGCACA 2

```
RESULT 70
US-09-102-977-14/c
; Sequence 14, Application US/09102977
; Patent No. 680550
; GENERAL INFORMATION:
; APPLICANT: WOYCHIK, RICHARD P.
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
; TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,977
; FILING DATE: 22-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/899,134
; FILING DATE: 23-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,732
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ORNL:014--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512)418-3000
; TELEFAX: (512)474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-102-977-14
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACCA 745
Db 13 AGAAGCAGCACCA 2

RESULT 71
US-09-034-088A-23/c
; Sequence 23, Application US/09034088A
; Patent No. 6310034
; GENERAL INFORMATION:
; APPLICANT: WOYCHIK, RICHARD P.
; APPLICANT: BULTMAN, SCOTT J.
; APPLICANT: MICHAUD, EDWARD J.
; TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
; FILE REFERENCE: 4310.001600
; CURRENT APPLICATION NUMBER: US/09/034,088A
; CURRENT FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 08/064,385
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; MEDIUM TYPE: Floppy disk
```

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; SEQ ID NO 23
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-034-088A-23
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACCA 745
Db 13 AGAAGCAGCACCA 2

RESULT 72
US-09-781-811-23/c
; Sequence 23, Application US/09781811
; Patent No. 6514747
; GENERAL INFORMATION:
; APPLICANT: WOYCHIK, RICHARD P.
; APPLICANT: BULTMAN, SCOTT J.
; APPLICANT: MICHAUD, EDWARD J.
; TITLE OF INVENTION: AGOUTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 4310.001682
; CURRENT APPLICATION NUMBER: US/09/781,811
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 09/034,088
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 08/064,385
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-781-811-23
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGCACCA 745
Db 13 AGAAGCAGCACCA 2

RESULT 73
US-08-808-474A-2
; Sequence 2, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,474A
FILING DATE: 03-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTDAL:001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (214) 740-8000
TELEFAX: (214) 740-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-808-474A-2

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGA 736
Db 1 TGCCCGAGA 10

RESULT 74
US-08-388-353-478
; Sequence 478, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 478:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-388-353-478
Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACACC 747
Db 1 AGAGAACACC 10

RESULT 75
US-08-488-551B-478
; Sequence 478, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0239
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 478:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-478

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACACC 747
Db 1 AGAGAACACC 10

RESULT 76
US-09-508-753B-19

; Sequence 19, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-19

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
| | | | |
Db 1 CTGGAGAAAC 10

RESULT 77
US-09-508-753B-41/c
; Sequence 41, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-41

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
| | | | |
Db 10 CTGGAGAAAC 1

RESULT 78
US-09-508-753B-127/c
; Sequence 127, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:

; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 127
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-127

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGA 742
| | | | |
Db 10 GAGAACAGA 1

RESULT 79
US-09-769-482-47/c
; Sequence 47, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-09-769-482-47

Query Match 38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACA 740
| | | | |
Db 10 AGGATAAACA 1

RESULT 80
US-09-332-319-18/c
; Sequence 18, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: 09/121,979
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 12
TYPE: RNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (11)...(12)
OTHER INFORMATION: Positions 11-12 are mutated.
US-09-332-319-18

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 745
Db 10 AAACAGAAC 1

RESULT 81
US-08-388-353-479
; Sequence 479, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-388-353-479
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 AGAACACC 747
Db 2 AGAACACC 9

RESULT 82
US-08-388-353-480
; Sequence 480, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-388-353-480
Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 AGAACACC 747
Db 1 AGAACACC 8

RESULT 83
US-08-488-551B-479
; Sequence 479, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper

```

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-479

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 AGAACACC 747
Db 2 AGAACACC 9

RESULT 84
US-08-488-551B-480
; Sequence 480, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 480:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-480

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 AGAACACC 747
Db 1 AGAACACC 8

RESULT 85
US-09-229-151C-15/c
; Sequence 15, Application US/09229151C
; Patent No. 653784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: KappaB3 sequence
; US-09-229-151C-15

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAAC 739
Db 10 GGAGAAAC 3

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RESULT 86

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US-08-671-824-12/c
; Sequence 12, Application US/08671824
; Patent No. 6025167
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Zaug, Arthur J.
; APPLICANT: Been, Michael D.
; TITLE OF INVENTION: RNA RIBOZYME POLYMERASES,
; TITLE OF INVENTION: DIPHOSPHORYLASES, RESTRICTION
; TITLE OF INVENTION: ENDORIBONUCLEASES AND METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671.824
; FILING DATE: June 5, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,624
; FILING DATE: July 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 220/166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-671-824-12

Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 738
Db 11 AGGAGAA 4

RESULT 87
US-08-231-227-5
; Sequence 5, Application US/08231227
; Patent No. 5631148
; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; TITLE OF INVENTION: RIBOZYMES WITH PRODUCT EJECTION BY
; TITLE OF INVENTION: STRAND DISPLACEMENT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,227
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth M.
; REFERENCE/DOCKET NUMBER: 0973.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; FEATURE:
; NAME/KEY: A
; LOCATION: 7
; OTHER INFORMATION: /label= variable
; OTHER INFORMATION: /note= an intervening sequence Nx of any length
; OTHER INFORMATION: may be inserted between nucleotides 7 and 8
US-08-231-227-5

Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAAC 739
Db 4 ANGAGAAC 12

RESULT 88
US-08-173-489C-10/c
; Sequence 10, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C.-G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from c-myc
DESCRIPTION: sequence region in Seq ID No. 58612449
HYPOTHETICAL: Yes
ANTI-SENSE: No
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 10 :FROM 1 TO 12
US-08-173-489C-10

Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 738
DB 8 AGGAGAA 1

RESULT 89
PCT-US95-04632-5
Sequence 5, Application PC/TUS9504632
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: RIBOZYMES WITH PRODUCT EJECTION BY
TITLE OF INVENTION: STRAND DISPLACEMENT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04632
FILING DATE: 14-APR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M.
REFERENCE/DOCKET NUMBER: 0973.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
FEATURE:

NAME/KEY: A
LOCATION: 7
OTHER INFORMATION: /label= variable
OTHER INFORMATION: /note= an intervening sequence Nx of any length
OTHER INFORMATION: may be inserted between nucleotides 7 and 8
PCT-US95-04632-5

Query Match 36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 80;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAA 739
DB 4 ANGAGAA 12
RESULT 90
US-08-173-489C-89
Sequence 89, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: superoxide dismutase gene (accession #
DESCRIPTION: J02947) nucleotides 21 to 31
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 21
MAP POSITION: 21q22.1
PUBLICATION INFORMATION:
AUTHORS: Hjalmarsson, K, Marklund, S L,
AUTHORS: Engstrom, A, Edlund, T.
TITLE: Isolation and sequence of
TITLE: complementary dna encoding human extracellular-
TITLE: superoxide dismutase
JOURNAL: Proceedings of the National Academy of
JOURNAL: Sciences, USA
VOLUME: 84
PAGES: 6340-6344
DATE: 1987
RELEVANT RESIDUES IN SEQ ID NO: 89 :FROM 1 TO 11
US-08-173-489C-89

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
|||||
Db 1 AGGAGAAAG 11

RESULT 91
US-08-687-916-14/c
; Sequence 14, Application US/08687916
; Patent No. 5908972
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: ISOLATED SPINACH
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,916
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/391,000
; FILING DATE: 21-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 028750-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-687-916-14

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
|||||
Db 11 GAGAAAAAAA 1

RESULT 92
US-09-072-435-8/c
; Sequence 8, Application US/09072435
; Patent No. 6215051
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; APPLICANT: Chan, Ming-Tsair

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 744
|||||
Db 11 AGAAACGCAAC 1

RESULT 93
US-09-138-614-14/c
; Sequence 14, Application US/09138614
; Patent No. 6245541
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: ISOLATED SPINACH
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,792
; FILING DATE: 29-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28123/34274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-072-435-8

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138.614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,916
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 028750-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-138-614-14

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
DB 11 GAGAAACAGAA 1

RESULT 94
US-08-083-945C-8
Sequence 8, Application US/08083945C
Patent No. 6274134
GENERAL INFORMATION:
APPLICANT: Beckner, Marie E.
APPLICANT: Liotta, Lance A.
APPLICANT: Krutzsch, Henry C.
TITLE OF INVENTION: AMP-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083.945C
FILING DATE: 25-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-083-945C-8

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 1 AGGAGAAACAG 11

RESULT 95
US-09-072-917A-10/C
Sequence 10, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-072-917A-10

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 744
DB 11 AGAAACAGAAC 1

RESULT 96


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QY      732 GGAGAAACAGA 742
      |||||
Db      12 GGGGAAGCAGA 2

RESULT 99
US-08-494-301A-3
; Sequence 3, Application US/08494301A
; Patent No. 5856461
; GENERAL INFORMATION:
; APPLICANT: Colote, Soudhir
; APPLICANT: Pirotzky, Eduardo
; TITLE OF INVENTION: Oligonucleotides to Inhibit the
; TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lucas & Just
; STREET: 205 E. 42nd Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 1.44 MB storage
; COMPUTER: IBM 486 Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; FILING DATE: 23-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9413035.8
; FILING DATE: 29-JUNE-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-494-301A-3

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
      |||||
Db      2 AGGAGTAGCAG 12

RESULT 100
US-08-173-489C-215
; Sequence 215, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C.-G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44mb storage
; COMPUTER: IBM PC/XT/AT

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; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23s rRNA gene from Escherichia coli
; DESCRIPTION: (Accession # M25458) nucleotides 212 to 223
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; STRAIN: MRE600
; PUBLICATION INFORMATION:
; AUTHORS: Branlant, C, Krol, A, Machatt, M, A,
; AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Roessel,
; AUTHORS: H.
; TITLE: Primary and secondary
; TITLE: structures of Escherichia coli MRE 600 23S
; TITLE: ribosomal RNA Comparison with models of
; TITLE: secondary structure for maize chloroplast 23S
; TITLE: rRNA and for large portions of mouse and human
; TITLE: 16S mitochondrial rRNAs
; JOURNAL: Nucleic Acids Research
; VOLUME: 9
; PAGES: 4303-4324
; DATE: 1981
; RELEVANT RESIDUES IN SEQ ID NO: 215 :FROM 1 TO 12
US-08-173-489C-215

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733 GGGAACAGAA 743
      |||||
Db      1 GAGGAAGAGAA 11

RESULT 101
US-08-173-489C-229
; Sequence 229, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C.-G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.

```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 229:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23S rRNA gene from Halococcus morrhuae
; DESCRIPTION: (Accession # X05481) nucleotides 1628 to 1639
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Halococcus morrhuae
; PUBLICATION INFORMATION:
; AUTHORS: Leffers, H, Kjems, J, Ostergaard, L,
; AUTHORS: Larsen, N, Garrett, R A.
; TITLE: Evolutionary Relationship
; TITLE: Amongst Archaeobacteria: A Comparative Study of
; TITLE: 23 S Ribosomal RNAs of a Sulphur-dependent
; TITLE: Extreme Thermophile, an Extreme Halophile and a
; TITLE: Thermophilic Methanogen
; JOURNAL: Journal of Molecular Biology
; VOLUME: 195
; PAGES: 43-61
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 229 :FROM 1 TO 12
;
; US-08-173-489C-229
;
; Query Match 35.5%; Score 7.8; DB 1; Length 12;
; Best Local Similarity 81.8%; Pred. No. 87;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 733 GAGAACAGAA 743
; Db |||||
; 1 GAGATAGAGAA 11
;
; RESULT 102
; US-08-173-489C-351
; Sequence 351, Application US/08173489C
; Patent No. 5661244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 229:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23S rRNA gene from Halococcus morrhuae
; DESCRIPTION: (Accession # X05481) nucleotides 1628 to 1639
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Halococcus morrhuae
; PUBLICATION INFORMATION:
; AUTHORS: Leffers, H, Kjems, J, Ostergaard, L,
; AUTHORS: Larsen, N, Garrett, R A.
; TITLE: Evolutionary Relationship
; TITLE: Amongst Archaeobacteria: A Comparative Study of
; TITLE: 23 S Ribosomal RNAs of a Sulphur-dependent
; TITLE: Extreme Thermophile, an Extreme Halophile and a
; TITLE: Thermophilic Methanogen
; JOURNAL: Journal of Molecular Biology
; VOLUME: 195
; PAGES: 43-61
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 229 :FROM 1 TO 12
;
; US-08-173-489C-229
;
; Query Match 35.5%; Score 7.8; DB 1; Length 12;
; Best Local Similarity 81.8%; Pred. No. 87;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 733 GAGAACAGAA 743
; Db |||||
; 1 GAGATAGAGAA 11
;
; RESULT 102
; US-08-173-489C-351
; Sequence 351, Application US/08173489C
; Patent No. 5661244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 351:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: p53 gene, nucleotides 1066-1077
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Harlow, E, Williamson, N M, Ralston, R,
; AUTHORS: Helfman, D M, Adams T E.
; TITLE: Molecular cloning and in
; TITLE: vitro expression of a cDNA for human cellular
; TITLE: tumor antigen p53
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; PAGES: 1601-1610
; DATE: 1985
; RELEVANT RESIDUES IN SEQ ID NO: 351 :FROM 1 TO 12
;
; US-08-173-489C-351
;
; Query Match 35.5%; Score 7.8; DB 1; Length 12;
; Best Local Similarity 81.8%; Pred. No. 87;
; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 733 GAGAACAGAA 743
; Db |||||
; 2 GAGGAGAGAA 12
;
; RESULT 103
; US-08-779-355-19
; Sequence 19, Application US/08779355
; Patent No. 6017701
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; APPLICANT: Mullinax, Rebecca L.
; TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
; TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,355
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/775,993
; FILING DATE: 03-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 43092CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)628-8800
; TELEFAX: (202)628-8844
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-779-355-19

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
Db 2 TGCGAAGAGAA 12

RESULT 104
US-08-938-835A-19
; Sequence 19, Application US/08938835A
; Patent No. 6060245
; GENERAL INFORMATION:
; APPLICANT: SORGE, Joseph A.
; APPLICANT: MULLINAX, Rebecca L.
; TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
; TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,835A
; FILING DATE: 26-SEPT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/775,993
; FILING DATE: 03-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/779,335
; FILING DATE: 06-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 04121.0044-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000

```

```

; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-938-835A-19

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
Db 2 TGCGAAGAGAA 12

RESULT 105
US-08-862-431-24
; Sequence 24, Application US/08862431
; Patent No. 6120994
; GENERAL INFORMATION:
; APPLICANT: TAM, SHUI-PANG
; TITLE OF INVENTION: ANTIOXIDANT RESPONSIVE ELEMENT
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,431
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kim, Judith U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 1669.0020000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-862-431-24

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGAAC 744
Db 1 AGAACACAGAC 11

RESULT 106
US-09-043-149-33/C
; Sequence 33, Application US/09043149
; Patent No. 6355418
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Gunter

```

;; TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
;; TITLE OF INVENTION: Identification of Antisense Binding Sites
;; FILE REFERENCE: 020600-272
;; CURRENT APPLICATION NUMBER: US/09/043,149
;; CURRENT FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: PCT/GB96/02275
;; PRIOR FILING DATE: 1996-09-13
;; PRIOR APPLICATION NUMBER: GB 9518864.5
;; PRIOR FILING DATE: 1995-09-14
;; NUMBER OF SEQ ID NOS: 54
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 33
;; LENGTH: 12
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: oligonucleotide
US-09-043-149-33

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAGACGAC 744
||| |||||
Db 12 AGGAAGACGAC 2

RESULT 107
US-09-513-783A-65
; Sequence 65, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase-6
; OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-65

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAGCA 742
||| |||||
Db 1 GTAGAAATAGA 11

RESULT 108
US-09-475-947A-59
; Sequence 59, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACA 740
||| |||||
Db 1 CAGCAGCAACA 11

RESULT 109
US-09-475-947A-329/c
; Sequence 329, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 329
; LENGTH: 12
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-329

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAGCA 742
||| |||||
Db 12 GGAGAGAGAGA 2

RESULT 110
US-08-887-916-11/c
; Sequence 11, Application US/08887916
; Patent No. 5908972
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: ISOLATED SPINACH
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
; TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,916
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

```
/ APPLICATION NUMBER: US 08/391,000
/ FILING DATE: 21-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dadio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 028750-138
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-687-916-11

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 9 GAGAAAAG 1

RESULT 111
US-09-138-614-11/c
/ Sequence 11, Application US/09138614
/ Patent No. 6245541
/ GENERAL INFORMATION:
/ APPLICANT: HOUTZ, Robert L.
/ TITLE OF INVENTION: ISOLATED SPINACH
/ TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
/ TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
/ TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
/ TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/138,614
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/687,916
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dadio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 028750-138
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-09-138-614-11

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 9 GAGAAAAG 1

RESULT 112
US-08-254-811D-5/c
/ Sequence 5, Application US/08254811D
/ Patent No. 5773213
/ GENERAL INFORMATION:
/ APPLICANT: Gullans, Steven R.
/ APPLICANT: Kojima, Ryoji
/ APPLICANT: Randail, Jeffrey
/ TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
/ TITLE OF INVENTION: Hybridization Steps
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Macwright, Robert S.
/ STREET: 1 Broadway
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 6.1 for Windows
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/254,811D
/ FILING DATE: 06-JUN-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Macwright, Robert S.
/ REGISTRATION NUMBER: 32,425
/ REFERENCE/DOCKET NUMBER: 1854/46101
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 425-7200
/ TELEFAX: (212) 425-5288
/ TELEX: 422141
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ HYPOTHETICAL: No
US-08-254-811D-5

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAG 742
Db 10 AGAACAG 2

RESULT 113
US-08-808-474A-3
/ Sequence 3, Application US/08808474A
/ Patent No. 5856103
/ GENERAL INFORMATION:
/ APPLICANT: Gray, Donald M.
/ APPLICANT: Clark, Chris L.
/ TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
/ TITLE OF INVENTION: FOR ANTISENSE TARGETING
/ NUMBER OF SEQUENCES: 37
```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Locke Purnell Rain Harrell
;; STREET: 2200 Ross Avenue, Suite 2200
;; CITY: Dallas
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 75201-6776
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/808,474A
;; FILING DATE: 03-MAR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mayfield, Denise L.
;; REGISTRATION NUMBER: 33,732
;; REFERENCE/DOCKET NUMBER: UTDA:001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (214) 740-8000
;; TELEFAX: (214) 740-8800
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-808-474A-3

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 1 GCCCGGAGA 9

RESULT 114
US-08-388-353-477
; Sequence 477, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343

;; TELEFAX: (516) 742-4366
;; TELEX: 230 901 SANS UR
;; INFORMATION FOR SEQ ID NO: 477:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-388-353-477

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
Db 2 ACAGAACAC 10

RESULT 115
US-08-488-551B-477
; Sequence 477, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-477

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;

```
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACAC 746
Db 2 AGAGAACAC 10

RESULT 116
US-08-522-384-3/c
; Sequence 3, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-3

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 10 GCCAGGAGA 2

RESULT 117
US-08-522-384-35/c
; Sequence 35, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-35

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 10 GCCAGGAGA 2

RESULT 118
US-08-522-384-36/c
; Sequence 36, Application US/08522384
; Patent No. 6110667
```

```
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-36

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 10 GCCAGGAGA 2

RESULT 119
US-08-522-384-93/c
; Sequence 93, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-93

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 9 GCCAGGAGA 1

RESULT 120
US-08-849-567A-41/c
; Sequence 41, Application US/08849567A
; Patent No. 6326174
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; APPLICANT: Breaker, Ronald R.
; TITLE OF INVENTION: ENZYMIC DNA MOLECULES
; FILE REFERENCE: SCR1943S
; CURRENT APPLICATION NUMBER: US/08/849,567A
; CURRENT FILING DATE: 1997-08-25
; PRIOR APPLICATION NUMBER: PCT/US95/15580
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/472,194
; PRIOR FILING DATE: 1995-06-07
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; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: substrate
; OTHER INFORMATION: binding region
US-08-849-567A-41

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      734 AGAAACAGCA 742
      |||||
Db      10 AGAAATAGA 2

RESULT 121
US-09-475-947A-135
; Sequence 135, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-135

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      737 AACAGAACCA 745
      |||||
Db      1 AACAGAATA 9

RESULT 122
US-09-508-753B-36/c
; Sequence 36, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHINAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

; PRIOR APPLICATION NUMBER: 08/349,023
; PRIOR FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; OTHER INFORMATION: 753B-36

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAAACAGAA 743
      |||||
Db      9 GAAGCAGAA 1

RESULT 123
PCT-US94-08023-32/c
; Sequence 32, Application PC/TUS9408023
; GENERAL INFORMATION:
; APPLICANT: de Kloet, Siwo R.
; TITLE OF INVENTION: Sex-Specific DNA Probe For Parrots,
; TITLE OF INVENTION: Methods And Kits
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08023
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,198
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: FL20979-34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-08023-32

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GGAGGAACA 740
      |||||
Db      10 GGAGAAAAA 2

RESULT 124
US-08-237-233-3/c
; Sequence 3, Application US/08237233
; Patent No. 5414077
; GENERAL INFORMATION:
; APPLICANT: LIN, KUEI-YING
; APPLICANT: MATTEUCCI, MARK
```

TITLE OF INVENTION: PSEUDONUCLEOSIDES AND
 TITLE OF INVENTION: PSEUDONUCLEOTIDES AND THEIR POLYMERS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IRELL & MANELLA
 STREET: 545 MIDDLEFIELD ROAD, SUITE 200
 CITY: MENLO PARK
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/237,233
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/594147
 FILING DATE: 09-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29959
 REFERENCE/DOCKET NUMBER: 4610-0006.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-327-7250
 TELEFAX: 415-327-2951
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-237-233-3

Query Match 33.6%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 91;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACCA 740
 Db 9 GGAGAAAAA 1

RESULT 125
 US-08-435-350-92
 ; Sequence 92, Application US/08435350
 ; Patent No. 5599704
 ; GENERAL INFORMATION:
 ; APPLICANT: James D. Thompson
 ; APPLICANT: Kenneth G. Draper
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: TREATMENT OF BREAST CANCER
 ; NUMBER OF SEQUENCES: 118
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 611 West Sixth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90017
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,350
 ; FILING DATE: 05-MAY-1995
 ; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/936,531
 ; FILING DATE: August 26, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wardburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 197/245
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 92:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-435-350-92

Query Match 33.6%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 77.8%; Pred. No. 91;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAG 735
 Db 1 UACCAGGAG 9

RESULT 126
 US-08-254-811D-6/c
 ; Sequence 6, Application US/08254811D
 ; Patent No. 5773213
 ; GENERAL INFORMATION:
 ; APPLICANT: Gullans, Steven R.
 ; APPLICANT: Kojima, Ryoji
 ; APPLICANT: Randall, Jeffrey
 ; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
 ; TITLE OF INVENTION: Hybridization Steps
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Macwright, Robert S.
 ; STREET: 1 Broadway
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 6.1 for Windows
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/254,811D
 ; FILING DATE: 06-JUN-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Macwright, Robert S.
 ; REGISTRATION NUMBER: 32,425
 ; REFERENCE/DOCKET NUMBER: 1854/46101
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 425-7200
 ; TELEFAX: (212) 425-5288
 ; TELEX: 422141
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; HYPOTHETICAL: No
 ; US-08-254-811D-6

Query Match 33.6%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAACAGCA 742
Db 11 AGAACAGCA 3

RESULT 127

US-08-764-522A-8
; Sequence 8, Application US/08764522A
; Patent No. 6090544
; GENERAL INFORMATION:
; APPLICANT: HARADA, SHUN-ICHI
; APPLICANT: SAMPATH, T. K.
; APPLICANT: RODAN, GIDSON A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,522A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-126
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..11
; OTHER INFORMATION: /product= "MEP-2 MUTANT CONSENSUS"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
Db 3 AAACATAAC 11

RESULT 128

US-08-764-528-8
; Sequence 8, Application US/08764528
; Patent No. 6103491
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, K. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,528
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: VITO, CHRISTINE C.
REGISTRATION NUMBER: 39,061
REFERENCE/DOCKET NUMBER: CRP-127
TELEPHONE: (617)-248-7000
TELEFAX: (617)-248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..11
OTHER INFORMATION: /product= "MEP-2 MUTANT CONSENSUS"

US-08-764-528-8
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
Db 3 AAACATAAC 11

RESULT 129

US-09-196-523-23
; Sequence 23, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-23

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
Db 11 CCAGGAGAA 11

```
Db      2  CCTGGAGAA 10

RESULT 130
US-08-930-828A-25
; Sequence 25, Application US/08930828A
; Patent No. 6261768
; GENERAL INFORMATION:
; APPLICANT: TODD, Alison
; TITLE OF INVENTION: METHOD FOR AMPLIFYING SPECIFIC NUCLEIC
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,828A
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KORNEAU, Anne M.
; REGISTRATION NUMBER: 25,864
; REFERENCE/DOCKET NUMBER: TODD-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-930-828A-25

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      729  CCAGGAGAA 737
Db      1  CCAGGAGAA 9

RESULT 131
US-08-722-015A-4
; Sequence 4, Application US/08722015A
; Patent No. 6379881
; GENERAL INFORMATION:
; APPLICANT: Fouchier, Ronaldus A.M.
; APPLICANT: Schuitemaker, Johanna
; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTII
; TITLE OF INVENTION: INDUCING AND NON SYNCYTII INDUCING VARIANTS OF THE HUMAN IMMUN
; FILE REFERENCE: 9250.25
; CURRENT APPLICATION NUMBER: US/08/722,015A
; CURRENT FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.

US-08-722-015A-4

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      729  CCAGGAGAA 737
Db      1  CCAGGAGAA 9

RESULT 132
US-09-249-155A-86
; Sequence 86, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-86

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      738  ACAGAACAC 746
Db      1  ACAGAACTC 9

RESULT 133
US-09-249-155A-124
; Sequence 124, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-124

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      738  ACAGAACAC 746
Db      1  ACAGAACTC 9

RESULT 134
US-08-930-828A-25
; Sequence 25, Application US/08930828A
; Patent No. 6261768
; GENERAL INFORMATION:
; APPLICANT: TODD, Alison
; TITLE OF INVENTION: METHOD FOR AMPLIFYING SPECIFIC NUCLEIC
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,828A
; FILING DATE: 16-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KORNEAU, Anne M.
; REGISTRATION NUMBER: 25,864
; REFERENCE/DOCKET NUMBER: TODD-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-930-828A-25

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      729  CCAGGAGAA 737
Db      1  CCAGGAGAA 9

RESULT 135
US-08-722-015A-4
; Sequence 4, Application US/08722015A
; Patent No. 6379881
; GENERAL INFORMATION:
; APPLICANT: Fouchier, Ronaldus A.M.
; APPLICANT: Schuitemaker, Johanna
; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTII
; TITLE OF INVENTION: INDUCING AND NON SYNCYTII INDUCING VARIANTS OF THE HUMAN IMMUN
; FILE REFERENCE: 9250.25
; CURRENT APPLICATION NUMBER: US/08/722,015A
; CURRENT FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.
```

Qy 738 ACAGAACAC 746
|| |||||
Db 3 ACCGACAC 11

RESULT 134
5214136-10/c
; APPLICANT: LIN, KUEI-YING; MATTEUCCI, MARK
; TITLE OF INVENTION: ANTHRAQUINONE-DERIVATIVES
; OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,941
; FILING DATE: 20-FEB-1990
; SEQ ID NO: 10:
; LENGTH: 11
5214136-10

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAAACA 740
|| |||||
Db 9 GGAGAAACA 1

RESULT 135
US-08-376-362A-3/c
; Sequence 3, Application US/08376362A
; Patent No. 5693756
; GENERAL INFORMATION:
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Blackshaw, Seth
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: AMILORIDE-SENSITIVE SODIUM CHANNEL AND
; TITLE OF INVENTION: METHOD OF IDENTIFYING SUBSTANCES WHICH STIMULATE OR BLOCK
; TITLE OF INVENTION: SALTY TASTE PERCEPTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/376,362A
; FILING DATE: 23-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan A., Sarah
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-376-362A-3

Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAG 735
|| |||||
Db 7 CCAGGAG 1

RESULT 136
US-08-859-954-30/c
; Sequence 30, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-30

Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 738 ACAGAAC 744
|| |||||
Db 8 ACAGAAC 2

RESULT 137
US-08-859-954-541/c
; Sequence 541, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.

APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 586
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 541:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-541

Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGA 736
Db 7 CAGGAGA 1

RESULT 138
US-09-985-799-19
Sequence 19, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-No. RE38392-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-985-799-19

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TGCCAGG 733
Db 4 TGCCAGG 10

RESULT 139
US-07-739-642-13
Sequence 13, Application US/07739642
Patent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Vectors And Hosts With Increased
TITLE OF INVENTION: Expression Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,642
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:


```
;
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-739-642-13

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 AACAGAA 743
Db 1 AACAGAA 7

RESULT 140
US-07-739-643-13
; Sequence 13, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee, Richard L.
; TITLE OF INVENTION: Increased Expression of HbcAg
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739.643
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-9228
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-739-142-13

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 AACAGAA 743
Db 1 AACAGAA 7

RESULT 142
US-08-548-199-14/c
; Sequence 14, Application US/08548199
; Patent No. 5652106
; GENERAL INFORMATION:
; APPLICANT: Plikeytis, Bonnie B.
; APPLICANT: Shinnick, Thomas M.
; APPLICANT: Crawford, Jack T.
; TITLE OF INVENTION: RAPID AMPLIFICATION-BASED SUBTYPING OF
; MYCOBACTERIUM TUBERCULOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 1200, The Candler Building
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/548.199
; FILING DATE: 25-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/072,450
; FILING DATE: 04 JUNE 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.062
```

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /number=10
; OTHER INFORMATION: /note="Consensus sequence of 10 bp tandem repeat
; OTHER INFORMATION: of MPTR (Hermans et al. 1992)"
US-08-548-199-14

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 742 AACACCG 748
Db 9 AACACCG 3

RESULT 143
US-08-440-787A-66/c
; Sequence 66, Application US/08440787A
; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440.787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-440-787A-70

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGAGAA 737
Db 9 AGAGAA 3

RESULT 145
US-08-594-031-19
; Sequence 19, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
```

```
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20004-2400
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/594,031
/ FILING DATE: 30-JAN-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/006,838
/ FILING DATE: 16-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Remenick, James
/ REGISTRATION NUMBER: 36,902
/ REFERENCE/DOCKET NUMBER: 0A146-0110
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-639-7700
/ TELEFAX: 202-639-7890
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ US-08-594-031-19

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TGCCAGG 733
Db 4 TGCCAGG 10

RESULT 146
US-08-388-353-481
; Sequence 481, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424

US-08-488-551B-481
; Sequence 481, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 481:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-481

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GAACACC 747
DB 1 GAACACC 7

RESULT 148
US-08-522-384-13/c

; Sequence 13, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-13

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGA 734
DB 9 GCCAGGA 3

RESULT 149
US-09-054-832-3

; Sequence 3, Application US/09054832
; Patent No. 6312894
; GENERAL INFORMATION:
; APPLICANT: Meyer, Rich
; TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
; TITLE OF INVENTION: MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
; TITLE OF INVENTION: CONJUGATED TO MINOR GROOVE BINDERS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Fast-SEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,832
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,370
; FILING DATE: 03-APR-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Brennan, Sean M
; REGISTRATION NUMBER: 39,917
; REFERENCE/DOCKET NUMBER: 34469-20004.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-054-832-3

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGA 742
DB 4 AAACAGA 10

RESULT 150

US-09-640-953-3
; Sequence 3, Application US/09640953
; Patent No. 6492346
; GENERAL INFORMATION:
; APPLICANT: Meyer, Rich
; TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
; TITLE OF INVENTION: MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
; CONJUGATED TO MINOR GROOVE BINDERS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Fast-SEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/640,953
; FILING DATE: 16-AUG-2000

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,832
; FILING DATE: 03-APR-1998
; APPLICATION NUMBER: 08/415,370
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brennan, Sean M
; REGISTRATION NUMBER: 39,917
; REFERENCE/DOCKET NUMBER: 34469-20004.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-640-953-3

Query Match 31.8%; Score 7; DB 1; Length 10;

```
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 736 AAACAGA 742
Db 4 AAACAGA 10
|||||

RESULT 151
US-09-867-915-21
; Sequence 21, Application US/09867915
; Patent No. 6521747
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Finkel, Kevin
; APPLICANT: Koshi, Beena
; APPLICANT: Lee, Helen H.
; TITLE OF INVENTION: HAPLOTYPES OF THE AGTR1 GENE
; CURRENT APPLICATION NUMBER: US/09/867,915
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/228,542
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-915-21

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 3 GAAACAG 9
|||||

RESULT 152
US-09-508-753B-135/c
; Sequence 135, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiichi OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 135
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-135

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAAA 738
Db 3 GGAGAAA 9
|||||

RESULT 153
US-09-508-753B-319/c
; Sequence 319, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiichi OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 319
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-319

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 8 GAAACAG 2
|||||

RESULT 154
US-09-769-482-22/c
; Sequence 22, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-22

Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 3 AGGAGAA 9
|||||
```

```
Db          9 AGGAGAA 3

RESULT 155
US-09-769-482-29
; Sequence 29, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-29

Query Match          31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          739 CAGAAC 745
Db          2 CAGAAC 8

RESULT 156
US-09-083-235A-52/c
; Sequence 52, Application US/09083235A
; Patent No. 6632919
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E
; APPLICANT: Haaima, Gerald
; APPLICANT: Eldrup, Anne B
; TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
; FILE REFERENCE: ISIS3044
; CURRENT APPLICATION NUMBER: US/09/083,235A
; CURRENT FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 08/862,629
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-52

Query Match          31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          740 AGAACAC 746
Db          8 AGAACAC 2

RESULT 157
US-09-083-235A-56/c
; Sequence 56, Application US/09083235A
; Patent No. 6632919
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E
; APPLICANT: Haaima, Gerald
; APPLICANT: Eldrup, Anne B
; TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
; FILE REFERENCE: ISIS3044
; CURRENT APPLICATION NUMBER: US/09/083,235A
; CURRENT FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 08/862,629
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-56

Query Match          31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          740 AGAACAC 746
Db          8 AGAACAC 2

RESULT 158
US-07-681-703B-55
; Sequence 55, Application US/07681703B
; Patent No. 5443965
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Moockli, Randolph
; TITLE OF INVENTION: Hepatitis C Virus Epitopes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/681,703B
; FILING DATE: 05-APR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,611
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 594,854
; FILING DATE: 09-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-076.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 55:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Codon Change, Example 20
US-07-681-703B-55

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGAGAA 743
Db 1 AGAAGAGAA 10

RESULT 159
US-08-049-283A-32/c
Sequence 32, Application US/08049283A
Patent No. 5502176
GENERAL INFORMATION:
APPLICANT: Tenen, Daniel G.
APPLICANT: Pahl, Heike L.
APPLICANT: Burn, Timothy C.
TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatenIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,283A
FILING DATE: 14-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,465
FILING DATE: 19-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/837,776
FILING DATE: 13-FEB-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BIH91-03'A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-049-283A-32

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
Db 10 GGAGAAGTAG 1

RESULT 160
US-07-949-541A-13
Sequence 13, Application US/07949541A
Patent No. 5552270
GENERAL INFORMATION:
APPLICANT: Khrapko, Konstantin R.
APPLICANT: Khorlin, Alexandr A.
APPLICANT: Ivanov, Igor B.
APPLICANT: Ershov, Gennady M.
APPLICANT: Lysov, Yuri P.
APPLICANT: Florentiev, Vladimir L.
APPLICANT: Mirzabekov, Andrei D.
TITLE OF INVENTION: Method for Determining a DNA Nucleotide
TITLE OF INVENTION: Sequence and a Device for Carrying Out Same
Patent No. 5552270
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/949,541A
FILING DATE: 09-No. 5552270-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/RU92/00052
FILING DATE: 18-Mar-1992
APPLICATION NUMBER: Russian Federation 4919321
FILING DATE: 18-Mar-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet I. Cord
REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U-8999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: chemically synthesized
MOLECULE TYPE: desoxyribonucleotide.
FEATURE: oligonucleotide was synthesized by phosphoramidite
FEATURE: method
OTHER INFORMATION: The sequence is listed from 3' to 5'
OTHER INFORMATION: left to right and this is a part of SEQ ID NO:4.
US-07-949-541A-13

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGAGAA 737
Db 1 GCCAGAGAA 10

RESULT 161
US-08-396-479B-16
; Sequence 16, Application US/08396479B
; Patent No. 5612455
; GENERAL INFORMATION:
; APPLICANT: HOEY, Timothy
; TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396.479B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59450-1/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 210 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-396-479B-16

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
Db 1 GGAAAAAAGT 10

RESULT 162
US-08-088-658-4
; Sequence 4, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M Ileggaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/088.658
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,363
; FILING DATE: 26-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-088-658-4

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAACA 745
Db 1 AAAAAGAAAA 10

RESULT 163
US-08-818-823-16
; Sequence 16, Application US/08818823
; Patent No. 5708158
; GENERAL INFORMATION:
; APPLICANT: HOEY, Timothy
; TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818.823
; FILING DATE: 14-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/396.479
; FILING DATE: 02-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59450-1/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 210 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-818-823-16

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741
|||||
Db 1 GGAAGAACTG 10

RESULT 164

US-08-686-116A-49
; Sequence 49, Application US/08686116A
; Patent No. 5714331

; GENERAL INFORMATION:

; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Binding Affinity, Sequence Specificity
Patent No. 5714331

; TITLE OF INVENTION: ans Solubility

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331 Iris LLP
; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/686,116A

; FILING DATE: July 24, 1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/108,591

; FILING DATE: 22-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Michael P. Straher

; REGISTRATION NUMBER: 38,325

; REFERENCE/DOCKET NUMBER: ISIS-2271

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-686-116A-49

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACA 745
|||||
Db 1 AAAAAGAAA 10

RESULT 165

US-08-685-484-49
; Sequence 49, Application US/08685484
; Patent No. 5719262

; GENERAL INFORMATION:

; APPLICANT: Buchardt et al.

; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid

; TITLE OF INVENTION: Side Chains

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262 Iris LLP
; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/685,484

; FILING DATE: 24-JUL-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/108,591

; FILING DATE: 22-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Michael P. Straher

; REGISTRATION NUMBER: 38,325

; REFERENCE/DOCKET NUMBER: ISIS-2270

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-685-484-49

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACA 745
|||||
Db 1 AAAAAGAAA 10

RESULT 166

US-08-847-108-49

; Sequence 49, Application US/08847108

; Patent No. 5736336

; GENERAL INFORMATION:

; APPLICANT: Buchardt et al.

; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced

; TITLE OF INVENTION: Binding Affinity, Sequence Specificity

; Patent No. 5736336

; TITLE OF INVENTION: and Solubility

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336 Iris LLP
; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/847,108

```

; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,116
; FILING DATE: July 24, 1996
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-847-108-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAAC 745
DB 1 AAAAAGAAAA 10

RESULT 167
US-08-686-113A-56
; Sequence 56, Application US/08686113A
; Patent No. 5766855
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Affinity And Sequence Specificity
; Patent No. 5766855
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,113A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2273
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-847-108-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAAC 745
DB 1 AAAAAGAAAA 10

RESULT 169
US-08-465-590-148
; Sequence 148, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
;
US-08-847-095A-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAAC 745
DB 1 AAAAAGAAAA 10

RESULT 168
US-08-847-095A-49
; Sequence 49, Application US/08847095A
; Patent No. 5786461
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
; TITLE OF INVENTION: Side Chains
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,095A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,484
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-847-095A-49
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACAGAAC 745
DB 1 AAAAAGAAAA 10

RESULT 169
US-08-465-590-148
; Sequence 148, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
;
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPEG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-465-590-148

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
|||
Db 1 AGGAGGAAAA 10

RESULT 170
US-08-808-474A-4
; Sequence 4, Application US/08808474A
; Patent No. 5856103
; GENERAL INFORMATION:
; APPLICANT: Gray, Donald M.
; APPLICANT: Clark, Chris L.
; TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
; TITLE OF INVENTION: FOR ANTISENSE TARGETING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Locke Purnell Rain Harrell
; STREET: 2200 Ross Avenue, Suite 2200
; CITY: Dallas
; STATE: Texas
; COUNTRY: USA
; ZIP: 75201-6776
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,474A

; FILING DATE: 03-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTDAL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 740-8000
; TELEFAX: (214) 740-8800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-808-474A-4

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
|||
Db 1 CCGGAGAGAGA 10

RESULT 171
US-08-173-489C-67
; Sequence 67, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: esterase D gene (Accession # M13450)
; DESCRIPTION: nucleotides 34 to 43
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:

ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 13
MAP POSITION: 13q14.1-q14.2
PUBLICATION INFORMATION:
AUTHORS: Lee, E Y H P, Lee, W H.
TITLE: Molecular cloning of the
TITLE: human esterase D gene, a genetic marker of
JOURNAL: Proceedings of the National Academy of
JOURNAL: Sciences, USA
VOLUME: 83
PAGES: 6337-6341
DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 67 :FROM 1 TO 10
US-08-173-489C-67

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
||| |||
DB 1 AGGAAAGAA 10

RESULT 172
US-08-173-489C-72/c
; Sequence 72, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
FILING DATE: 22 DEC 1993
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from esterase D
HYPOTHETICAL: Yes
ANTI-SENSE: No

; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 72 :FROM 1 TO 10
US-08-173-489C-72
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 743
||| |||
DB 10 AGAAAGGAA 1
RESULT 173
US-08-173-489C-151/c
; Sequence 151, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
FILING DATE: 22 DEC 1993
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 29 OCT 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus ayw isolate,
DESCRIPTION: nucleotides 807 to 816
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: ayw
PUBLICATION INFORMATION:
AUTHORS: Galibert, F, Mandart, E, Pitoussi, F,
AUTHORS: Tiollais, P, Charnay, P.
TITLE: Nucleotide sequence of the
TITLE: Hepatitis B virus genome (subtype ayw) cloned
TITLE: in E coli
JOURNAL: Nature
VOLUME: 281
PAGES: 646-650
DATE: 1979

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; RELEVANT RESIDUES IN SEQ ID NO: 151 :FROM 1 TO 10
US-08-173-489C-151

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAA 743
   |||||
Db 10 AGAAGACAGAA 1

RESULT 174
US-08-173-489C-175
; Sequence 175, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus adw2 isolate,
; DESCRIPTION: nucleotides 563 to 572
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: adw2
; PUBLICATION INFORMATION:
; AUTHORS: Valenzuela, P, Quiroga, M, Zaldivar, J,
; AUTHORS: Gray, P, Ruter, W J.
; TITLE: The nucleotide sequence of
; TITLE: the Hepatitis B viral genome and the
; TITLE: identification of the major viral genes
; JOURNAL: In "Animal Virus Genetics", Fields, B N,
; VOLUME: Jaenisch, R, Fox C F eds
; PAGES: 57-70
; DATE: 1980

; RELEVANT RESIDUES IN SEQ ID NO: 175 :FROM 1 TO 10
US-08-173-489C-175

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAA 743
   |||||
Db 1 AGAAGACAGAA 10

RESULT 175
US-08-173-489C-205
; Sequence 205, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus adr isolate,
; DESCRIPTION: nucleotides 2241 to 2250
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: adr
; PUBLICATION INFORMATION:
; AUTHORS: Fujiyama, A, Miyanochara, A, No. 5861244aki, C,
; AUTHORS: Toneyama, T, Ohromo, N, Matsubara, K.
; TITLE: Cloning and structural
; TITLE: analysis of Hepatitis B virus DNAs subtype adr
; JOURNAL: Nucleic Acids Research
; VOLUME: 11
; PAGES: 4601-4610
; DATE: 1983
; RELEVANT RESIDUES IN SEQ ID NO: 205 :FROM 1 TO 10
US-08-173-489C-205
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schultz1-727.rni

Mon Oct 18 14:40:09 2004

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; LOCATION: 1..10
; US-08-286-819A-48
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAGACGAA 743
||| |||
Db 1 AGAAGACGAA 10

RESULT 176
US-08-286-819A-48
; Sequence 48, Application US/08286819A
; Patent No. 5971910
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-WALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPROTEIDS, IN PARTICULAR
; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.819A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174.682
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/917.146
; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5871910man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: RBS

; Query Match 30.9%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 1e+02;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAGACGAA 743
||| |||
Db 1 AGAAGACGAA 10

RESULT 177
US-08-545-253A-5
; Sequence 5, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Amerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdNA
; US-08-545-253A-5

; Query Match 30.9%; Score 6.8; DB 1; Length 10;
; Best Local Similarity 80.0%; Pred. No. 1e+02;
; Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 739 CAGAACACCG 748
||| |||
Db 1 CCGAACACCG 10

RESULT 178
US-08-471-907A-4
; Sequence 4, Application US/08471907A
; Patent No. 5986053

```

GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Berg, Rolf H.
APPLICANT: M. Ilegard, Niels E.
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-471-907A-4

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 745
Db 1 AAAAAAGAAA 10

RESULT 179
US-08-388-353-73
Sequence 73, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-73

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGAGAA 737
Db 1 GCCAGAGCA 10

RESULT 180
US-08-388-353-175
Sequence 175, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs

```
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-175

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 734 AGAAGACAA 743
Db 1 AGAAGACAA 10

RESULT 181
US-08-388-353-186
; Sequence 186, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-187

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 732 GGAGAACAG 741
Db 1 GGAGAACAG 10

RESULT 183
US-08-980-357-48
; Sequence 48, Application US/08980357
; Patent No. 6013508
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-MALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; EXPRESSION OF RESISTANCE TO GLYCOPROTEINS, IN PARTICULAR
; IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-186

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 731 AGGAGAACAA 740
Db 1 AGGAGAACAA 10

RESULT 182
US-08-388-353-187
; Sequence 187, Application US/08388353
; Patent No. 6010895
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: RBS
LOCATION: 1..10
US-08-980-357-48

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGA 736
||| |||||
Db 1 TGAAGGAGA 10

RESULT 184
US-08-488-551B-73
; Sequence 73, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,357
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 96062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-73

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAA 737
|||||
Db 1 GCCAGGAGCA 10

RESULT 185
US-08-488-551B-175
; Sequence 175, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95

```

; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-175

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAA 743
Db 1 AGAAGACAA 10

RESULT 186
US-08-488-551B-186
; Sequence 186, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-187

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 CGAGGACAG 741
Db 1 CGAGGACAG 10

RESULT 188
US-08-488-551B-188
; Sequence 188, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-186
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US-08-993-303-2
; Sequence 2, Application US/08993303
; Patent No. 6020132
; GENERAL INFORMATION:
; APPLICANT: ORUM, Henrik
; APPLICANT: KOCH, Troels
; APPLICANT: BORRE, Martin
; APPLICANT: HANSEN, Henrik Frydenlund
; TITLE OF INVENTION: METHOD OF ANALYSIS USING SIGNAL
; TITLE OF INVENTION: AMPLIFICATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street, N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,303
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berman, Richard B.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P1614-7082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OLIGODEOXYRIBONUCLEOTIDE"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "AT THE TERMINUS IS AN AMINOHXYL
; OTHER INFORMATION: "ALKYLATED GROUP"
US-08-993-303-2
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 731 AGGAGAAACA 740
DB 1 AAGAGAAA 10
RESULT 189
US-08-719-337-5
; Sequence 5, Application US/08719337
; Patent No. 6054634
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte

STATE: No. 6054634th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,337
FILING DATE: 25-SEP-1996
CLASSIFICATION: 047
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,567
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-719-337-5
Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 739 CAGACACCG 748
DB 1 CCGACACCG 10
RESULT 190
US-08-724-466B-26
; Sequence 26, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344

```

; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-724-466B-26

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
Db 1 TGCCAGTGA 10

RESULT 191
US-08-522-384-121/c
; Sequence 121, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; FILE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522.384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-121

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
Db 10 GCCAGCAGGA 1

RESULT 192
US-08-711-417C-148
; Sequence 148, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711.417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-08-711-417C-148

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
Db 1 AGGAGGAAAA 10

RESULT 193
US-08-088-661F-20
; Sequence 20, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
; APPLICANT: No. 6228982den, Bengel
; APPLICANT: Wittung, Pernilla
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf
; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
; FILE REFERENCE: IS11108
; CURRENT APPLICATION NUMBER: US/08/088,661F
; CURRENT FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982e1 Sequence
US-08-088-661F-20

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAAACA 745
Db 1 AAAAAGAAAA 10

RESULT 194
US-08-088-661F-30

```

; Sequence 30, Application US/08088661F
 ; Patent No. 6228982
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6228982den, Bengel
 ; APPLICANT: Wittung, Perrilla
 ; APPLICANT: Buchardt, Ole
 ; APPLICANT: Egholm, Michael
 ; APPLICANT: Nielsen, Peter E.
 ; APPLICANT: Berg, Rolf
 ; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
 ; FILE REFERENCE: IS181108
 ; CURRENT APPLICATION NUMBER: US/08/088,661F
 ; CURRENT FILING DATE: 1993-07-02
 ; PRIOR FILING DATE: 1993-04-26
 ; PRIOR APPLICATION NUMBER: PCT/EP92/01219
 ; PRIOR FILING DATE: 1992-05-19
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
 US-08-088-661P-30

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACACAG 743
 Db 1 AAAAAACAAA 10

RESULT 195
 US-09-245-041-129
 ; Sequence 129, Application US/09245041
 ; Patent No. 6274339
 ; GENERAL INFORMATION:
 ; APPLICANT: Moore, K.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
 ; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
 ; FILE REFERENCE: 7853-136
 ; CURRENT APPLICATION NUMBER: US/09/245,041
 ; CURRENT FILING DATE: 1998-02-05
 ; EARLIER APPLICATION NUMBER: 60/093,630
 ; EARLIER FILING DATE: 1998-07-21
 ; EARLIER APPLICATION NUMBER: 60/104,978
 ; EARLIER FILING DATE: 1998-10-20
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 129
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-09-245-041-129

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAACAG 741
 Db 1 GGACACAG 10

RESULT 196
 US-08-882-164D-26

; Sequence 26, Application US/08882164D
 ; Patent No. 6306624
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.,
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5L 1A9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/882,164D
 ; FILING DATE: June 25, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; APPLICATION NUMBER: 08/724,466
 ; FILING DATE: October 1, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00010
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-882-164D-26

Query Match 30.9%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGA 736
 Db 1 TGCCAGTGGA 10

RESULT 197
 US-08-150-156A-5
 ; Sequence 5, Application US/08150156A
 ; Patent No. 6357163
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
 ; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
 ; NUMBER OF SEQUENCES: 40
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/150,156A
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 0986/91
 ; FILING DATE: 24-MAY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 0987/91

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; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-5

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAA 745
Db 1 AAAAAGAAAA 10

RESULT 198
US-08-150-156A-6
; Sequence 6, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-6

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 1 AAAAAGAAAA 10

RESULT 199
US-08-150-156A-14/c
; Sequence 14, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-14

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAA 745
Db 1 AAAAAGAAAA 10

RESULT 200
US-08-150-156A-17/c
; Sequence 17, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-6

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 1 AAAAAGAAAA 10

```

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Db 1 AAAAACAAAA 10

RESULT 199
US-08-150-156A-14/c
; Sequence 14, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-14

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAA 745
Db 1 AAAAAGAAAA 10

RESULT 200
US-08-150-156A-17/c
; Sequence 17, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150.156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; US-08-150-156A-17

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      731 AGGAGAAACA 740
Db      10 AGAAGAAAAA 1

RESULT 201
US-08-618-834C-33
; Sequence 33, Application US/08618834C
; Patent No. 6361937
; GENERAL INFORMATION:
; APPLICANT: Stryer, Lubert
; TITLE OF INVENTION: Computer-Aided Nucleic Acid
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: CA
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,834C
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFYP002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-618-834C-45

Query Match          30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      739 CAGAACACCG 748
Db      1 CACATCACCG 10

RESULT 203
US-08-108-591B-8
; Sequence 8, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Sgholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-8

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACAA 745
DB      10 AAAAAAGAAAA 1

RESULT 204
US-08-108-591B-9
; Sequence 9, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-9

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACAA 745
DB      10 AAAAAAGAAAA 10

RESULT 205
US-08-108-591B-12/c
; Sequence 12, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-12

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACAA 745
DB      10 AAAAAAGAAAA 10

RESULT 206
US-08-108-591B-15/c
; Sequence 15, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-15

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGAACAA 740
DB      10 AGAGAGAAAA 1

RESULT 207
US-08-108-591B-28
; Sequence 28, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-28

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAACAGAA 743
DB      1 AAAAAACAAAA 10
```


RESULT 208
US-08-686-114B-56
; Sequence 56, Application US/08686114B
; Patent No. 6414112
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,114B
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-686-114B-56

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAGACA 745
Db 1 AAAAGAGAAA 10

RESULT 209
US-09-154-750A-14/c
; Sequence 14, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-154-750A-14

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAGACA 745
Db 10 AACAGAGACA 1

RESULT 210
US-09-154-750A-54
; Sequence 54, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-154-750A-54

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
Db 1 GGAAGACAGA 10

RESULT 211
US-09-394-457C-7/c
; Sequence 7, Application US/09394457C
; Patent No. 6440705
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 246/020
; CURRENT APPLICATION NUMBER: US/09/394,457C
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
; US-09-394-457C-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAGACA 740
Db 10 AGGAGAGACA 1

RESULT 212

US-08-275-951-61/c
; Sequence 61, Application US/08275951
; Patent No. 6451968

GENERAL INFORMATION:

; APPLICANT: Egholm, Michael
; APPLICANT: Kiely, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilson, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif

; TITLE OF INVENTION: Linked Peptide Nucleic Acids

; FILE REFERENCE: IS181577

; CURRENT APPLICATION NUMBER: US/08/275,951

; CURRENT FILING DATE: 1994-07-15

; PRIOR APPLICATION NUMBER: 08/108,591

; PRIOR FILING DATE: 1993-11-22

; PRIOR APPLICATION NUMBER: 08/088,658

; PRIOR FILING DATE: 1993-07-02

; PRIOR APPLICATION NUMBER: 08/088,661

; PRIOR FILING DATE: 1993-07-02

; PRIOR APPLICATION NUMBER: PCT/EP92/01219

; PRIOR FILING DATE: 1992-05-22

; PRIOR APPLICATION NUMBER: 986/91

; PRIOR FILING DATE: 1991-05-22

; PRIOR APPLICATION NUMBER: 987/91

; PRIOR FILING DATE: 1991-05-24

; PRIOR APPLICATION NUMBER: 510/92

; PRIOR FILING DATE: 1991-04-15

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 61

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence

US-08-275-951-61

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGAGAGAA 743

Db 10 AGAAGAGAGAA 1

RESULT 213

US-09-709-596A-7/c

; Sequence 7, Application US/09709596A

; Patent No. 6458945

GENERAL INFORMATION:

; APPLICANT: Variagenics, Inc.

; TITLE OF INVENTION: A Method for Analyzing Polynucleotides

; FILE REFERENCE: 258/239

; CURRENT APPLICATION NUMBER: US/09/709,596A

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hypothetical sequence to demonstrate application.

US-09-709-596A-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740

Db 10 AGGAGAAACA 1

RESULT 214

US-09-486-853-8/c

; Sequence 8, Application US/09486853

; Patent No. 6461871

GENERAL INFORMATION:

; APPLICANT: KUBISTA, MIKHAEL

; APPLICANT: SVANVIK, NICKIE

; APPLICANT: WESTMAN, GUNNAR

; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROBE FOR NUCLEIC ACID HYBRIDIZATION

; FILE REFERENCE: GOTEPO29US

; CURRENT APPLICATION NUMBER: US/09/486,853

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: PCT/SE98/01580

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: SE 9703251-0

; PRIOR FILING DATE: 1997-05-09

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 10

; TYPE: DNA

; ORGANISM: synthetic construct

US-09-486-853-8

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741

Db 10 GGAGAAAGGAG 1

RESULT 215

US-09-475-947A-106/c

; Sequence 106, Application US/09475947A

; Patent No. 6472154

GENERAL INFORMATION:

; APPLICANT: Garner, Harold R.

; APPLICANT: Wren, Jonathan D.

; APPLICANT: Minna, John D.

; TITLE OF INVENTION: Polymorphic Repeats in Human Genes

; FILE REFERENCE: UTSD0667

; CURRENT APPLICATION NUMBER: US/09/475,947A

; CURRENT FILING DATE: 1999-12-31

; NUMBER OF SEQ ID NOS: 346

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 106

; LENGTH: 10

; TYPE: DNA

; ORGANISM: human

US-09-475-947A-106

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Length 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGAGAGAA 743

Db 10 AGAAGAGAGAA 1

RESULT 216

US-09-475-947A-122/c

; Sequence 122, Application US/09475947A

; Patent No. 6472154

GENERAL INFORMATION:

; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-122

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGAA 743
Db 10 AGAAAAAAA 1

RESULT 217
US-09-914-259-101/c
; Sequence 101, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
US-09-914-259-101

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 733 GAGAAACAGA 742
Db 10 GAGAGAGAGA 1

RESULT 218
US-09-916-228-7
; Sequence 7, Application US/09916228
; Patent No. 6498013
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Sparks, Andrew
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Serial analysis of transcript expression
; FILE REFERENCE: 001107.00172
; CURRENT APPLICATION NUMBER: US/09/916,228
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,556
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/233,431

; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tag or tag concatenamer
US-09-916-228-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACAA 745
Db 1 AAACAAATCA 10

RESULT 219
US-09-655-104A-7/c
; Sequence 7, Application US/09655104A
; Patent No. 6500650
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Identifying Polymorphisms
; FILE REFERENCE: 257/078
; CURRENT APPLICATION NUMBER: US/09/655,104A
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-09-655-104A-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAACAA 740
Db 10 AGGAGGAATA 1

RESULT 220
US-08-301-037-7/c
; Sequence 7, Application US/08301037
; Patent No. 6528313
; GENERAL INFORMATION:
; APPLICANT: Le Mouellic, Herve
; Brulet, Philippe
; TITLE OF INVENTION: Procedure for Specific Replacement of a Copy of a
; Gene Present in the Recipient Genome by the Integration of
; That Where the Integration is Made
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-37

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAG 741
||| |||
Db 1 GGAAAGCAG 10

RESULT 224
US-09-508-753B-51
; Sequence 51, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-51

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
||| |||
Db 1 CACCAGAAAC 10

RESULT 225
US-09-508-753B-76/c
; Sequence 76, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 76
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-76

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAG 741
||| |||
Db 10 GGAAAGCAG 1

RESULT 226
US-09-508-753B-79/c
; Sequence 79, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 79
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-79

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAAAC 739
||| |||
Db 10 CACCAGAAAC 1

RESULT 227
US-09-508-753B-82
; Sequence 82, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI

```

; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; CURRENT FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; PRIOR FILING DATE: 1997-09-18
; SEQ ID NO 82
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-82

```

```

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 735 GAAACAGAAC 744
||| ||| |||
DB 1 GAGACACAAC 10

```

```

RESULT 228
US-09-508-753B-126
; Sequence 126, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; CURRENT FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 126
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-126

```

```

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 735 GAAACAGAAC 744
||| ||| |||
DB 1 GAAACTGAGC 10

```

```

RESULT 229
US-09-508-753B-131/c
; Sequence 131, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

```

```

; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 131
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-131

```

```

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 735 GAAACAGAAC 744
||| ||| |||
DB 10 GAAACTGAGC 1

```

```

RESULT 230
US-09-508-753B-133/c
; Sequence 133, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 133
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-133

```

```

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 729 CCAGAGAGAA 738
||| ||| |||
DB 10 CCAGAGAGAA 1

```

```

RESULT 231
US-09-508-753B-157/c
; Sequence 157, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16

```

```

; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 157
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Primer
US-09-508-753B-157

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches      8; Conservative 0; Mismatches 0;

Qy      735 GAAACAGAAC 744
Db      10 GAGACACAAC 1

RESULT 232
US-09-508-753B-160
; Sequence 160, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 160
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Primer
US-09-508-753B-160

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches      8; Conservative 0; Mismatches 0;

Qy      738 ACAGAACACC 747
Db      1 ACTGACTCC 10

RESULT 233
US-10-042-111-42
; Sequence 42, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 42
; LENGTH: 10
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Primer
US-10-042-111-42

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches      8; Conservative 0; Mismatches 0;

Qy      738 ACAGAACACC 747
Db      1 ACTGAAGGCC 10

RESULT 234
US-10-042-111-43/c
; Sequence 43, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Primer
US-10-042-111-43

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches      8; Conservative 0; Mismatches 0;

Qy      738 ACAGAACACC 747
Db      10 ACGAGACACC 1

RESULT 235
US-09-394-467-7/c
; Sequence 7, Application US/09394467
; Patent No. 6566059
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 245/287
; CURRENT APPLICATION NUMBER: US/09/394,467
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Used to demonstrate how indicated aspect of invention works.
US-09-394-467-7

Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches      8; Conservative 0; Mismatches 0;

Qy      731 AGGAGAAACA 740

```

```
DB      .      10 AGGAGGAATA 1
||||| |||
RESULT 236
US-10-104-818-7/c
; Sequence 7, Application US/10104818
; Patent No. 6582923
; GENERAL INFORMATION:
; APPLICANT: Varigenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 265/034
; CURRENT APPLICATION NUMBER: US/10/104,818
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/394,774
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-10-104-818-7
Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      731 AGGAGGAACA 740
||||| |||
DB      10 AGGAGGAATA 1

RESULT 237
US-09-989-789-1332/c
; Sequence 1332, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1332
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1332
Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      737 AACAGAACAC 746
||||| |||
DB      10 ACCAGCACAC 1

RESULT 238
US-09-989-789-1333/c
; Sequence 1333, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1333
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1333
Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      737 AACAGAACAC 746
||||| |||
DB      10 ACCAGCACAC 1

RESULT 239
US-09-989-789-1334/c
; Sequence 1334, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1334
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1334
Query Match      30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      737 AACAGAACAC 746
||||| |||
DB      10 ACCAGCACAC 1

RESULT 240
US-09-989-789-1335/c
; Sequence 1335, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1335
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1335
```


; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1335

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACGAGACAC 746
Db 10 ACCAGCACAC 1

RESULT 241

US-09-337-304-56
; Sequence 56, Application US/09337304
; Patent No. 6613873
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS-3809
; CURRENT APPLICATION NUMBER: US/09/337,304
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 08/847,110
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 08/686,114
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 810/92
; PRIOR FILING DATE: 1992-04-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-337-304-56

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACAC 745
Db 1 AAAAAAGAAA 10

RESULT 242

US-09-855-159A-7/c
; Sequence 7, Application US/09855159A
; Patent No. 6620595
; GENERAL INFORMATION:
; APPLICANT: Cannon, Paula
; APPLICANT: Barcova, Maria
; TITLE OF INVENTION: Retroviral Vectors Comprising An Enhanced 3' Transcription Termin
; FILE REFERENCE: 4-31439A/USC
; CURRENT APPLICATION NUMBER: US/09/855,159A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/203,884
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Adenovirus type 2
US-09-855-159A-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGAA 743
Db 10 ACAAAGAA 1

RESULT 243

US-09-723-909-148
; Sequence 148, Application US/09723909
; Patent No. 6630141
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,909
; FILING DATE: 28-NO. 6630141-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417
; FILING DATE: 05-SEP-1996
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-09-723-909-148

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
Db 1 AGGAGAGAAA 10

```

RESULT 244
US-08-466-699-7/c
; Sequence 7, Application US/08466699
; Patent No. 6638768
; GENERAL INFORMATION:
; APPLICANT: Le Mouellic, Herve
; TITLE OF INVENTION: Procedure for Specific Replacement of a Copy
; TITLE OF INVENTION: of a Gene Present in the Recipient Genome by the Integration o
; TITLE OF INVENTION: Different From That Where the Integration is Made
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Durner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/466,699
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/301,037
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,744
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/598,679
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR90/00185
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8903630
; FILING DATE: 20-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 02356-0053-06000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-466-699-7

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGGAAC 739
DB 10 CATCGAAC 1

RESULT 245
PCT-US91-03680-75/c
; Sequence 75, Application PC/TUS9103680

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
DB 10 GAGAGAGA 1

RESULT 246
PCT-US93-08743-148
; Sequence 148, Application PC/TUS9308743

GENERAL INFORMATION:
APPLICANT: Matteucci, Mark D.
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
TITLE OF INVENTION: DUPLEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 2
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
FEATURE:
NAME/KEY: modified_base
LOCATION: 5
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
FEATURE:
NAME/KEY: modified_base
LOCATION: 8
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
FEATURE:
NAME/KEY: modified_base
LOCATION: 10
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "T-T, linking group o-xyloso (nucleotides
OTHER INFORMATION: that have xylose sugar linked via the o-xylo
OTHER INFORMATION: ring)"
PCT-US91-03680-75

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
DB 10 GAGAGAGA 1

RESULT 246
PCT-US93-08743-148
; Sequence 148, Application PC/TUS9308743
```

GENERAL INFORMATION:
APPLICANT: IKAROS: A T CELL PATHWAY REGULATORY GENE
TITLE OF INVENTION: 152
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-08743-148

Query Match 30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2;

QY 731 AGGAGAAACA 740
Db 1 AGGAGGAAAA 10

RESULT 247
US-07-739-642-14
Sequence 14, Application US/07739642
Patent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Vectors And Hosts With Increased
Expression Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,642
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear

US-07-739-642-14

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; Indels 0;
Matches 7; Conservative 0; Mismatches 1;

QY 737 AACAGAAC 744
Db 1 AACAGACC 8

RESULT 248
US-07-739-643-14
Sequence 14, Application US/07739643
Patent No. 5175094
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Increased Expression Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,643
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-739-643-14

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; Indels 0;
Matches 7; Conservative 0; Mismatches 1;

QY 737 AACAGAAC 744
Db 1 AACAGACC 8

RESULT 249
US-07-739-142-14
Sequence 14, Application US/07739142
Patent No. 5175272
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: DNA Sequences With Increased Expression
Of Hbcag
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey

COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,142
FILING DATE: 19910801
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: 33,213
REFERENCE/DOCKET NUMBER: P-2271
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-739-142-14

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

QY 737 AACAGAAC 744
|||||
Db 1 AACAGACC 8

RESULT 250
US-08-465-590-117
Sequence 117, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-465-590-117
Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0
QY 731 AGGAGAAA 738
|||||
Db 1 AGGGGAAA 8

RESULT 251
US-08-859-954-38/C
Sequence 38, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-38

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

QY 740 AGAACACC 747

Db	AGATCACC 1	AGATCACC 1
Db	8	AGATCACC 1
RESULT 252		
US-08-859-954-205		
Sequence 205, Application US/08859954		
Patent No. 6083695		
GENERAL INFORMATION:		
APPLICANT: Hardin, Susan H.		
APPLICANT: Homayouni, Ramin		
APPLICANT: Hardin, Paul E.		
TITLE OF INVENTION: Design and Optimized Primer Library for		
NUMBER OF SEQUENCES: 566		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: Fulbright & Jaworski L.L.P.		
STREET: 1301 McKinney, Suite 5100		
CITY: Houston		
STATE: Texas		
COUNTRY: U.S.A.		
ZIP: 77010-3095		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: Patent In Release #1.0, Version #1.30		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/859,954		
FILING DATE:		
CLASSIFICATION:		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: 08/632,782		
FILING DATE:		
ATTORNEY/AGENT INFORMATION:		
NAME: Paul, Thomas D.		
REGISTRATION NUMBER: 32,714		
REFERENCE/DOCKET NUMBER: D-5900		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 713/651-5325		
TELEFAX: 713/651-5246		
INFORMATION FOR SEQ ID NO: 205:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 8 base pairs		
TYPE: nucleic acid		
STRANDEDNESS: single		
TOPOLOGY: linear		
MOLECULE TYPE: other nucleic acid		
DESCRIPTION: /desc = "oligonucleotide"		
HYPOTHETICAL: YES		
ANTI-SENSE: YES		
US-08-859-954-375		
Query Match	29.1%	Score 6.4; DB 1; Length 8;
Best Local Similarity	87.5%	Pred. No. 7e+02;
Matches	7;	Conservative 0; Mismatches 1; Indels 0;
Qy	735	GAACACAGA 742
Db	1	GAGACAGA 8
RESULT 253		
US-08-859-954-375		
Sequence 375, Application US/08859954		
Patent No. 6083695		
GENERAL INFORMATION:		
APPLICANT: Hardin, Susan H.		
APPLICANT: Homayouni, Ramin		
APPLICANT: Hardin, Paul E.		
TITLE OF INVENTION: Design and Optimized Primer Library for		
NUMBER OF SEQUENCES: 566		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: Fulbright & Jaworski L.L.P.		
STREET: 1301 McKinney, Suite 5100		
CITY: Houston		
STATE: Texas		
COUNTRY: U.S.A.		
ZIP: 77010-3095		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: Patent In Release #1.0, Version #1.30		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/859,954		
FILING DATE:		
CLASSIFICATION:		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: 08/632,782		
FILING DATE:		
ATTORNEY/AGENT INFORMATION:		
NAME: Paul, Thomas D.		
REGISTRATION NUMBER: 32,714		
REFERENCE/DOCKET NUMBER: D-5900		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 713/651-5325		
TELEFAX: 713/651-5246		
INFORMATION FOR SEQ ID NO: 205:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 8 base pairs		
TYPE: nucleic acid		
STRANDEDNESS: single		
TOPOLOGY: linear		
MOLECULE TYPE: other nucleic acid		
DESCRIPTION: /desc = "oligonucleotide"		
HYPOTHETICAL: YES		
ANTI-SENSE: YES		
US-08-859-954-205		
Query Match	29.1%	Score 6.4; DB 1; Length 8;
Best Local Similarity	87.5%	Pred. No. 7e+02;
Matches	7;	Conservative 0; Mismatches 1; Indels 0;
Qy	735	GAACACAGA 742
Db	1	GAGACAGA 8
RESULT 254		
US-08-711-417C-117		
Sequence 117, Application US/08711417C		
Patent No. 6228611		
GENERAL INFORMATION:		
APPLICANT: Georgopoulos, Katia A.		
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE		
NUMBER OF SEQUENCES: 202		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: Fish & Richardson P.C.		
STREET: 225 Franklin Street		
CITY: Boston		
STATE: MA		
COUNTRY: USA		
ZIP: 02110-2804		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Diskette		
COMPUTER: IBM Compatible		
OPERATING SYSTEM: Windows 95		
SOFTWARE: FastSeq for Windows Version 2.0b		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/711,417C		
FILING DATE: 05-Sep-1996		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: 08/238,212		
FILING DATE: 02-MAY-1994		

```
;
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-08-711-417C-117

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
DB 1 AGGGGAAA 8

RESULT 255
PCT-US93-08743-117
; Sequence 117, Application PC/TUS9308743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08743
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US93-08743-117

Query Match 29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
DB 1 AGGGGAAA 8

RESULT 257
US-08-088-658-5
; Sequence 5, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M. Illegard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
```

STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 19930702
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,363
FILING DATE: 26-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-088-658-5

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAA 738
DB 1 AAGAGAA 8

RESULT 258
US-08-410-779B-28/c
Sequence 28, Application US/08410779B
Patent No. 5814517
GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
STREET: 9393 TOWNE CENTRE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,779B
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/228,935
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: JURGENSEN, THOMAS E
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0013A.US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 550-7675
TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
SYNTHETIC DNA"
US-08-410-779B-28

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGA 734
DB 9 TTCCAGGA 2

RESULT 259
US-08-465-590-126
Sequence 126, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-590-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 CGAGAAC 739
|||||
Db 1 CGAGAAC 8

RESULT 260

US-08-605-163-7/c
; Sequence 7, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-605-163-7

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
|||||
Db 8 CAGAGCAC 1

RESULT 261

US-08-605-163-18/c
; Sequence 18, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These

; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-605-163-18

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
|||||
Db 8 CAGAGCAC 1

RESULT 262

US-08-471-907A-5
; Sequence 5, Application US/08471907A
; Patent No. 5986053
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M. Ilegard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,907A


```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/088,658
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-471-907A-5

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAA 738
Db 1 AAGAGAAA 8

RESULT 263
US-08-461-607-21/c
; Sequence 21, Application US/08461607
; Patent No. 6054633
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Stanbrook, Peter J.
; TITLE OF INVENTION: Live Animal Mutagenesis Systems for
; TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,607
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,105
; FILING DATE:
; APPLICATION NUMBER: US 07/874,974
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..9
; OTHER INFORMATION: /note="This sequence represents
; OTHER INFORMATION: mutation of base 2486 of Seq Id No. 60546333"
US-08-461-607-21

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAG 735
Db 8 GCCAGCAG 1

RESULT 264
US-08-711-417C-126
; Sequence 126, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-08-711-417C-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAAAC 739
Db 1 GGAGGAAC 8

```

```

; TITLE OF INVENTION: KNOWN AND NOVEL MEMBERS OF GENE FAMILIES
; FILE REFERENCE: VCUIP4B
; CURRENT APPLICATION NUMBER: US/09/163,485
; CURRENT FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide, consensus sequence from human
; OTHER INFORMATION: matrix metalloproteinases
; US-09-163-485-23

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. NO. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGAGAAA 738
Db 1 AGAGGAA 8

RESULT 267
US-09-327-138C-13
; Sequence 13, Application US/09327138C
; Patent No. 6541244
; GENERAL INFORMATION:
; APPLICANT: AUERNHAMMER, CHRISTOPH J.
; TITLE OF INVENTION: SUPPRESSOR OF CYTOKINE SIGNALING
; TITLE OF INVENTION: (SOCS)-3 PROMOTER AND METHODS FOR ITS USE IN GENETIC THERAPY
; FILE REFERENCE: P07 42591 (18810-803)
; CURRENT APPLICATION NUMBER: US/09/327,138C
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (-74)...(-66)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (0)...(0)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO 66
; US-09-327-138C-13

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. NO. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGA 734
Db 1 TTCCAGGA 8

RESULT 268
US-09-989-789-530/c
; Sequence 530, Application US/09989789
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
```

```

; TITLE OF INVENTION: Live Animal Mutagenesis Systems for
; TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/363,600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,607
; FILING DATE:
; APPLICATION NUMBER: US 07/874,974
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..9
; OTHER INFORMATION: /note= "This sequence represents
; OTHER INFORMATION: mutation of base 2486 of Seq Id No. 62325243"
; US-09-363-600-21

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. NO. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
Db 8 GCCAGCAG 1

RESULT 266
US-09-163-485-23
; Sequence 23, Application US/09163485
; Patent No. 6277571
; GENERAL INFORMATION:
; APPLICANT: FILMORE, HELEN
; APPLICANT: BROADBUDS, WILLIAM
; APPLICANT: GILLIES, GEORGE
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
```

```
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 530
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-530

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      729 CCAGGAGA 736
      |||||
Db      8 CCAGCAGA 1

RESULT 269
US-09-989-789-2021
; Sequence 2021, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2021
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2021

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      730 CAGGAGAA 737
      |||||
Db      1 CAGGAAAA 8

RESULT 270
US-09-989-789-2022
; Sequence 2022, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2022
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; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2022

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      730 CAGGAGAA 737
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Db      1 CAGGAAAA 8

RESULT 271
US-09-989-789-2401
; Sequence 2401, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2401
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2401

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      731 AGGAGAAA 738
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Db      2 AGGAAAAA 9

RESULT 272
US-09-989-789-2402
; Sequence 2402, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2402
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2402

Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 2 AGGAGAAA 9

RESULT 273
US-09-989-789-2403
; Sequence 2403, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2403
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2403

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
Db 2 AGGAGAAA 9

RESULT 274
US-09-723-909-126
; Sequence 126, Application US/09723909
; Patent No. 6630141
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,909
; FILING DATE: 28-NOV-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417
; FILING DATE: 05-SEP-1996
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-723-909-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGGAAC 739
Db 1 GGAGGAAC 8

RESULT 275
PCT-US93-08743-126
; Sequence 126, Application PC/TUS9308743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08743
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-08743-126

Query Match 29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGGAAC 739
Db 1 GGAGGAAC 8

RESULT 276
PCT-US95-0477-28/c
; Sequence 28, Application PC/TUS950477
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
PCT-US95-04477-28

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Query Match      29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 727 TGCCAGGA 734
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Db 9 TTCCAGGA 2

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Search completed: October 18, 2004, 14:09:44
Job time : 1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:11:18 ; Search time 0.001 Seconds
(without alignments)
165.484 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tgcagagagaacagacacg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 286 seqs, 3761 residues

Total number of hits satisfying chosen parameters: 572

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 286 summaries

Database : rnpb1-727.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	16.4	74.5	22	1	US-10-321-039-633	Sequence 633, App
3	15.4	70.0	18	1	US-09-736-084-45	Sequence 45, Appl
4	15	68.2	18	1	US-10-453-792-274	Sequence 274, App
5	14.6	66.4	22	1	US-10-270-258-7	Sequence 7, Appli
6	14.6	66.4	22	1	US-10-270-258-11	Sequence 11, Appl
7	14.6	66.4	22	1	US-10-270-258-17	Sequence 17, Appl
8	14.2	64.5	21	1	US-09-904-368A-29	Sequence 29, Appl
9	14	63.6	18	1	US-10-453-792-276	Sequence 276, App
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11	13.4	60.9	18	1	US-10-453-792-272	Sequence 272, App
12	13.4	60.9	18	1	US-10-453-792-273	Sequence 273, App
13	12.8	58.2	17	1	US-10-060-756A-1254	Sequence 1254, App
14	12.8	58.2	17	1	US-10-060-756A-1255	Sequence 1255, App
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19	12.4	56.4	19	1	US-09-998-533-28	Sequence 28, Appl
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21	12	54.5	17	1	US-10-676-154-188	Sequence 188, App
22	11.8	53.6	17	1	US-09-877-478-169	Sequence 169, App
23	11.8	53.6	17	1	US-09-877-478-170	Sequence 170, App
24	11.8	53.6	17	1	US-09-877-478-178	Sequence 178, App
25	11.8	53.6	17	1	US-10-342-902-169	Sequence 169, App
26	11.8	53.6	17	1	US-10-342-902-170	Sequence 170, App
27	11.8	53.6	17	1	US-10-342-902-878	Sequence 878, App
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32	11.8	53.6	17	1	US-10-339-793-241	Sequence 241, App
33	11.8	53.6	17	1	US-10-138-674-9242	Sequence 9242, App

17	1	US-10-287-949A-9242	Sequence 9242, App
17	1	US-10-669-841-169	Sequence 169, App
17	1	US-10-669-841-170	Sequence 170, App
17	1	US-10-669-841-878	Sequence 878, App
18	1	US-08-911-824-42	Sequence 42, Appl
18	1	US-10-453-792-289	Sequence 289, App
18	1	US-10-453-792-271	Sequence 271, App
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12	1	US-10-146-058-125	Sequence 125, App
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15	1	US-09-504-231A-715	Sequence 715, App
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15	1	US-09-274-553D-715	Sequence 715, App
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14	1	US-09-504-231A-1341	Sequence 1341, App
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14	1	US-10-146-058-126	Sequence 126, App
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12	1	US-10-100-957A-73	Sequence 73, Appl
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14	1	US-10-073-377-32	Sequence 32, Appl
14	1	US-10-073-377-39	Sequence 39, Appl
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14	1	US-10-146-058-35	Sequence 35, Appl
10	1	US-10-033-145-1787	Sequence 1787, App
10	1	US-10-033-145-1921	Sequence 1921, App
11	1	US-10-450-797-167	Sequence 167, App
12	1	US-09-288-959-843	Sequence 843, App
12	1	US-10-100-957A-61	Sequence 61, Appl
12	1	US-10-100-957A-75	Sequence 75, Appl
12	1	US-09-981-803-47	Sequence 47, Appl
12	1	US-10-275-071-28	Sequence 28, Appl
12	1	US-10-091-281-393	Sequence 393, App
12	1	US-10-684-830-34	Sequence 34, Appl
12	1	US-10-684-830-37	Sequence 37, Appl

C 107	8.8	40.0	13	1	US-09-152-059-3	Sequence 3, Appl	C 180	8.4	38.2	10	1	US-10-330-627-1363	Sequence 1363, Ap
C 108	8.8	40.0	13	1	US-09-152-059-4	Sequence 4, Appl	C 181	8.4	38.2	10	1	US-10-434-479-47	Sequence 47, Appl
C 109	8.8	40.0	13	1	US-09-152-059-5	Sequence 5, Appl	C 182	8.4	38.2	11	1	US-10-450-797-47	Sequence 47, Appl
C 110	8.8	40.0	13	1	US-09-152-059-6	Sequence 6, Appl	C 183	8.4	38.2	11	1	US-10-450-797-332	Sequence 532, App
C 111	8.8	40.0	13	1	US-09-152-059-7	Sequence 7, Appl	C 184	8.4	38.2	11	1	US-10-450-797-537	Sequence 537, App
C 112	8.8	40.0	13	1	US-09-152-059-8	Sequence 8, Appl	C 185	8.4	38.2	11	1	US-10-450-797-613	Sequence 613, App
C 113	8.8	40.0	13	1	US-09-152-059-9	Sequence 9, Appl	C 186	8.4	38.2	11	1	US-10-450-797-741	Sequence 741, App
C 114	8.8	40.0	13	1	US-09-152-059-28	Sequence 28, Appl	C 187	8.4	38.2	12	1	US-09-179-536B-81	Sequence 81, Appl
C 115	8.8	40.0	13	1	US-09-152-059-29	Sequence 29, Appl	C 188	8.4	38.2	12	1	US-09-179-536B-86	Sequence 86, Appl
C 116	8.8	40.0	13	1	US-09-152-059-30	Sequence 30, Appl	C 189	8.4	38.2	12	1	US-09-263-959-477	Sequence 477, App
C 117	8.8	40.0	13	1	US-09-152-059-31	Sequence 31, Appl	C 190	8.4	38.2	12	1	US-09-263-959-492	Sequence 492, App
C 118	8.8	40.0	13	1	US-09-152-059-32	Sequence 32, Appl	C 191	8.4	38.2	12	1	US-09-263-959-755	Sequence 755, App
C 119	8.8	40.0	13	1	US-09-152-059-43	Sequence 43, Appl	C 192	8.4	38.2	12	1	US-09-263-959-850	Sequence 850, App
C 120	8.8	40.0	13	1	US-09-152-059-44	Sequence 44, Appl	C 193	8.4	38.2	12	1	US-09-845-938A-4	Sequence 4, Appl
C 121	8.8	40.0	13	1	US-09-152-059-46	Sequence 46, Appl	C 194	8.4	38.2	12	1	US-09-845-938A-7	Sequence 7, Appl
C 122	8.8	40.0	13	1	US-09-152-059-47	Sequence 47, Appl	C 195	8.4	38.2	12	1	US-09-845-938A-81	Sequence 81, Appl
C 123	8.8	40.0	13	1	US-09-152-059-48	Sequence 48, Appl	C 196	8.4	38.2	12	1	US-09-297-576A-86	Sequence 86, Appl
C 124	8.8	40.0	13	1	US-09-152-059-71	Sequence 71, Appl	C 197	8.4	38.2	12	1	US-10-164-875C-3	Sequence 3, Appl
C 125	8.8	40.0	13	1	US-09-152-059-74	Sequence 74, Appl	C 198	8.4	38.2	12	1	US-10-164-875C-5	Sequence 5, Appl
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C 127	8.8	40.0	13	1	US-09-781-811-23	Sequence 23, Appl	C 200	8.4	38.2	12	1	US-10-661-165-433	Sequence 222, App
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C 130	8.8	40.0	13	1	US-10-008-029-3	Sequence 3, Appl	C 203	8	36.4	10	1	US-10-329-465-139	Sequence 139, App
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C 132	8.8	40.0	13	1	US-10-008-029-5	Sequence 5, Appl	C 205	8	36.4	10	1	US-10-330-627-77	Sequence 26, Appl
C 133	8.8	40.0	13	1	US-10-008-029-6	Sequence 6, Appl	C 206	8	36.4	10	1	US-10-330-627-77	Sequence 79, Appl
C 134	8.8	40.0	13	1	US-10-008-029-7	Sequence 7, Appl	C 207	8	36.4	10	1	US-10-330-627-77	Sequence 77, Appl
C 135	8.8	40.0	13	1	US-10-008-029-8	Sequence 8, Appl	C 208	8	36.4	10	1	US-10-330-627-85	Sequence 85, Appl
C 136	8.8	40.0	13	1	US-10-008-029-9	Sequence 9, Appl	C 209	8	36.4	10	1	US-10-330-627-85	Sequence 85, Appl
C 137	8.8	40.0	13	1	US-10-008-029-28	Sequence 28, Appl	C 210	8	36.4	10	1	US-10-330-627-1321	Sequence 1321, Ap
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C 139	8.8	40.0	13	1	US-10-008-029-30	Sequence 30, Appl	C 212	8	36.4	11	1	US-09-828-211A-8	Sequence 8, Appl
C 140	8.8	40.0	13	1	US-10-008-029-31	Sequence 31, Appl	C 213	8	36.4	11	1	US-09-918-715-65	Sequence 65, Appl
C 141	8.8	40.0	13	1	US-10-008-029-32	Sequence 32, Appl	C 214	8	36.4	11	1	US-10-266-138B-6	Sequence 6, Appl
C 142	8.8	40.0	13	1	US-10-008-029-43	Sequence 43, Appl	C 215	8	36.4	11	1	US-10-055-728-27	Sequence 27, Appl
C 143	8.8	40.0	13	1	US-10-008-029-46	Sequence 46, Appl	C 216	8	36.4	11	1	US-10-265-509B-6	Sequence 6, Appl
C 144	8.8	40.0	13	1	US-10-008-029-46	Sequence 46, Appl	C 217	8	36.4	11	1	US-10-310-677-27	Sequence 27, Appl
C 145	8.8	40.0	13	1	US-10-008-029-48	Sequence 48, Appl	C 218	8	36.4	11	1	US-10-450-797-452	Sequence 452, App
C 146	8.8	40.0	13	1	US-10-008-029-48	Sequence 48, Appl	C 219	8	36.4	11	1	US-10-450-797-714	Sequence 714, App
C 147	8.8	40.0	13	1	US-10-008-029-74	Sequence 74, Appl	C 220	8	36.4	11	1	US-10-450-797-1387	Sequence 1387, Ap
C 148	8.8	40.0	13	1	US-10-008-029-77	Sequence 77, Appl	C 221	8	36.4	11	1	US-10-723-940-88	Sequence 88, Appl
C 149	8.8	40.0	13	1	US-10-008-029-77	Sequence 77, Appl	C 222	8	36.4	12	1	US-09-765-061B-30	Sequence 30, Appl
C 150	8.8	40.0	13	1	US-10-208-650-3	Sequence 3, Appl	C 223	7.8	35.5	11	1	US-09-245-155-39	Sequence 49, Appl
C 151	8.8	40.0	13	1	US-10-208-650-4	Sequence 4, Appl	C 224	7.8	35.5	11	1	US-09-918-715-49	Sequence 63, Appl
C 152	8.8	40.0	13	1	US-10-208-650-5	Sequence 5, Appl	C 225	7.8	35.5	11	1	US-10-620-514-6	Sequence 73, Appl
C 153	8.8	40.0	13	1	US-10-208-650-6	Sequence 6, Appl	C 226	7.8	35.5	11	1	US-10-314-322-73	Sequence 297, App
C 154	8.8	40.0	13	1	US-10-208-650-7	Sequence 7, Appl	C 227	7.8	35.5	11	1	US-10-450-797-297	Sequence 1044, Ap
C 155	8.8	40.0	13	1	US-10-208-650-8	Sequence 8, Appl	C 228	7.8	35.5	11	1	US-09-365-029-21	Sequence 21, Appl
C 156	8.8	40.0	13	1	US-10-208-650-9	Sequence 9, Appl	C 229	7.8	35.5	12	1	US-09-804-481-9	Sequence 9, Appl
C 157	8.8	40.0	13	1	US-10-208-650-28	Sequence 28, Appl	C 230	7.8	35.5	12	1	US-09-828-034-24	Sequence 24, Appl
C 158	8.8	40.0	13	1	US-10-208-650-29	Sequence 29, Appl	C 231	7.8	35.5	12	1	US-09-828-034-24	Sequence 65, Appl
C 159	8.8	40.0	13	1	US-10-208-650-30	Sequence 30, Appl	C 232	7.8	35.5	12	1	US-10-100-957A-65	Sequence 3, Appl
C 160	8.8	40.0	13	1	US-10-208-650-31	Sequence 31, Appl	C 233	7.8	35.5	12	1	US-10-073-377-3	Sequence 4, Appl
C 161	8.8	40.0	13	1	US-10-208-650-32	Sequence 32, Appl	C 234	7.8	35.5	12	1	US-10-073-377-4	Sequence 359, App
C 162	8.8	40.0	13	1	US-10-208-650-43	Sequence 43, Appl	C 235	7.8	35.5	12	1	US-10-211-088-359	Sequence 41, Appl
C 163	8.8	40.0	13	1	US-10-208-650-44	Sequence 44, Appl	C 236	7.8	35.5	12	1	US-10-273-334-41	Sequence 14, Appl
C 164	8.8	40.0	13	1	US-10-208-650-46	Sequence 46, Appl	C 237	7.8	35.5	12	1	US-10-427-629-14	Sequence 13, Appl
C 165	8.8	40.0	13	1	US-10-208-650-47	Sequence 47, Appl	C 238	7.4	33.6	9	1	US-10-455-101-13	Sequence 14, Appl
C 166	8.8	40.0	13	1	US-10-208-650-47	Sequence 47, Appl	C 239	7.4	33.6	10	1	US-10-283-741-14	Sequence 14, Appl
C 167	8.8	40.0	13	1	US-10-208-650-71	Sequence 71, Appl	C 240	7.4	33.6	10	1	US-09-910-469-55	Sequence 55, Appl
C 168	8.8	40.0	13	1	US-10-208-650-71	Sequence 71, Appl	C 241	7.4	33.6	10	1	US-09-910-469-56	Sequence 56, Appl
C 169	8.8	40.0	13	1	US-10-208-650-77	Sequence 77, Appl	C 242	7.4	33.6	10	1	US-10-293-232-212	Sequence 212, App
C 170	8.8	40.0	13	1	US-10-091-281-199	Sequence 199, App	C 243	7.4	33.6	10	1	US-10-033-145-75	Sequence 75, Appl
C 171	8.8	40.0	13	1	US-10-194-882-5	Sequence 5, Appl	C 244	7.4	33.6	10	1	US-10-033-145-196	Sequence 196, App
C 172	8.6	39.1	13	1	US-10-073-377-8	Sequence 8, Appl	C 245	7.4	33.6	10	1	US-10-033-145-236	Sequence 236, App
C 173	8.4	38.2	10	1	US-10-033-145-331	Sequence 331, App	C 246	7.4	33.6	10	1	US-10-033-145-339	Sequence 339, App
C 174	8.4	38.2	10	1	US-10-033-145-1175	Sequence 1175, Ad	C 247	7.4	33.6	10	1	US-10-033-145-373	Sequence 373, App
C 175	8.4	38.2	10	1	US-10-033-145-1215	Sequence 1215, Ap	C 248	7.4	33.6	10	1	US-10-033-145-595	Sequence 595, App
C 176	8.4	38.2	10	1	US-10-390-045-47	Sequence 47, Appl	C 249	7.4	33.6	10	1	US-10-033-145-780	Sequence 780, App
C 177	8.4	38.2	10	1	US-10-330-627-834	Sequence 834, App	C 250	7.4	33.6	10	1	US-10-033-145-794	Sequence 794, App
C 178	8.4	38.2	10	1	US-10-330-627-834	Sequence 834, App	C 251	7.4	33.6	10	1	US-10-033-145-813	Sequence 813, App
C 179	8.4	38.2	10	1	US-10-330-627-1293	Sequence 1293, App	C 252	7.4	33.6	10	1	US-10-033-145-835	Sequence 835, App

c 253 7.4 33.6 10 1 US-10-033-145-1342 Sequence 1342, Ap
254 7.4 33.6 10 1 US-10-033-145-1396 Sequence 1396, Ap
255 7.4 33.6 10 1 US-10-033-145-1419 Sequence 1419, Ap
256 7.4 33.6 10 1 US-10-033-145-1496 Sequence 1496, Ap
257 7.4 33.6 10 1 US-10-033-145-1773 Sequence 1773, Ap
258 7.4 33.6 10 1 US-10-033-145-1999 Sequence 1999, Ap
259 7.4 33.6 10 1 US-10-010-802-261 Sequence 261, Ap
260 7.4 33.6 10 1 US-10-010-802-287 Sequence 287, Ap
261 7.4 33.6 10 1 US-10-176-464A-59 Sequence 59, Ap
262 7.4 33.6 10 1 US-10-329-465-95 Sequence 95, Ap
263 7.4 33.6 10 1 US-10-330-627-238 Sequence 238, Ap
264 7.4 33.6 10 1 US-10-330-627-399 Sequence 399, Ap
265 7.4 33.6 10 1 US-10-193-507-79 Sequence 79, Ap
266 7.4 33.6 10 1 US-09-735-363A-82 Sequence 82, Ap
267 7.4 33.6 10 1 US-09-249-155-86 Sequence 86, Ap
268 7.4 33.6 10 1 US-09-249-155-124 Sequence 124, Ap
269 7.4 33.6 10 1 US-09-918-715-66 Sequence 66, Ap
270 7.4 33.6 10 1 US-10-191-302-8 Sequence 8, Ap
271 7.4 33.6 10 1 US-10-314-322-86 Sequence 86, Ap
272 7.4 33.6 10 1 US-10-314-322-124 Sequence 124, Ap
273 7.4 33.6 10 1 US-10-612-224-71 Sequence 71, Ap
274 7.4 33.6 10 1 US-10-450-797-51 Sequence 51, Ap
275 7.4 33.6 10 1 US-10-450-797-110 Sequence 110, Ap
276 7.4 33.6 10 1 US-10-450-797-284 Sequence 284, Ap
277 7.4 33.6 10 1 US-10-450-797-285 Sequence 285, Ap
278 7.4 33.6 10 1 US-10-450-797-335 Sequence 335, Ap
279 7.4 33.6 10 1 US-10-450-797-538 Sequence 538, Ap
280 7.4 33.6 10 1 US-10-450-797-626 Sequence 626, Ap
281 7.4 33.6 10 1 US-10-450-797-662 Sequence 662, Ap
282 7.4 33.6 10 1 US-10-450-797-681 Sequence 681, Ap
283 7.4 33.6 10 1 US-10-450-797-1118 Sequence 1118, Ap
284 7.4 33.6 10 1 US-10-450-797-1280 Sequence 1280, Ap
285 7.4 33.6 10 1 US-10-450-797-1286 Sequence 1286, Ap
286 7.4 33.6 10 1 US-10-450-797-1320 Sequence 1320, Ap

ALIGNMENTS

RESULT 1
US-10-409-107A-1
; Sequence 1, Application US/10409107A
; Publication No. US20040053288A1
; GENERAL INFORMATION:
; APPLICANT: YANAI, Yoshiaki
; APPLICANT: YAMAMOTO, Shigeto
; APPLICANT: YAMAMOTO, Kozo
; APPLICANT: IKEGAMI, Hakuo
; TITLE OF INVENTION: Method for estimating therapeutic efficacy of tumor necrosis
; TITLE OF INVENTION: factor
; FILE REFERENCE: YANAI=3
; CURRENT APPLICATION NUMBER: US/10/409,107A
; PRIOR FILING DATE: 2003-04-19
; PRIOR FILING DATE: 2003-04-19
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of TNF-R55 mRNA
US-10-409-107A-1

Query Match 90.9%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 727 TGCCAGGAGAAACAGAAC 746
|||||
Db 3 TGCCAGGAGAAACAGAAC 22

RESULT 2
US-10-321-039-633
; Sequence 633, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Jurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 633
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-633

Query Match 74.5%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 8.8; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1

QY 727 TGCCAGGAGAAACAGAAC 744
|||||
Db 5 TGCCAGGAGACACAGAAC 22

RESULT 3
US-09-736-084-45/c
; Sequence 45, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,084
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. US20020107211A1
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.


```
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-270-258-11

Query Match      66.4%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 727 TGCAGGAGAAACAGAACAC 747
Db 22 TCCAGAAGACACAGAGACC 2

RESULT 7
US-10-270-258-17/c
; Sequence 17, Application US/10270258
; Publication No. US20030148951A1
; GENERAL INFORMATION:
; APPLICANT: Hsi-Hsien, Lin
; APPLICANT: Gordon, Siamon
; APPLICANT: McKnight, Andrew J.
; APPLICANT: Stacey, Martin
; APPLICANT: Isis Innovation Limited
; TITLE OF INVENTION: Human EMR2, A G-Protein Coupled Receptor from the EGF-TM7 Family
; FILE REFERENCE: 1365.061US1
; CURRENT APPLICATION NUMBER: US/10/270,258
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: PCT/GB01/01729
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: GB 0009181.9
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-270-258-17

Query Match      66.4%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 727 TGCAGGAGAAACAGAACAC 747
Db 22 TCCAGAAGACACAGAGACC 2

RESULT 8
US-09-904-968A-29
; Sequence 29, Application US/09904968A
; Publication No. US2003008289A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHADDEKITCHARON, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
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; FEATURE:
; OTHER INFORMATION: PCR primer 5F1
US-09-904-968A-29

Query Match      64.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAACAC 746
Db 3 GCCAGGAGAGCAGAACCC 21

RESULT 9
US-10-453-792-276/c
; Sequence 276, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-453-792-276

Query Match      63.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAACAG 5
```

```
RESULT 10
US-10-453-792-270/c
; Sequence 270, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 04-Jun-2003
; APPLICATION NUMBER: US/10/453,792
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 270:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-10-453-792-270

Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
Db 18 GCCAAGAGAAACAGA 4

RESULT 11
US-10-453-792-272/c
; Sequence 272, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-453-792-272

Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
Db 18 GCCATGAGAAACAGA 4

RESULT 12
US-10-453-792-273/c
; Sequence 273, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-10-453-792-273

Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACACA 742
Db 18 GCCAGGAGAAACGGA 4
|||||

RESULT 13
US-10-060-756A-1254/c
; Sequence 1254, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1254
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1254

Query Match 58.2%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACACA 742
Db 17 TGCCAGGAGAAACACA 2
|||||

RESULT 14
US-10-060-756A-1255/c
; Sequence 1255, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1255
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1255

Query Match 58.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACACA 742
Db 16 TGCCAGGAGAAACACA 1
|||||

RESULT 15
US-10-060-756A-1256/c
; Sequence 1256, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/327,898
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Aecmica Sequence Listing Engine
 ; SEQ ID NO 1256
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-060-756A-1256

Query Match 56.4%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 32;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACA 740
 Db 15 TGCCAGGTGAAACA 2

RESULT 16
 US-10-060-756A-1257/c
 ; Sequence 1257, Application US/10060756A
 ; Publication No. US20030046717A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Jian
 ; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
 ; FILE REFERENCE: PB0177
 ; CURRENT APPLICATION NUMBER: US/10/060,756A
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/327,898
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Aecmica Sequence Listing Engine
 ; SEQ ID NO 1257
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-060-756A-1257

Query Match 56.4%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 32;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACA 740
 Db 14 TGCCAGGTGAAACA 1

RESULT 17
 US-10-453-792-275/c
 ; Sequence 275, Application US/10453792
 ; Publication No. US20040029110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STUYVER, LIEVEN
 ; ROSSAU, RUDI
 ; MAERTENS, GEERT
 ; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION NUMBER: US/10/453,792
 ; FILING DATE: 04-Jun-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/155,885A
 ; FILING DATE: 08-Oct-1998
 ; APPLICATION NUMBER: PCT/EP97/02002
 ; FILING DATE: 21-APR-1997
 ; APPLICATION NUMBER: EP 96870053.4
 ; FILING DATE: 19-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/POCKET NUMBER: 2551-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 275:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEetical: NO
 ; ANTI-SENSE: NO
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 275:
 US-10-453-792-275

Query Match 56.4%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 33;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
 Db 18 GCCAGGAGAAACGG 5

RESULT 18
 US-10-453-792-278/c
 ; Sequence 278, Application US/10453792
 ; Publication No. US20040029110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STUYVER, LIEVEN
 ; ROSSAU, RUDI
 ; MAERTENS, GEERT
 ; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
 ; NUMBER OF SEQUENCES: 313
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 278:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 278:
US-10-453-792-278

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 33;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAG 741
Db 18 GCCATGAGAAACAG 5

RESULT 19

US-09-898-533-28/c
Sequence 28, Application US/09898533
Patent No. US20020106656A1
GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC9, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
FILE REFERENCE: 93445-00004
CURRENT APPLICATION NUMBER: US/09/898,533
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US/09/268,140
PRIOR FILING DATE: 2000-03-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-898-533-28

Query Match 56.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 34;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACA 740
Db 16 TGCCAGGAGAAACA 3

RESULT 20

US-10-349-143-4649/c

Sequence 4649, Application US/10349143
Publication No. US2004000584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4649
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
US-10-349-143-4649

Query Match 55.5%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAACACC 747
Db 17 AGGAGAAACAGAGGAAC 1

RESULT 21

US-10-676-154-188/c
Sequence 188, Application US/10676154
Publication No. US20040081996A1
GENERAL INFORMATION:
APPLICANT: John Landers
APPLICANT: David Houseman
APPLICANT: Barbara Jordan
APPLICANT: Alain Charest
TITLE OF INVENTION: Methods and Products Related to
FILE REFERENCE: M0656/7045 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/676,154
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US 60/101,757
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22283
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 691
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 188
LENGTH: 17
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-676-154-188

Query Match 54.5%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 13 AAACAGAACACC 2

```
RESULT 22
US-09-877-478-169/c
; Sequence 169, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 17 GCCAAGAGAAACGGA 3

RESULT 23
US-09-877-478-170/c
; Sequence 170, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 17 GCCAAGAGAAACGGA 3

RESULT 24
US-09-877-478-878/c
; Sequence 878, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 878
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-878

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 15 GCCAAGAGAAACGGA 1

RESULT 25
US-10-342-902-169/c
; Sequence 169, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
```


APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 169
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
||| ||||| ||
Db 17 GCCAAGAGAAACGGA 3

RESULT 26
US-10-342-902-170/c
Sequence 170, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 170
LENGTH: 17
TYPE: RNA

ORGANISM: Hepatitis B virus
US-10-342-902-170
Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
||| ||||| ||
Db 16 GCCAAGAGAAACGGA 2

RESULT 27
US-10-342-902-878/c
Sequence 878, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 878
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-878
Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
||| ||||| ||
Db 15 GCCAAGAGAAACGGA 1

RESULT 28
US-10-060-756A-1253/c
Sequence 1253, Application US/10060756A
Publication No. US20030046717A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 1253
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1253

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACACA 742
||||| |||||
DB 17 GCCAGGTGAACACA 3

RESULT 29
US-10-156-306-4512/c
; Sequence 4512, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4512
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-4512

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
||||| |||||
DB 17 TCCAGGAGAAACAG 3

RESULT 30
US-10-156-306-5193/c
; Sequence 5193, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5193
; LENGTH: 17
; TYPE: RNA

; ORGANISM: Homo sapiens
US-10-156-306-5193

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
||||| |||||
DB 16 TCCAGGAGAAACAG 2

RESULT 31
US-10-156-306-5194/c
; Sequence 5194, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5194
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5194

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
||||| |||||
DB 15 TCCAGGAGAAACAG 1

RESULT 32
US-10-339-793-241
; Sequence 241, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-241

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCAGGAGAAACAG 741
||||| |||||
DB 3 TCCAGGAGAAATCAG 17

RESULT 33
US-10-138-674-9242/c
; Sequence 9242, Application US/10138674

```
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9242
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-9242

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGACACCG 748
Db 17 AGAAACAGACACCG 3

RESULT 34
US-10-287-949A-9242/c
; Sequence 9242, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9242
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-9242

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGACACCG 748
Db 17 AGAAACAGACACCG 3

RESULT 35
US-10-669-841-169/c
; Sequence 169, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
```

```
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 169
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-169

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGAGAAACAGA 742
Db 17 GCCAGAGAAACCGA 3

RESULT 36
US-10-669-841-170/c
; Sequence 170, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
```

```
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-170

Query Match      53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
DB 16 GCCAGGAGAAACGGA 2

RESULT 37
US-10-669-841-878/c
; Sequence 878, Application US/10669841
; Publication No. US2004012746A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCI/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 878
; LENGTH: 17
```

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; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-878

Query Match      53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
DB 15 GCCAGGAGAAACGGA 1

RESULT 38
US-08-911-824-42
; Sequence 42, Application US/08911824
; Publication No. US20030004323A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Hackett, John R., Jr.
; APPLICANT: Yamaguchi, Julie
; APPLICANT: Golden, Alan M.
; APPLICANT: Brennan, Catherine A.
; APPLICANT: Hickman, Robert K.
; APPLICANT: Devare, Sushil G.
; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
; FILE REFERENCE: 6165 US 01
; CURRENT APPLICATION NUMBER: US/08/911,824
; CURRENT FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; OTHER INFORMATION: PCR Primer 41sy-3
US-08-911-824-42

Query Match      53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
DB 3 CAGCAGGAGAAACAGAAC 17

RESULT 39
US-10-453-792-269/c
; Sequence 269, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
```

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/ REFERENCE/DOCKET NUMBER: 2551-5
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 816-4000
/ TELEFAX: (703) 816-4100
/ INFORMATION FOR SEQ ID NO: 271:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 271:
/
/ US-10-453-792-271
/
Query Match          53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
QY      728 GCCAGGAGAAACGAGA 742
Db      18 GCCATGGAACGGA 4
/
RESULT 41
US-08-841-636A-40
/ Sequence 40, Application US/08841636A
/ Publication No. US20020168751A1
/ GENERAL INFORMATION:
/ APPLICANT: Miettinen-Oinonen, Arja
/ APPLICANT: Londeborough, John
/ APPLICANT: Vehmaanper Jari
/ APPLICANT: Haakana, Heli
/ APPLICANT: M ntyl , Arja
/ APPLICANT: Lantto, Raija
/ APPLICANT: Elovainio, Minna
/ APPLICANT: Joutsjoki, Vesa
/ APPLICANT: Paloheimo, Marja
/ APPLICANT: Suominen, Pirkko
/ TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
/ NUMBER OF INVENTION: 45
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
/ STREET: 1100 New York Avenue, N.W., Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/841.636A
/ FILING DATE: 30-APR-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/005,335
/ FILING DATE: 17-OCT-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/007,926
/ FILING DATE: 04-DEC-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/020,840
/ FILING DATE: 28-JUN-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/732,181
/ FILING DATE: 16-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/FI96/00550

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; FILING DATE: 17-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Timothy J. Shea, Jr.
; REGISTRATION NUMBER: 41,306
; REFERENCE/DOCKET NUMBER: 1716.0510005/WAC/TJS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-841-636A-40

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db |||||:|:|:|:|:|:|

RESULT 42
US-10-060-756A-1258/c
; Sequence 1258, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PR0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1258
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-060-756A-1258

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```

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGGAAC 739
Db |||||:|:|:|:|:|:|
13 TGCCAGGTGAAC 1

RESULT 43
US-10-138-674-2390
; Sequence 2390, Application US/10138674
; Publication No. US20040077565A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2390
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-138-674-2390

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745
Db |||||:|:|:|:|:|:|
2 GAGAAAUAGAAC 14

RESULT 44
US-10-287-949A-2390
; Sequence 2390, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2390
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-287-949A-2390

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 46;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745
Db |||||:|:|:~|:~|:~|:~|:~|
2 GAGAAAUAGAAC 14

RESULT 45
US-10-782-002-40
; Sequence 40, Application US/10782002
; Publication No. US2004014244A1
; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Londenborough, John
; APPLICANT: Vehmaanpera, Jari
; APPLICANT: Haakana, Heli
; APPLICANT: Mantlya, Arja
; APPLICANT: Lantto, Raija
; APPLICANT: Elovainio, Minna
; APPLICANT: Joutsjoki, Vesa

```

APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Novel Cellulases, The Genes Encoding Them and Uses Thereof
FILE REFERENCE: 1716.051000A
CURRENT APPLICATION NUMBER: US/10/782,002
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US 08/841,636
PRIOR FILING DATE: 1997-04-30
PRIOR APPLICATION NUMBER: PCT/FI96/00550
PRIOR FILING DATE: 1996-10-17
PRIOR APPLICATION NUMBER: US 08/732,181
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/020,840
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: US 60/007,926
PRIOR FILING DATE: 1995-12-04
PRIOR APPLICATION NUMBER: US 60/005,335
PRIOR FILING DATE: 1995-10-17
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
LENGTH: 17
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PCR Primer
NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: n is a, c, g, or t
US-10-782-002-40

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 1; Indels 0; Gaps 0;
QY 735 GAAACAGAACACCG 748
Db 4 GARACNGARCAVMG 17
||:||||:|

RESULT 46
US-10-825-378-40
Sequence 40, Application US/10825378
Publication No. US20040185498A1
GENERAL INFORMATION:
APPLICANT: Miettinen-Oinonen, Arja
APPLICANT: Londeborough, John
APPLICANT: Vehmaanpera, Jari
APPLICANT: Haakana, Heli
APPLICANT: Mantyla, Arja
APPLICANT: Laitto, Raija
APPLICANT: Elovaainio, Minna
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Novel Cellulases, The Genes Encoding Them and Uses Thereof
FILE REFERENCE: 1716.0510009
CURRENT APPLICATION NUMBER: US/10/825,378
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 08/841,636
PRIOR FILING DATE: 1997-04-30
PRIOR APPLICATION NUMBER: PCT/FI96/00550
PRIOR FILING DATE: 1996-10-17
PRIOR APPLICATION NUMBER: US 08/732,181
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/020,840
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: US 60/007,926
PRIOR FILING DATE: 1995-12-04
PRIOR APPLICATION NUMBER: US 60/005,335
PRIOR FILING DATE: 1995-10-17
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2

SEQ ID NO 40
LENGTH: 17
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PCR Primer
NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: n is a, c, g, or t
US-10-825-378-40
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAACACCG 748
Db 4 GARACNGARCAVMG 17
||:||||:|

RESULT 47
US-09-776-474-983
Sequence 983, Application US/09776474
Publication No. US20030087847A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Bocher, Robert
APPLICANT: Holman, Patricia
APPLICANT: Fattaey, Ali
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK-1)
FILE REFERENCE: MEH00-955-A (400/008)
CURRENT APPLICATION NUMBER: US/09/776,474
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,983
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2992
SOFTWARE: PatentIn version 3.0
SEQ ID NO 983
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-983
Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 731 AGGAGAACACGACAC 746
Db 2 AGGAGAACACGACAC 17
|||||||

RESULT 48
US-10-238-700-133
Sequence 133, Application US/10238700
Publication No. US20030153521A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
FILE REFERENCE: 400/057 (MBH01-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR FILING DATE: 2001-09-10

US-09-504-231A-653/c
; Sequence 653, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 653
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-653

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCG 748
Db 15 GAAACAGTACTG 2

RESULT 54
US-09-274-553D-653/c
; Sequence 653, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 653
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-653/c

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCG 748
Db 15 GAAACAGTACTG 2

US-09-274-553D-653
Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCG 748
Db 15 GAAACAGTACTG 2

RESULT 55
US-10-056-414-10/c
; Sequence 10, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-056-414-10

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAAC 744
Db 14 AGGGGAAACAGATC 1

```
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (616577)...(616592)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 743
US-10-339-674-558

Query Match 49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db 16 GAAACAGAACACCG 3

RESULT 59
US-10-339-674-1160/c
; Sequence 1160, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1160
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1302700)...(1302715)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1513
US-10-339-674-1160

Query Match 49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db 16 GAAACAGAACACCG 3

RESULT 60
US-10-717-897-78
; Sequence 78, Application US/10717897
; Publication No. US20040163146A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: PUTHIGAE, SATHISH
; APPLICANT: YAO, JIALONG
; APPLICANT: FLINN, BARRY
; APPLICANT: FORSTER, RICHARD S.
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTERS
; FILE REFERENCE: 044463-0264
; CURRENT APPLICATION NUMBER: US/10/717,897
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/428,287
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 78
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide motif sequence
```

```
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (616577)...(616592)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 743
US-10-339-674-558

Query Match 49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db 16 GAAACAGAACACCG 3

RESULT 59
US-10-339-674-1160/c
; Sequence 1160, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1160
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1302700)...(1302715)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1513
US-10-339-674-1160

Query Match 49.1%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
Db 16 GAAACAGAACACCG 3

RESULT 60
US-10-717-897-78
; Sequence 78, Application US/10717897
; Publication No. US20040163146A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: PUTHIGAE, SATHISH
; APPLICANT: YAO, JIALONG
; APPLICANT: FLINN, BARRY
; APPLICANT: FORSTER, RICHARD S.
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTERS
; FILE REFERENCE: 044463-0264
; CURRENT APPLICATION NUMBER: US/10/717,897
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/428,287
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 78
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide motif sequence
```

US-10-717-897-78

Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAGAA 743
Db 1 GGAGAACAGAA 12
|||||

RESULT 61
US-10-146-058-125
; Sequence 125, Application US/10146058
; Publication No. US2003004099A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-125

US-09-877-478-6035/c

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGAGAAAC 739
Db 12 GCCAGAGAAAC 1
|||||

RESULT 62
US-09-877-478-6035/c
; Sequence 6035, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6035
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-6035

US-10-146-058-125

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 742
Db 1 AGGAGAACAGAA 12
|||||

RESULT 63
US-10-342-902-6035/c
; Sequence 6035, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07

US-10-342-902-6035/c

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGAGAAAC 739
Db 12 GCCAGAGAAAC 1
|||||

RESULT 63
US-10-342-902-6035/c
; Sequence 6035, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07

; PRIOR APPLICATION NUMBER: US 07/882,712
 ; PRIOR FILING DATE: 1992-05-14
 ; PRIOR APPLICATION NUMBER: US 09/436,430
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 6592
 ; SOFTWARE: Patent version 3.2
 ; SEQ ID NO 6035
 ; LENGTH: 15
 ; TYPE: RNA
 ; ORGANISM: Hepatitis B virus
 US-10-342-902-6035

Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 60;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAC 739
 DB 12 GCCAGGAGAAC 1

RESULT 64

US-10-339-674-1179/c
 ; Sequence 1179, Application US/10339674
 ; Publication No. US20030204318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/339,674
 ; CURRENT FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 3537
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1179
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
 ; FEATURE:
 ; LOCATION: (1357006) ... (1357020)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1542
 US-10-339-674-1179

Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 60;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGACACC 747
 DB 13 AACAGACACC 2

RESULT 65

US-10-339-674-3197/c
 ; Sequence 3197, Application US/10339674
 ; Publication No. US20030204318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/339,674
 ; CURRENT FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 3537
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 3197
 ; LENGTH: 15
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
 ; FEATURE:
 ; LOCATION: (4276408) ... (4276422)
 ; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4240
 US-10-339-674-3197

Query Match 47.3%; Score 10.4; DB 1; Length 15;

Best Local Similarity 91.7%; Pred. No. 60;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGACACC 747
 DB 13 AACAGACACC 2

RESULT 66

US-10-056-414-11/c
 ; Sequence 11, Application US/10056414
 ; Publication No. US20030003469A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Dan T.
 ; Draper, Kenneth G.
 ; McSwigen, James
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; DISEASES OR CONDITIONS
 ; RELATED TO LEVELS OF
 ; NF-KB

NUMBER OF SEQUENCES: 830
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/056,414
 FILING DATE: 23-Jan-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/291,932A
 FILING DATE: August 15, 1994
 APPLICATION NUMBER: 08/245,466
 FILING DATE: May 18, 1994
 APPLICATION NUMBER: 07/987,132
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-10-056-414-11

Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 60;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGGAACAGA 742
 DB 13 AGGGAACAGA 2

RESULT 67

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; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-597-326-2

Query Match          47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GGAGAAACAGAA 743
      |||||
Db       16 GGGAAACAGAA 5

RESULT 69
US-09-504-231A-715/c
; Sequence 715, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McGswiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 715
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-715

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      729 CCAGGAGAAACAGAA 743
      |||||
Db       15 CCAGGAGAGAGAAA 1

RESULT 70
US-09-504-231A-716/c
; Sequence 716, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McGswiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15

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; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 716
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-716

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 742
DB 15 GCCAGGAGAGGAGAAA 1

RESULT 71
US-09-274-553D-715/c
; Sequence 715, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 715
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-715

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAGAA 743
DB 15 CCAGGAGAGGAGAAA 1

RESULT 72
US-09-274-553D-716/c
; Sequence 716, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
```

```
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 716
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-716

Query Match          46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGAA 742
DB 15 GCCAGGAGAGGAGAAA 1

RESULT 73
US-09-835-694-19
; Sequence 19, Application US/09835694
; Publication No. US20040087521A1
; GENERAL INFORMATION:
; APPLICANT: DONNELLY, JOHN J.
; APPLICANT: DWARKI, VARAVANI J.
; APPLICANT: LIU, MARGARET A.
; APPLICANT: MONTGOMERY, DONNA L.
; APPLICANT: PARKER, SUEZANNE E.
; APPLICANT: SHIVER, JOHN W.
; APPLICANT: ULMER, JEFFREY B.
; TITLE OF INVENTION: NUCLEIC ACID PHARMACEUTICALS - INFLUENZA MATRIX
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,694
; FILING DATE: 16-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,268
; FILING DATE: 05-June-1995
; APPLICATION NUMBER: PCT/US94/02751
; FILING DATE: 14-March-1994
; APPLICATION NUMBER: 08/089,985
; FILING DATE: 08-July-1993
; APPLICATION NUMBER: 08/032,383
; FILING DATE: 18-March-1993
```

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18972PCA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-835-694-19

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGACA 745
Db 1 AGCAGAGCAGACA 15

RESULT 74
US-10-339-674-420
; Sequence 420, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 420
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (435971)...(435985)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 553
US-10-339-674-420

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 727 TGCAGGAGAAACAG 741
Db 1 TGCCAGGGCAAAAG 15

RESULT 75
US-10-339-674-421
; Sequence 421, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 421
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (435971)...(435985)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 552
US-10-339-674-421

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACAG 741
Db 1 TGCCAGGGCAAAAG 15

RESULT 76
US-09-504-231A-717/c
; Sequence 717, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 717
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-717

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAA 737
Db 13 GCCAGGAGAA 4

RESULT 77
US-09-274-553D-717/c
; Sequence 717, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; FILE REFERENCE: rpi 247/282
US-09-274-553D-717/c
```

; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 717
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-717

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAA 737
|||
Db 13 GCCAGGAGAA 4

RESULT 78
US-09-504-231A-1341/c
; Sequence 1341, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT FILING DATE: 2000-02-15
; CURRENT APPLICATION NUMBER: US/09/504,231A
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1341
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1341

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GCAGAACAGAAC 744
|||
Db 13 GGTGAACAGTAC 1

RESULT 79
US-09-274-553D-1341/c
; Sequence 1341, Application US/09274553D
; Patent No. US20020082225A1

; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1341
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1341

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GCAGAACAGAAC 744
|||
Db 13 GGTGAACAGTAC 1

RESULT 80
US-10-146-058-126
; Sequence 126, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta ()
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/PS8418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202)393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-126

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 728 GCCAGGAGAAACA 740
||| ||||| |||
Db 2 GCAAGGAGAGCA 14

RESULT 81

US-10-104-025-9
Sequence 9, Application US/10104025
Publication No. US20030165876A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA SA
APPLICANT: CAMERON, Beatrice
TITLE OF INVENTION: PROCESSES FOR PURIFYING AND FOR DETECTING TARGET DOUBLE-STRANDED
TITLE OF INVENTION: SEQUENCES BY TRIPLE HELIX INTERACTION
FILE REFERENCE: 03806.0546
CURRENT APPLICATION NUMBER: US/10/104,025
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US 60/285,272
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: FR 0103953
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 14
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-025-9

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 731 AGGAGAAACAGAA 743
||| ||||| |||
Db 2 AGGAGAGAGAA 14

RESULT 82

US-10-324-409B-21
Sequence 21, Application US/10324409B
Publication No. US2004008680A1
GENERAL INFORMATION:
APPLICANT: Sampson, et al.
TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
TITLE OF INVENTION: Secondary Structure
FILE REFERENCE: 2003309-0028
CURRENT APPLICATION NUMBER: US/10/324,409B
CURRENT FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Predicted
OTHER INFORMATION: Thermodynamic Parameters.
US-10-324-409B-21

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 734 AGAAGACAGAACAC 746
||| ||||| |||
Db 2 AGAGACTGAACAC 14

RESULT 83

US-09-504-231A-654/C
Sequence 654, Application US/09504231A
Patent No. US20020013458A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REFERENCE: rpi 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SOFTWARE: PatentIn version 3.0
SEQ ID NO 654
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-654

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAAC 744
||| ||||| |||
Db 13 GGTGAACACAGTAC 1

RESULT 84

US-09-274-553D-654/C
Sequence 654, Application US/09274553D
Patent No. US2002008225A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: ipi 247/282
CURRENT APPLICATION NUMBER: US/09/274.553D
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PatentIn version 3.0
SEQ ID NO 654
TYPE: RNA
LENGTH: 15
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-654

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACGAC 744
DB 13 GGTGAAACAGTAC 1

RESULT 85
US-10-347-510A-95/c
Sequence 95, Application US/10347510A
Publication No. US20040063110A1
GENERAL INFORMATION:
APPLICANT: Henrik Stender
Kaare Lund
Tina Anderson Hollerup
TITLE OF INVENTION: No. US20040063110A1el Process For The Detection of Mycobact
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
STREET: 1300 I ST. NW
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/347,510A
FILING DATE: 21-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,392
FILING DATE: 15-Oct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-Oct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-May-97
APPLICATION NUMBER: 08/943,777
FILING DATE: 3-Oct-97
ATTORNEY/AGENT INFORMATION:
NAME: Anthony C. Tridico
REGISTRATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4173
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 basepairs
TYPE: nucleic acid basepairs
STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-347-510A-95

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAACAG 742
DB 14 CAGGACGACAG 2

RESULT 86
US-09-544-934B-95/c
Sequence 95, Application US/09544934B
Publication No. US20020137035A1
GENERAL INFORMATION:
APPLICANT: Henrik Stender
Kaare Lund
Tina Anderson Hollerup
TITLE OF INVENTION: Novel Process For The Detection of Mycobacteria
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
STREET: 1300 I ST. NW
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/544,934B
FILING DATE: 07-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,392
FILING DATE: 15-Oct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-Oct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-May-97
APPLICATION NUMBER: 08/943,777
FILING DATE: 3-Oct-97
ATTORNEY/AGENT INFORMATION:
NAME: Anthony C. Tridico
REGISTRATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4173
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 basepairs
TYPE: nucleic acid basepairs
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-544-934B-95

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAACAG 742
DB 14 CAGGACGACAG 2

RESULT 87
US-10-339-674-1871/c

```
; Sequence 1871, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1871
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2551260)...(2551274)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2480
US-10-339-674-1871

Query Match      44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      729 CCAGGAGAAACAG 741
Db      13 CCAGGTTAAACAG 1
      ||||| |||||

RESULT 88
US-10-450-797-1219/c
; Sequence 1219, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1219
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1219

Query Match      42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      734 AGAAACAGATC 744
Db      11 AGAAACAGATC 1
      ||||| |||||

RESULT 89
US-10-100-957A-73
; Sequence 73, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-LIA
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180

; Sequence 1871, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1871
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2551260)...(2551274)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2480
US-10-339-674-1871

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GCAGAAACAG 742
Db      1 GTAGAAACAG 11
      ||||| |||||

RESULT 90
US-10-073-377-5/c
; Sequence 5, Application US/10073377
; Publication No. US2003009670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; TITLE OF INVENTION: Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified
; OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-5

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
Db      12 AGTAGAAACAG 2
      ||||| |||||

RESULT 91
US-10-073-377-6/c
; Sequence 6, Application US/10073377
; Publication No. US2003009670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; TITLE OF INVENTION: Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified
; OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-6
```

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAACAC 2

RESULT 92
US-10-076-597-32
; Sequence 32, Application US/10076597
; Publication No. US20030045490A1
; GENERAL INFORMATION:
; APPLICANT: Dale, Roderic M. K.
; APPLICANT: Arrow, Amy
; APPLICANT: Thompson, Terry
; TITLE OF INVENTION: Antisense Phosphodiesterase Inhibitors
; FILE REFERENCE: OLIG-003CIP
; CURRENT APPLICATION NUMBER: US/10/076,597
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/364,626
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/223,586
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Oligonucleotide
US-10-076-597-32

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
Db 3 TGTCAGGAGAA 13

RESULT 93
US-10-073-377-19/c
; Sequence 19, Application US/10073377
; Publication No. US20030093670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified Influenza C 3'-sequence
US-10-073-377-19

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741

Db 14 AGTAGAAACAG 4

RESULT 94
US-10-191-997-1
; Sequence 1, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their Use
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ASM oligonucleotide
US-10-191-997-1

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
Db 3 TGTCAGGAGAA 13

RESULT 95
US-10-146-058-35
; Sequence 35, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of immunosuppression
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (TGF-beta)
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-10-146-058-35

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 87;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 730 CAGGAGAACAGAA 743
Db 1 CATGAGAGCAGGA 14

RESULT 96
US-10-033-145-1787
Sequence 1787, Application US/10033145
Publication No. US2002015151A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAO201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18.
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1787
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-1787

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 734 AGAACAGA 742
Db 2 AGAACAGA 10

RESULT 97
US-10-033-145-1921/c
Sequence 1921, Application US/10033145
Publication No. US2002015151A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAO201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1921
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-033-145-1921

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 738 ACAGAACAC 746
Db 9 ACAGAACAC 1

RESULT 98
US-10-450-797-167
Sequence 167, Application US/10450797
Publication No. US20040142335A1
GENERAL INFORMATION:
APPLICANT: Petersohn, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 101 00 121.5
PRIOR FILING DATE: 2001-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
SEQ ID NO 167
LENGTH: 11
TYPE: DNA
ORGANISM: Homo sapiens
US-10-450-797-167

Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
Db 3 CCAGGAGAA 11

RESULT 99
US-09-263-959-843/c
Sequence 843, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/263,959
 ; FILING DATE: 05-MAR-1999
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mcmasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 920010.426C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 843:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-263-959-843

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 AACAGACACA 745
 DB 11 AACAGACACA 3

RESULT 100
 US-10-100-957A-61
 ; Sequence 61, Application US/10100957A
 ; Publication No. US20030096322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Giuliano, Kenneth A.
 ; APPLICANT: Kapur, Ravi
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97-022-LIA
 ; CURRENT APPLICATION NUMBER: US/10/100,957A
 ; CURRENT FILING DATE: 2002-03-19
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 61
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-3
 ; OTHER INFORMATION: substrate recognition sequence
 US-10-100-957A-61

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACACAGA 742
 DB 3 AGAAACACAGA 11

RESULT 101
 US-10-100-957A-75
 ; Sequence 75, Application US/10100957A
 ; Publication No. US20030096322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Giuliano, Kenneth A.
 ; APPLICANT: Kapur, Ravi
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97-022-LIA
 ; CURRENT APPLICATION NUMBER: US/10/100,957A
 ; CURRENT FILING DATE: 2002-03-19
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75

; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-8
 ; OTHER INFORMATION: substrate recognition sequence
 US-10-100-957A-75

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACACAGA 742
 DB 3 AGAAACACAGA 11

RESULT 102
 US-09-981-803-47/c
 ; Sequence 47, Application US/09981803
 ; Publication No. US2003032092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Joel CROUZET-
 ; APPLICANT: Daniel SCHERMAN
 ; APPLICANT: Beatrice CAMERON
 ; APPLICANT: Pierre WILS
 ; APPLICANT: Anne-Marie DARQUET
 ; TITLE OF INVENTION: DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY
 ; FILE REFERENCE: MINICIRCLE
 ; CURRENT APPLICATION NUMBER: US/09/981,803
 ; CURRENT FILING DATE: 2001-10-19
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence:
 ; OTHER INFORMATION: oligonucleotide
 US-09-981-803-47

Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 91;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
 DB 12 AGGAGAAACAGA 1

RESULT 103
 US-10-273-071-28/c
 ; Sequence 28, Application US/10275071
 ; Publication No. US20030186268A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Crouzet, Joel
 ; APPLICANT: Scherman, Daniel
 ; APPLICANT: Wils, Pierre
 ; APPLICANT: Cameron, Beatrice
 ; APPLICANT: Blanche, Francis
 ; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
 ; FILE REFERENCE: 08888.0138-02
 ; FILE REFERENCE: IMMobilized OLIGONUCLEOTIDE
 ; CURRENT APPLICATION NUMBER: US/10/275,071
 ; CURRENT FILING DATE: 2003-04-07
 ; PRIOR APPLICATION NUMBER: 09/580,923
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 08/860,038
 ; PRIOR FILING DATE: 1997-06-09
 ; PRIOR APPLICATION NUMBER: PCT/FR95/01468
 ; PRIOR FILING DATE: 1995-11-08
 ; NUMBER OF SEQ ID NOS: 36

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-275-071-28

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 12 AGGAAAAAAGA 1

RESULT 104
US-10-091-281-393
; Sequence 393, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091.281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 393
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative SORY/SRY.01 motif
US-10-091-281-393

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAAACAGAACCA 745
Db 1 AAAAAACAAACA 12

RESULT 105
US-10-684-830-34/c
; Sequence 34, Application US/10684830
; Publication No. US20040142452A1
; GENERAL INFORMATION:
; APPLICANT: Gencell S.A.; Aventis Pharmaceuticals, Inc.
; APPLICANT: Soubrier, Fabienne
; TITLE OF INVENTION: Circular DNA Molecule with Conditional Origin of Replication, Met
; TITLE OF INVENTION: Preparing Same, and Use Thereof in Gene Therapy
; FILE REFERENCE: 8888.0132-02
; CURRENT APPLICATION NUMBER: US/10/684.830
; CURRENT FILING DATE: 2003-10-15
; PRIOR FILING DATE: 1998-01-16
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 09/043,193
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/FR96/01414
; PRIOR FILING DATE: 1996-09-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA
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```
; ORGANISM: Escherichia coli
US-10-684-830-34

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 12 AGGAAAAAAGA 1

RESULT 106
US-10-684-830-37/c
; Sequence 37, Application US/10684830
; Publication No. US20040142452A1
; GENERAL INFORMATION:
; APPLICANT: Gencell S.A.; Aventis Pharmaceuticals, Inc.
; APPLICANT: Soubrier, Fabienne
; TITLE OF INVENTION: Circular DNA Molecule with Conditional Origin of Replication, Met
; TITLE OF INVENTION: Preparing Same, and Use Thereof in Gene Therapy
; FILE REFERENCE: 8888.0132-02
; CURRENT APPLICATION NUMBER: US/10/684.830
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 10/268,948
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 09/043,193
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/FR96/01414
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-684-830-37

Query Match          40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGA 742
Db 12 AGGAAAAAAGA 1

RESULT 107
US-09-152-059-3/c
; Sequence 3, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-3

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      736 AAACAGACACC 747
      ||||| |||||
Db      12 AAACAACACC 1

```

```

RESULT 108
US-09-152-059-4/c
; Sequence 4, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-4

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      736 AAACAGACACC 747
      ||||| |||||
Db      12 AAACAACACC 1

```

```

RESULT 109
US-09-152-059-5/c
; Sequence 5, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL

```

```

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-5

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      736 AAACAGACACC 747
      ||||| |||||
Db      12 AAACAACACC 1

```

```

RESULT 110
US-09-152-059-6/c
; Sequence 6, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```


; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-6

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1

RESULT 111
US-09-152-059-7/c
; Sequence 7, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)

; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-7

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1

RESULT 112
US-09-152-059-8/c
; Sequence 8, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-8

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1

RESULT 113
US-09-152-059-9/c
; Sequence 9, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide

```

US-09-152-059-9
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
    ||||| ||||
Db 12 AAACAAACCACC 1

RESULT 114
US-09-152-059-28/c
; Sequence 28, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-29
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
    ||||| ||||
Db 12 AAACAAACCACC 1

RESULT 116
US-09-152-059-30/c
; Sequence 30, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-30
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
    ||||| ||||
Db 12 AAACAAACCACC 1

RESULT 115
US-09-152-059-29/c
; Sequence 29, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591

```

```
Db      12 AACACAAACCACC 1

RESULT 117
US-09-152-059-31/c
; Sequence 31, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION: Description of Artificial Sequence: Probe
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-31

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACACGAAACC 747
      ||||| |||||
Db      12 AACACAAACCACC 1

RESULT 118
US-09-152-059-43/c
; Sequence 43, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-43

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACACGAAACC 747
      ||||| |||||
Db      12 AACACAAACCACC 1

RESULT 120
US-09-152-059-44/c
; Sequence 44, Application US/09152059
; Patent No. US20020068708A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-44

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 121
US-09-152-059-46/c
; Sequence 46, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-46/c
```

```
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-09-152-059-46

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 122
US-09-152-059-47/c
; Sequence 47, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-47

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
      ||||| |||||
Db      12 AAACAAACCACC 1

RESULT 123
US-09-152-059-48/c
; Sequence 48, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-48

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACAGAACACC 747
Db      12 AACAAACCACC 1
|||||
RESULT 124
US-09-152-059-71/c
; Sequence 71, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-71

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACAGAACACC 747
Db      12 AACAAACCACC 1
|||||
RESULT 125
US-09-152-059-74/c
; Sequence 74, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-74

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AACAGAACACC 747
Db      12 AACAAACCACC 1
|||||
RESULT 126
US-09-152-059-77/c
; Sequence 77, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-77
```

; PRIOR APPLICATION NUMBER: 60/088,309
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/094,355
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 77
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (1)..(12)
 ; OTHER INFORMATION: LNA monomer
 ; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
 ; OTHER INFORMATION: oligonucleotide
 US-09-152-059-77

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747
 Db 12 AAACAGACACC 1

RESULT 127

US-09-781-811-23/c
 ; Sequence 23, Application US/09781811
 ; Patent No. US20020151463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WOYCHIK, RICHARD P.
 ; APPLICANT: BULTMAN, SCOTT J.
 ; APPLICANT: MICHAUD, EDWARD J.
 ; TITLE OF INVENTION: AGOUTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
 ; FILE REFERENCE: 4310.001682
 ; CURRENT APPLICATION NUMBER: US/09/781,811
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 09/034,088
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: 08/064,385
 ; PRIOR FILING DATE: 1993-05-21
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 ; OTHER INFORMATION: OLIGONUCLEOTIDE
 US-09-781-811-23

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGACACA 745
 Db 13 AGAACAGACACA 2

RESULT 128

US-10-027-632-177279/c
 ; Sequence 177279, Application US/10027632
 ; Publication No. US2002019837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 177279
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-177279

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCACAGAGAAA 738
 Db 12 TTCTGGAGAAA 1

RESULT 129

US-10-027-632-177279/c
 ; Sequence 177279, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 177279
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-177279

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TCCACAGAGAAA 738
 Db 12 TTCTGGAGAAA 1

RESULT 130
US-10-008-029-3/c
; Sequence 3, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/088,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-3

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747
|||||
Db 12 AAACAAACCACC 1

RESULT 131
US-10-008-029-4/c
; Sequence 4, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/088,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747
|||||
Db 12 AAACAAACCACC 1

; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-4

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747
|||||
Db 12 AAACAAACCACC 1

RESULT 132
US-10-008-029-5/c
; Sequence 5, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-5

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747
|||||
Db 12 AAACAAACCACC 1

```
RESULT 133
US-10-008-029-6/c
; Sequence 6, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-008-029-6
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 12 AAACAAACCACC 1
|||||

RESULT 134
US-10-008-029-7/c
; Sequence 7, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
```

```

; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
US-10-008-029-7
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 12 AAACAAACCACC 1
|||||

RESULT 135
US-10-008-029-8/c
; Sequence 8, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-8
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 12 AAACAAACCACC 1
|||||
```


Db 12 AACAAACACC 1

RESULT 136

US-10-008-029-9/c

Sequence 9, Application US/10008029

Publication No. US20030134808A1

GENERAL INFORMATION:

APPLICANT: WENGEL, JESPER

APPLICANT: NIELSEN, POUL

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165-C2(71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 09/152,059

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/071,682

PRIOR FILING DATE: 1998-01-16

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR FILING DATE: 1998-03-03

PRIOR APPLICATION NUMBER: 60/083,507

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/088,309

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/094,355

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 146

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 13

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: LNA modified

NAME/KEY: modified base

LOCATION: (1)..(12)

OTHER INFORMATION: LNA monomer

US-10-008-029-9

Query Match 40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 95;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACACGAACACC 747

Db 12 AACAAACACC 1

RESULT 137

US-10-008-029-28/c

Sequence 28, Application US/10008029

Publication No. US20030134808A1

GENERAL INFORMATION:

APPLICANT: WENGEL, JESPER

APPLICANT: NIELSEN, POUL

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165-C2(71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 09/152,059

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/071,682

PRIOR FILING DATE: 1998-01-16

PRIOR APPLICATION NUMBER: 60/076,591

US-10-008-029-9

Query Match 40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 95;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACACGAACACC 747

Db 12 AACAAACACC 1

RESULT 138

US-10-008-029-29/c

Sequence 29, Application US/10008029

Publication No. US20030134808A1

GENERAL INFORMATION:

APPLICANT: WENGEL, JESPER

APPLICANT: NIELSEN, POUL

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165-C2(71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 09/152,059

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/071,682

PRIOR FILING DATE: 1998-01-16

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR FILING DATE: 1998-03-03

PRIOR APPLICATION NUMBER: 60/083,507

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/088,309

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/094,355

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 146

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 28

LENGTH: 13

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Probe

NAME/KEY: modified base

LOCATION: (1)..(12)

OTHER INFORMATION: LNA monomer

US-10-008-029-29

Query Match 40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 95;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACACGAACACC 747

Db 12 AACAAACACC 1

RESULT 139
US-10-008-029-30/c
; Sequence 30, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-30

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACACC 1

RESULT 140
US-10-008-029-31/c
; Sequence 31, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-008-029-31

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACACC 1

RESULT 141
US-10-008-029-32/c
; Sequence 32, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-32

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACACC 1

RESULT 140
US-10-008-029-31/c
; Sequence 31, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACAAACACC 1

```
RESULT 142
US-10-008-029-43/c
; Sequence 43, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JESPER
; APPLICANT: WENDEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-43
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1

RESULT 143
US-10-008-029-44/c
; Sequence 44, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JESPER
; APPLICANT: WENDEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-44
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1

RESULT 144
US-10-008-029-46/c
; Sequence 46, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENDEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-46
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1

RESULT 145
US-10-008-029-47/c
; Sequence 47, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, JESPER
; APPLICANT: WENDEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-47
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1
```

```
US-10-008-029-47/c
; Sequence 47, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: LNA monomer
US-10-008-029-47
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACAACACC 1
```

```
RESULT 146
US-10-008-029-48/c
; Sequence 48, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
```

```
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-008-029-48
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACAACACC 1
```

```
RESULT 147
US-10-008-029-71/c
; Sequence 71, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-71
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACAACACC 1
```

```
RESULT 148
US-10-008-029-74/c
; Sequence 74, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
```

```
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-74

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 149
US-10-008-029-77/c
; Sequence 77, Application US/10008029
; Publication No. US2003013480A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-74

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 149
US-10-008-029-77/c
; Sequence 77, Application US/10008029
; Publication No. US2003013480A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-008-029-77

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 150
US-10-208-650-3/c
; Sequence 3, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-3

Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAAACACC 1

RESULT 151
US-10-208-650-4/c
```

; Sequence 4, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-4

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACAGAACACC 1

RESULT 152
US-10-208-650-5/c
; Sequence 5, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-5

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACAGAACACC 1

RESULT 153
US-10-208-650-6/c
; Sequence 6, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-6

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;

```

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
    ||||| |||||
Db 12 AACAAACACC 1

RESULT 154
US-10-208-650-7/c
; Sequence 7, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-7
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
    ||||| |||||
Db 12 AACAAACACC 1

RESULT 155
US-10-208-650-8/c
; Sequence 8, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05

```

```

; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-8
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
    ||||| |||||
Db 12 AACAAACACC 1

RESULT 156
US-10-208-650-9/c
; Sequence 9, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-3

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

```

```

RESULT 157
US-10-208-650-28/c
; Sequence 28, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; ORGANISM: Artificial Sequence
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe

```

```

US-10-208-650-29
; Sequence 29, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; ORGANISM: Artificial Sequence
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

```

```

RESULT 158
US-10-208-650-29/c
; Sequence 29, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; ORGANISM: Artificial Sequence
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

```

```

RESULT 159
US-10-208-650-30/c
; Sequence 30, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; ORGANISM: Artificial Sequence
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309

```

```

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-29

```

```

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      736 AAACAGAACACC 747
Db      12 AAACAAACCACC 1

```

```

RESULT 159
US-10-208-650-30/c
; Sequence 30, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309

```



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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-31
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 160
US-10-208-650-31/c
; Sequence 31, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,293
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-31
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 160
US-10-208-650-31/c
; Sequence 31, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,293
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-208-650-31
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

```

```

RESULT 161
US-10-208-650-32/c
; Sequence 32, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,293
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-32
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

RESULT 162
US-10-208-650-43/c
; Sequence 43, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,293
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-208-650-43
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AACAGAACACC 747
Db 12 AACAAACCACC 1

```

```
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 43
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-44
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACACC 1

RESULT 163
US-10-208-650-44/c
; Sequence 44, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 44
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-44
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACACC 1

RESULT 164
US-10-208-650-46/c
; Sequence 46, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-46
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACAAACACC 1

RESULT 165
US-10-208-650-47/c
; Sequence 47, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
```

```
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
;
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: LNA monomer
US-10-208-650-47
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1
```

```
RESULT 166
US-10-208-650-48/c
; Sequence 48, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-48
```

```
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1
```

```
RESULT 167
US-10-208-650-71/c
; Sequence 71, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-71

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 736 AAACAGAACACC 747
Db 12 AAACAAACCACC 1
```

```
RESULT 168
US-10-208-650-74/c
; Sequence 74, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
```

; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-74

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
|||||
Db 12 AAACAGAACACC 1

RESULT 169
US-10-208-650-77/c
; Sequence 77, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENDEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(12)
; OTHER INFORMATION: LNA monomer
US-10-208-650-77

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
|||||
Db 12 AAACAGAACACC 1

RESULT 170
US-10-091-281-199
; Sequence 199, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative IRPF/IRF2.01 motif
US-10-091-281-199

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGAACACC 746
|||||
Db 2 GAACAGAACACC 13

RESULT 171
US-10-194-882-5/c
; Sequence 5, Application US/10194882
; Publication No. US20040014042A1
; GENERAL INFORMATION:
; APPLICANT: JU, JINGYUE
; TITLE OF INVENTION: Multiplex Genotyping Using Solid Phase Capturable Dideoxynucleotides
; FILE REFERENCE: 0575/66833/JPW/ADM
; CURRENT APPLICATION NUMBER: US/10/194,882
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: internal mass standard

```

US-10-194-882-5
Query Match          40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred.No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAACACGAACA 745
Db      13 AGAAAAAGAAAA 2
      ||||| |||||
      ||||| |||||

RESULT 172
US-10-073-377-8
; Sequence 8, Application US/10073377
; Publication No. US20030099670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
; TITLE OF INVENTION: Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Influenza B virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: n = any nucleotide

US-10-073-377-8
Query Match          39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred.No. 1e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
Db      1 AGAGWAACAR 11
      ||||| |||||
      ||||| |||||

RESULT 173
US-10-257-021-102
; Sequence 102, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-257-021-102
Query Match          38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred.No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

; APPLICANT: ROBERTS, BRUCE
 ; APPLICANT: SHANKARA, SRINIVAS
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: GA0201C
 ; CURRENT APPLICATION NUMBER: US/10/033,145
 ; CURRENT FILING DATE: 2001-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 2137
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1215
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-033-145-1215

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAAA 738
 |||||
 Db 1 CCAGGAGGAA 10

RESULT 177
 US-10-390-045-47/C
 ; Sequence 47, Application US/10390045
 ; Publication No. US20030170713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOUL, JUDD W.
 ; APPLICANT: XU, LINDA L.
 ; APPLICANT: SEGAWA, TAKEHIKO
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 ; FILE REFERENCE: 04995.0057-00000
 ; CURRENT APPLICATION NUMBER: US/10/390,045
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US/09/769,482
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: oligonucleotide
 US-10-390-045-47

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGATAAACA 740
 |||||
 Db 10 AGGATAAACA 1

RESULT 178
 US-10-330-627-834
 ; Sequence 834, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W.
 ; APPLICANT: Vogelstein, Bert

; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 834
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-834

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAAA 738
 |||||
 Db 1 CCAGGAGGAA 10

RESULT 179
 US-10-330-627-1293/c
 ; Sequence 1293, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W.
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1293
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-1293

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGATAAACA 740
 |||||
 Db 10 AGGATAAACA 1

RESULT 180
 US-10-330-627-1363/c
 ; Sequence 1363, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W.
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1363
 ; LENGTH: 10
 ; TYPE: DNA

OY 739 CAGAACACCG 748
Db 1 CGAACACCG 10

RESULT 185

US-10-450-797-613/c
; Sequence 613, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 613
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-613

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 734 AGAACACGAA 743
Db 10 AGAACACGAA 1

RESULT 186

US-10-450-797-741
; Sequence 741, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 741
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-741

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 729 CCAGGAGAAA 738
Db 1 CCAGGAGAAA 10

RESULT 187

US-09-179-536B-81

; Sequence 81, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; APPLICANT: David M. Lough
; APPLICANT: Guobing Xiang
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,536B
; FILING DATE: 26-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/20444
; FILING DATE: 06-NOV-1997
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-NO. US20020042112A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-NO. US20020042112A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-NO. US20020042112A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-NO. US20020042112A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 81
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-09-179-536B-81

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 188
US-09-179-536B-86
; Sequence 86, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; David M. Lough
; Guobing Xiang
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,536B
; FILING DATE: 26-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/20444
; FILING DATE: 06-NOV-1997
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20020042112A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-179-536B-86

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGACAA 737

Db 2 GCCAGGACAA 11
|||||
RESULT 189
US-09-263-959-477/c
; Sequence 477, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-477

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGACAA 745
|||||
Db 12 AACAGACAA 3

RESULT 190
US-09-263-959-492/c
; Sequence 492, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-09-263-959-492

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 492:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-492

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. le+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1;

QY 736 AACAGAACAC 745
DB 11 AACACACAC 2

RESULT 191
US-09-263-959-755/c
Sequence 755, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 755:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-755

Query Match 38.2%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. le+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACAGAACAC 745
DB 11 AACACACAC 2

RESULT 192
US-09-263-959-850/c
Sequence 850, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 850:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-850

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. le+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1;

QY 737 AACAGAACAC 746
DB 12 AACACACAC 3

RESULT 193
US-09-845-938A-4/c
Sequence 4, Application US/09845938A
Publication No. US20030118550A1
GENERAL INFORMATION:
APPLICANT: Kabanov, Alexander V
APPLICANT: Benieux, Pierre
APPLICANT: Yulievich, Valery
TITLE OF INVENTION: Compositions and Methods for Inducing Activation of Dendritic Cell
FILE REFERENCE: 3874-129 US
CURRENT APPLICATION NUMBER: US/09/845,938A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1

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; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-09-845-938A-4

Query Match      38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730 CAGAGGAAC 739
Db      11 CAGAGGAAC 2

RESULT 194
US-09-845-938A-7/c
; Sequence 7, Application US/09845938A
; Publication No. US20030118550A1
; GENERAL INFORMATION:
; APPLICANT: Kabanov, Alexander V
; APPLICANT: Lenieux, Pierre
; APPLICANT: Yulievich, Valery
; APPLICANT: Vincigradov, Sergey V.
; TITLE OF INVENTION: Compositions and Methods for Inducing Activation of Dendritic Cell
; FILE REFERENCE: 3874-129 US
; CURRENT APPLICATION NUMBER: US/09/845,938A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Herpes Simplex Virus type 1
US-09-845-938A-7

Query Match      38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730 CAGAGGAAC 739
Db      11 CAGAGGAAC 2

RESULT 195
US-09-297-576A-81
; Sequence 81, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:

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```

; APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20030129589A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-450-8499
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
US-09-297-576A-81

Query Match      38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      728 GCCAGGAGAA 737
Db      2 GCCAGGAGAA 11

RESULT 196
US-09-297-576A-86
; Sequence 86, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```


; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 10/376,770
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-661-165-433

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGAACAC 746
||| |||
Db 10 AACAGAACAC 1

RESULT 200
US-10-667-891-32
; Sequence 32, Application US/10667891
; Publication No. US20040171024A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, CHARLES W.
; APPLICANT: SREY, PAUL T.
; APPLICANT: HOLM, INGE
; APPLICANT: GRAILLES, MARINE
; APPLICANT: RHETSKY, ANDREY
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
; FILE REFERENCE: 03495.0294-00000
; CURRENT APPLICATION NUMBER: US/10/667,891
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/413,469
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-667-891-32

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGAACAC 746
||| |||
Db 2 AACAGAACAC 11

RESULT 201
US-10-091-281-222/c
; Sequence 222, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 222
; LENGTH: 9

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AREB/AREB6.04 motif
US-10-091-281-222

Query Match 36.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 734 AGAAACAG 741
||| |||
Db 8 AGAAACAG 1

RESULT 202
US-10-293-222-96/c
; Sequence 96, Application US/10293222
; Publication No. US2004003932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-96

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 GCCAGGAG 735
||| |||
Db 10 GCCAGGAG 3

RESULT 203
US-10-033-145-537
; Sequence 537, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 537
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-537

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GAACACCG 748
Db 1 GAACACCG 8

RESULT 204

US-10-329-465-139
; Sequence 139, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-139

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
Db 2 AGGAGAAA 9

RESULT 205

US-10-355-820-2
; Sequence 2, Application US/10355820
; Publication No. US20030166282A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, DAVID
; APPLICANT: FORD, LANCE
; APPLICANT: JARVIS, RICH
; APPLICANT: PALLOTTA, VINCE
; APPLICANT: PASLOSKE, BRITTAN
; TITLE OF INVENTION: HIGH POTENCY siRNAs FOR REDUCING THE EXPRESSION OF
; TITLE OF INVENTION: TARGET GENES
; FILE REFERENCE: AM61-077US
; CURRENT APPLICATION NUMBER: US/10/355,820
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353,332
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-355-820-2

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAAC 739
Db 1 GGAGAAAC 9

Db 2 GGAGAAAC 9

RESULT 206

US-10-330-627-26
; Sequence 26, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-26

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 AGAACACCC 747
Db 1 AGAACACCC 8

RESULT 207

US-10-330-627-77
; Sequence 77, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-77

Query Match 36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAA 743
Db 3 AAACAGAA 10

RESULT 208

US-10-330-627-79
; Sequence 79, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert

```
/ ORGANISM: Homo sapiens
/ US-10-330-627-1321

Query Match      36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
Db 10 GCCAGGAG 3

RESULT 211
US-10-302-547-55/c
/ Sequence 55, Application US/10302547
/ Publication No. US20040142448A1
/ GENERAL INFORMATION:
/ APPLICANT: MURPHY, BRIAN R.
/ APPLICANT: COLLINS, PETER L.
/ APPLICANT: SKIADOPOULOS, MARIO H.
/ APPLICANT: NEWMAN, JASON T.
/ TITLE OF INVENTION: RECOVERY OF RECOMBINANT HUMAN PARAINFLUENZA VIRUS TYPE
/ TITLE OF INVENTION: 1 (HPV1) FROM CDNA AND USE OF RECOMBINANT HPV1 IN
/ TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AND AS VECTORS TO ELICIT
/ TITLE OF INVENTION: IMMUNE RESPONSES AGAINST PIV AND OTHER HUMAN PATHOGENS
/ FILE REFERENCE: 2303-37-3
/ CURRENT APPLICATION NUMBER: US/10/302,547
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: 60/331,961
/ PRIOR FILING DATE: 2001-11-21
/ NUMBER OF SEQ ID NOS: 137
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 55
/ LENGTH: 10
/ TYPE: RNA
/ ORGANISM: Bovine parainfluenza virus 3
/ US-10-302-547-55

Query Match      36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAA 738
Db 10 AGGAGAAA 3

RESULT 212
US-09-828-211A-8/c
/ Sequence 8, Application US/09828211A
/ Publication No. US20010034029A1
/ GENERAL INFORMATION:
/ APPLICANT: FUJIWAKE, Hideshi
/ TITLE OF INVENTION: Method of Detecting Mutation in Base Sequence of Nucleic Acid
/ FILE REFERENCE: NOG-0009
/ CURRENT APPLICATION NUMBER: US/09/828,211A
/ CURRENT FILING DATE: 2001-04-09
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 11
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence 17a in Fig. 3 (5' to 3')
/ US-09-828-211A-8

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAACAGAGA 742
Db 10 GAACAGAGA 3

/ TITLE OF INVENTION: Human Transcriptomes
/ FILE REFERENCE: 001107.00319
/ CURRENT APPLICATION NUMBER: US/10/330,627
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 09/448,480
/ PRIOR FILING DATE: 1999-11-24
/ NUMBER OF SEQ ID NOS: 1564
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 79
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-330-627-79

Query Match      36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAA 743
Db 3 AAACAGAA 10

RESULT 209
US-10-330-627-85
/ Sequence 85, Application US/10330627
/ Publication No. US20030175771A1
/ GENERAL INFORMATION:
/ APPLICANT: Velculescu, Victor E.
/ APPLICANT: Kinzler, Kenneth W.
/ APPLICANT: Vogelstein, Bert
/ TITLE OF INVENTION: Human Transcriptomes
/ FILE REFERENCE: 001107.00319
/ CURRENT APPLICATION NUMBER: US/10/330,627
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 09/448,480
/ PRIOR FILING DATE: 1999-11-24
/ NUMBER OF SEQ ID NOS: 1564
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 85
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-330-627-85

Query Match      36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAA 743
Db 3 AAACAGAA 10

RESULT 210
US-10-330-627-1321/c
/ Sequence 1321, Application US/10330627
/ Publication No. US20030175771A1
/ GENERAL INFORMATION:
/ APPLICANT: Velculescu, Victor E.
/ APPLICANT: Kinzler, Kenneth W.
/ APPLICANT: Vogelstein, Bert
/ TITLE OF INVENTION: Human Transcriptomes
/ FILE REFERENCE: 001107.00319
/ CURRENT APPLICATION NUMBER: US/10/330,627
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 09/448,480
/ PRIOR FILING DATE: 1999-11-24
/ NUMBER OF SEQ ID NOS: 1564
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1321
/ LENGTH: 10
/ TYPE: DNA
```

```
Db      8 GAAACAGA 1

RESULT 213
US-09-918-715-65/c
; Sequence 65, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-65

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      11 GCCAGGAG 4

RESULT 214
US-10-266-138B-6
; Sequence 6, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; FILE REFERENCE: J6664US(ED:EP/JVT)seq13sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq. # 56 of
; OTHER INFORMATION: Table I
US-10-266-138B-6

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      1 GCCAGGAG 8

RESULT 215
US-10-055-728-27
; Sequence 27, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
; APPLICANT: van der Kuyt, Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
; CURRENT APPLICATION NUMBER: US/10/055,728
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,722
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TAG sequence Hs23579
US-10-055-728-27

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
      |||||
Db      4 CAGGAGAA 11

RESULT 216
US-10-265-509B-6
; Sequence 6, Application US/10265509B
; Publication No. US20030170739A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: GENE EXPRESSION FOR ANALYZING PHOTODAMAGE
; FILE REFERENCE: J6663US(ED:EP/JVT)seq13sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/265,509B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/337,856
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq. # 56 of
; OTHER INFORMATION: Table I
US-10-265-509B-6

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      1 GCCAGGAG 8

RESULT 217
US-10-266-138B-6
; Sequence 6, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; FILE REFERENCE: J6664US(ED:EP/JVT)seq13sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq. # 56 of
; OTHER INFORMATION: Table I
US-10-266-138B-6

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      |||||
Db      1 GCCAGGAG 8
```


US-10-310-677-27
; Sequence 27, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
; APPLICANT: Kuyt v.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TAG sequence
; OTHER INFORMATION: Hs23579
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
US-10-310-677-27
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 730 CAGGAGAA 737
Db 4 CAGGAGAA 11
RESULT 218
US-10-450-797-452/c
; Sequence 452, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 452
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-452
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 736 AAACAGAA 743
Db 11 AAACAGAA 4
RESULT 219

US-10-450-797-714
; Sequence 714, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 714
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-714
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 728 GCCAGGAG 735
Db 1 GCCAGGAG 8
RESULT 220
US-10-450-797-1387
; Sequence 1387, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1387
Query Match 36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 733 GAGAAACA 740
Db 1 GAGAAACA 8
RESULT 221
US-10-723-940-88/c
; Sequence 88, Application US/10723940
; Publication No. US20040195468A1
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freeman, Robert
; TITLE OF INVENTION: Promoter Variants in the Alpha-7 Nicotinic Acetylcholine Receptor

; TITLE OF INVENTION: Gene
 ; FILE REFERENCE: VARD-07989
 ; CURRENT APPLICATION NUMBER: US/10/723,940
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 08/956,518
 ; PRIOR FILING DATE: 1997-10-23
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 88
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-723-940-88

Query Match 36.4%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAG 741
 DB 8 AGAAACAG 1

RESULT 222

US-09-765-061B-30/c
 ; Sequence 30, Application US/09765061B
 ; Publication No. US2003002165A1
 ; GENERAL INFORMATION:

; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene 17
 ; FILE REFERENCE: 96606/16UTL
 ; CURRENT APPLICATION NUMBER: US/09/765,061B
 ; CURRENT FILING DATE: 2001-01-17
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 30
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: mutation
 ; LOCATION: (4)...(4)
 ; OTHER INFORMATION: a to c mutation: IVS2-10A to C Benign

US-09-765-061B-30
 Query Match 36.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAAC 739
 DB 9 GGAGAAAC 2

RESULT 223

US-09-249-155-73/c
 ; Sequence 73, Application US/09249155
 ; Publication No. US20030037345A1
 ; GENERAL INFORMATION:

; APPLICANT: Heber-Katz, Ellen
 ; TITLE OF INVENTION: Compositions and Methods for Wound
 ; FILE REFERENCE: 00486.78503
 ; CURRENT APPLICATION NUMBER: US/09/249,155
 ; CURRENT FILING DATE: 1999-02-12
 ; EARLIER APPLICATION NUMBER: 60/074,737
 ; EARLIER FILING DATE: 1998-02-13
 ; EARLIER APPLICATION NUMBER: 60/097,937
 ; EARLIER FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: 60/102,051

; EARLIER FILING DATE: 1998-09-28
 ; NUMBER OF SEQ ID NOS: 254
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 73
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-249-155-73

Query Match 35.5%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
 DB 11 GCAGAAACCGA 1

RESULT 224

US-09-918-715-49
 ; Sequence 49, Application US/09918715
 ; Publication No. US20030017157A1
 ; GENERAL INFORMATION:

; APPLICANT: Brad St. Croix
 ; APPLICANT: Bert Vogelstein
 ; APPLICANT: Kenneth Kinzler
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107.00134
 ; CURRENT APPLICATION NUMBER: US/09/918,715
 ; CURRENT FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/222,599
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: 60/224,360
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 49
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-918-715-49

Query Match 35.5%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
 DB 1 TGCCAGGTGCA 11

RESULT 225

US-10-620-514-6
 ; Sequence 6, Application US/10620514
 ; Publication No. US20040068762A1
 ; GENERAL INFORMATION:

; APPLICANT: Attar, Ricardo M.
 ; APPLICANT: Bol, David K.
 ; APPLICANT: Gottardis, Marco
 ; APPLICANT: Mookhtiar, Kasim
 ; APPLICANT: Rowley, Ronald B.
 ; APPLICANT: Ostrowski, Jacek
 ; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING A REPORTER NUCLEIC ACID
 ; FILE REFERENCE: D0287 NP
 ; CURRENT APPLICATION NUMBER: US/10/620,514
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: US 60/396,501
 ; PRIOR FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DR-1
US-10-620-514-6

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      735 GAAACAGAACCA 745
DB      1 GGAACGGACCA 11
      |||||
RESULT 226
US-10-314-322-73/c
; Sequence 73, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-73

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAAACAGA 742
DB      11 GGAGAAACCGA 1
      |||||
RESULT 227
US-10-450-797-297/c
; Sequence 297, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 297
; LENGTH: 11

QY      732 GGAGAAACAGA 742
DB      11 GGAGAAACCGA 1
      |||||
RESULT 228
US-10-450-797-1044/c
; Sequence 1044, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1044
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1044

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAAACAGA 742
DB      11 GGAGATACAGA 1
      |||||
RESULT 229
US-09-365-029-21
; Sequence 21, Application US/09365029
; Patent No. US20010021772A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, Eugen
; APPLICANT: PEYMAN, Anuschirwan
; APPLICANT: BITONTI, Alan J.
; APPLICANT: WOESSNER, Richard D.
; TITLE OF INVENTION: SHORT OLIGONUCLEOTIDES FOR THE INHIBITION OF VEGF
; FILE REFERENCE: 26083/208
; CURRENT APPLICATION NUMBER: US/09/365,029
; CURRENT FILING DATE: 1999-08-02
; EARLIER APPLICATION NUMBER: EP 98114853.9
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF antisense
; OTHER INFORMATION: oligonucleotide
US-09-365-029-21
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Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCACGAGAAA 738
| | | | |
Db 1 GACAGCAGAAA 11

RESULT 230

US-09-804-481-9
; Sequence 9, Application US/09804481
; Patent No. US20020058287A1
; GENERAL INFORMATION:
; APPLICANT: de Graaf, David
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: Small Nuclear RNA Vectors and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 2825.1023-001
; CURRENT APPLICATION NUMBER: US/09/804,481
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modification fragment
US-09-804-481-9

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGAAC 744
| | | | |
Db 2 ACAACACAGAAC 12

RESULT 231

US-09-828-034-24
; Sequence 24, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-24

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGAAC 744
| | | | |
Db 2 AAAACAGUAC 12

RESULT 232
US-10-100-957A-65
; Sequence 65, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1A
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase-6
; OTHER INFORMATION: substrate recognition sequence
US-10-100-957A-65

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GCAGAACAGAGA 742
| | | | |
Db 1 GTAGAAATAGA 11

RESULT 233

US-10-073-377-3/c
; Sequence 3, Application US/10073377
; Publication No. US20030099670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Influenza C virus
US-10-073-377-3

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
| | | | |
Db 12 AGCAGAGCAG 2

RESULT 234

US-10-073-377-4/c
; Sequence 4, Application US/10073377
; Publication No. US20030099670A1
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gert
; APPLICANT: Menke, Annette
; TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and Replicative Capacities
; FILE REFERENCE: 010293us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/073,377
US-10-073-377-4/c

```
/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Modified
/ OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-4

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAAACACG 2

RESULT 235
US-10-211-088-359/c
/ Sequence 359, Application US/10211088
/ Publication No. US20030104479A1
/ GENERAL INFORMATION:
/ APPLICANT: Bright, Gary R.
/ APPLICANT: Premkumar, D. David
/ APPLICANT: Chen, Yih-Tai
/ TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular B
/ FILE REFERENCE: 01-1022-US
/ CURRENT APPLICATION NUMBER: US/10/211,088
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: 60/309,395
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/341,589
/ PRIOR FILING DATE: 2001-12-13
/ NUMBER OF SEQ ID NOS: 366
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 359
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence encoding post-translational modification site
US-10-211-088-359

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAC 746
Db 12 AGACAGACGC 2

RESULT 236
US-10-273-334-41/c
/ Sequence 41, Application US/10273334
/ Publication No. US20030129631A1
/ GENERAL INFORMATION:
/ APPLICANT: Pasternack, Gary R.
/ APPLICANT: Kocheavar, Gerald J.
/ APPLICANT: Brody, Jonathan R.
/ APPLICANT: Kodkol, Shrihari S.
/ TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
/ FILE REFERENCE: 031787.0076
/ CURRENT APPLICATION NUMBER: US/10/273,334
/ CURRENT FILING DATE: 2002-10-18
/ PRIOR APPLICATION NUMBER: US/09/591,500
/ PRIOR FILING DATE: 2000-12-06
/ PRIOR APPLICATION NUMBER: PCT/US98/26433
/ PRIOR FILING DATE: 1998-12-11

/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Modified
/ OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-4

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAAACACG 2

RESULT 235
US-10-211-088-359/c
/ Sequence 359, Application US/10211088
/ Publication No. US20030104479A1
/ GENERAL INFORMATION:
/ APPLICANT: Bright, Gary R.
/ APPLICANT: Premkumar, D. David
/ APPLICANT: Chen, Yih-Tai
/ TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular B
/ FILE REFERENCE: 01-1022-US
/ CURRENT APPLICATION NUMBER: US/10/211,088
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: 60/309,395
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/341,589
/ PRIOR FILING DATE: 2001-12-13
/ NUMBER OF SEQ ID NOS: 366
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 359
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence encoding post-translational modification site
US-10-211-088-359

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGACAC 746
Db 12 AGACAGACGC 2

RESULT 236
US-10-273-334-41/c
/ Sequence 41, Application US/10273334
/ Publication No. US20030129631A1
/ GENERAL INFORMATION:
/ APPLICANT: Pasternack, Gary R.
/ APPLICANT: Kocheavar, Gerald J.
/ APPLICANT: Brody, Jonathan R.
/ APPLICANT: Kodkol, Shrihari S.
/ TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
/ FILE REFERENCE: 031787.0076
/ CURRENT APPLICATION NUMBER: US/10/273,334
/ CURRENT FILING DATE: 2002-10-18
/ PRIOR APPLICATION NUMBER: US/09/591,500
/ PRIOR FILING DATE: 2000-12-06
/ PRIOR APPLICATION NUMBER: PCT/US98/26433
/ PRIOR FILING DATE: 1998-12-11

/ CURRENT FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Modified
/ OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-4

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 745
Db 12 GAAACAGAAC 2

RESULT 237
US-10-427-629-14
/ Sequence 14, Application US/10427629
/ Publication No. US20040078834A1
/ GENERAL INFORMATION:
/ APPLICANT: Croce, Carlo M.
/ TITLE OF INVENTION: Human Chronic Lymphocytic Leukemia Modeled In Mouse By Targeted
/ TITLE OF INVENTION: TCL1 Expression
/ FILE REFERENCE: TJU2851
/ CURRENT APPLICATION NUMBER: US/10/427,629
/ CURRENT FILING DATE: 2003-04-29
/ PRIOR APPLICATION NUMBER: 60/376,464
/ PRIOR FILING DATE: 2002-04-29
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 14
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-10-427-629-14

Query Match          35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAC 740
Db 2 CAGGAGACAG 12

RESULT 238
US-10-455-101-13
/ Sequence 13, Application US/10455101
/ Publication No. US20040038405A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Dakai
/ APPLICANT: Rabbani, Elazar
/ TITLE OF INVENTION: VECTORS AND VIRAL VECTORS, AND PACKAGING CELL LINES FOR
/ TITLE OF INVENTION: PROPOGATING SAME
/ FILE REFERENCE: Enz-56(D2)SequenceListing051199
/ CURRENT APPLICATION NUMBER: US/10/455,101
/ CURRENT FILING DATE: 2003-06-04
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/046,841
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-24
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/822,963
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-21
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 9
/ TYPE: DNA
/ ORGANISM: human glucocorticoid
```

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:nucleic acid,
; OTHER INFORMATION: double stranded, linear topology
US-10-455-101-13

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred.No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
||| |||||
Db 1 CAGAACATC 9

RESULT 239

US-10-283-741-14/c
; Sequence 14, Application US/10283741
; Publication No. US20030182068A1

GENERAL INFORMATION:

APPLICANT: Battersby, Bronwyn J.
APPLICANT: Miller, Christopher R.

APPLICANT: Trau, Matthias
APPLICANT: Way, Jeffery C.

APPLICANT: Johnston, Angus

TITLE OF INVENTION: Device and Methods For Directed
FILE REFERENCE: 50277/003002

CURRENT APPLICATION NUMBER: US/10/283,741
CURRENT FILING DATE: 2002-10-30

PRIOR APPLICATION NUMBER: US 60/330,759
PRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14

LENGTH: 9
TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-283-741-14

Query Match 33.6%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred.No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
||| |||||
Db 9 GAGTAACAG 1

RESULT 240

US-09-910-469-55/c
; Sequence 55, Application US/09910469
; Publication No. US20030175702A1

GENERAL INFORMATION:

APPLICANT: Schweitzer, Markus
APPLICANT: Anderson, Richard R.

APPLICANT: Mueller, Jochen

APPLICANT: Fiechter, Michael

APPLICANT: Bruecher, Christoph

APPLICANT: Kienle, Stefan

APPLICANT: Orwick, Jill

APPLICANT: Pignot, Marc

APPLICANT: Raddatz, Stefan

APPLICANT: Schneider, Eberhard

TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthetic

FILE REFERENCE: 264/217 Nanogen Recognomics

CURRENT APPLICATION NUMBER: US/09/910,469

CURRENT FILING DATE: 2001-07-19

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.1

SEQ ID NO 55
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic binding system
NAME/KEY: modified base
LOCATION: (1)..(10)
OTHER INFORMATION: pyranosyl RNA
US-09-910-469-55

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
||| |||||
Db 9 GATACAGAA 1

RESULT 241

US-09-910-469-56

Sequence 56, Application US/09910469
Publication No. US20030175702A1

GENERAL INFORMATION:

APPLICANT: Schweitzer, Markus
APPLICANT: Anderson, Richard R.

APPLICANT: Mueller, Jochen

APPLICANT: Fiechter, Michael

APPLICANT: Bruecher, Christoph

APPLICANT: Kienle, Stefan

APPLICANT: Orwick, Jill

APPLICANT: Pignot, Marc

APPLICANT: Raddatz, Stefan

APPLICANT: Schneider, Eberhard

TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthetic

FILE REFERENCE: 264/217 Nanogen Recognomics

CURRENT APPLICATION NUMBER: US/09/910,469

CURRENT FILING DATE: 2001-07-19

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.1

SEQ ID NO 56

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic binding system

NAME/KEY: modified base

LOCATION: (1)..(10)

OTHER INFORMATION: pyranosyl RNA

US-09-910-469-56

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
||| |||||
Db 2 GATACAGAA 10

RESULT 242

US-10-293-222-212

Sequence 212, Application US/10293222

Publication No. US2004003932A1

GENERAL INFORMATION:

APPLICANT: Versteeg, Rogier

APPLICANT: Caron, Hubertus N.

TITLE OF INVENTION: MYC targets

FILE REFERENCE: 2183-5580US

CURRENT APPLICATION NUMBER: US/10/293,222

100

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RESULT 247
US-10-033-145-373/c
; Sequence 373, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 373
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-373

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAGACAGAA 743
DB      10 GAGACAGAA 2
|||||

RESULT 248
US-10-033-145-595/c
; Sequence 595, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 595
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-595

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      730 CAGCAGAAA 738
DB      10 CAGCAGAAA 2
|||||

RESULT 249
US-10-033-145-780/c
; Sequence 780, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

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; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 780
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-780

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      727 TGCCAGGAG 735
DB      9 TTCCAGGAG 1
|||||

RESULT 250
US-10-033-145-794
; Sequence 794, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 794
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-794

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      735 GAAACAGAA 743
DB      1 GAAACTGAA 9
|||||

RESULT 251
US-10-033-145-813/c
; Sequence 813, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 813
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-10-033-145-813

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
|||||||
DB 9 GCCAGGATA 1

RESULT 252

US-10-033-145-835
; Sequence 835, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 835
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-835

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
|||||||
DB 2 AGGAGAATC 10

RESULT 253

US-10-033-145-1342/c
; Sequence 1342, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1342
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1342

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 CAAGAGAA 743
|||||||
DB 9 CAAGAGAA 1

RESULT 254

US-10-033-145-1396
; Sequence 1396, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1396
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1396

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAA 738
|||||||
DB 1 CAGGAGACA 9

RESULT 255

US-10-033-145-1419
; Sequence 1419, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1419
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1419

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAA 745
|||||||
DB 1 AACAGATA 9

RESULT 256

US-10-033-145-1496
; Sequence 1496, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145

; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1496
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1496

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 745
DB 1 ACCAGAAC 9

RESULT 257

US-10-033-145-1773
; Sequence 1773, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1773

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
DB 2 GAGAAACAG 10

RESULT 258

US-10-033-145-1999/c
; Sequence 1999, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1999
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1999

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
DB 9 GAGAAACAG 1

RESULT 259

US-10-010-802-261/c
; Sequence 261, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Duda, Amy
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Windemuth, Andreas
; TITLE OF INVENTION: Drug Target Isoenes: Polymorphisms in the Interleukin
; TITLE OF INVENTION: 4 Receptor Alpha Gene
; FILE REFERENCE: MMH-0002US2 IL4R alpha
; CURRENT APPLICATION NUMBER: US/10/010,802
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/19094
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 261
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-802-261

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAG 735
DB 10 TCCAGGAG 2

RESULT 260

US-10-010-802-287/c
; Sequence 287, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Duda, Amy
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Windemuth, Andreas
; TITLE OF INVENTION: Drug Target Isoenes: Polymorphisms in the Interleukin
; TITLE OF INVENTION: 4 Receptor Alpha Gene
; FILE REFERENCE: MMH-0002US2 IL4R alpha
; CURRENT APPLICATION NUMBER: US/10/010,802
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/19094
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-802-287

Query Match 33.6%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

Qy 739 CAGACACC 747
Db 10 CAGACACC 2

RESULT 261

US-10-176-464A-59
; Sequence 59, Application US/10176464A
; Publication No. US20030165902A1
; GENERAL INFORMATION:
; APPLICANT: Bieganski, Karyn
; APPLICANT: Lee, Helen
; APPLICANT: Messer, Chad
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOTYPES OF THE F2R GENE
; FILE REFERENCE: F2R MWH-1457US
; CURRENT APPLICATION NUMBER: US/10/176,464A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/30876
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/236,603
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-176-464A-59

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAACACAGA 742
Db 1 AGAACACAGA 9

RESULT 262

US-10-329-465-95/c
; Sequence 95, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-95

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 10 CAGGAGAAA 2

RESULT 263

US-10-330-627-238/c
; Sequence 238, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-238

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TCCAGGAG 735
Db 9 TCCAGGAG 1

RESULT 264

US-10-330-627-399/c
; Sequence 399, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-399

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 10 CAGGAGAAA 2

RESULT 265

US-10-193-507-79
; Sequence 79, Application US/10193507
; Publication No. US20040018493A1
; GENERAL INFORMATION:
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Kazemi, Amir
; APPLICANT: Lachowicz, Michael F.
; APPLICANT: Pabon, Vicente
; APPLICANT: Shah, Nisha

```

; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
; FILE REFERENCE: MW-2790US
; CURRENT APPLICATION NUMBER: US/10/193,507
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,573
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-507-79

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      731 AGGAGAAC 739
Db      2 AGGGAAC 10

```

```

RESULT 266
US-09-735-363A-82/c
; Sequence 82, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel

```

```

; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

```

```

; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-82

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      736 AACAGAAC 744
Db      10 AACAAAC 2

```

```

RESULT 267
US-09-249-155-86
; Sequence 86, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051

```

```

; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-86

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      738 ACAGAACAC 746
Db      1 ACAGAACAC 9

```

```

RESULT 268
US-09-249-155-124
; Sequence 124, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:

```

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; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-124

```

```

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      738 ACAGAACAC 746
Db      3 ACCGAACAC 11

```

```

RESULT 269
US-09-918-715-66/c
; Sequence 66, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66

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; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-66

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      734 AGAAGACAGA 742
      |||||
Db      9 AGAAGCAGA 1

RESULT 270
US-10-191-302-8
; Sequence 8, Application US/10191302
; Publication No. US20030092065A1
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, K. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/191,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,528
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..11
; OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS"
US-10-191-302-8

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      736 AAACAGAAC 744
      |||||
Db      3 AAACATAAC 11

RESULT 271
US-10-314-322-86
; Sequence 86, Application US/10314322
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```
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-86

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
      |||||
Db      1 ACAGAACTC 9

RESULT 272
US-10-314-322-124
; Sequence 124, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-124

Query Match          33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      738 ACAGAACAC 746
      |||||
Db      3 ACCGAACAC 11

RESULT 273
US-10-612-224-78
; Sequence 78, Application US/10612224
; Publication No. US20040137011A1
```

; GENERAL INFORMATION:
 ; APPLICANT: Cunningham, Philip R.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 ; IDENTIFICATION OF ANTIBIOTICS THAT ARE NOT SUSCEPTIBLE TO
 ; TITLE OF INVENTION: IDENTIFICATION OF ANTIBIOTIC RESISTANCE
 ; FILE REFERENCE: HSK-2597
 ; CURRENT APPLICATION NUMBER: US/10/612,224
 ; CURRENT FILING DATE: 2003-07-01
 ; PRIOR APPLICATION NUMBER: 60/393237
 ; PRIOR FILING DATE: 2002-07-01
 ; PRIOR APPLICATION NUMBER: 60/452012
 ; PRIOR FILING DATE: 2003-03-05
 ; NUMBER OF SEQ ID NOS: 245
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 78
 ; LENGTH: 11
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer
 US-10-612-224-78

Query Match 33.6%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
 Db 2 ACAGAACAC 10

RESULT 274
 US-10-450-797-51/c
 ; Sequence 51, Application US/10450797
 ; Publication No. US20040142335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Petersohn, Dirk
 ; APPLICANT: Conradt, Marcus
 ; APPLICANT: Hofmann, Kay
 ; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
 ; FILE REFERENCE: HSK-0041
 ; CURRENT APPLICATION NUMBER: US/10/450,797
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: PCT/EP01/15178
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: DE 101 00 121.5
 ; PRIOR FILING DATE: 2001-01-03
 ; NUMBER OF SEQ ID NOS: 1435
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 51
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-450-797-51

Query Match 33.6%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
 Db 11 CAGAACACC 3

RESULT 275
 US-10-450-797-110/c
 ; Sequence 110, Application US/10450797
 ; Publication No. US20040142335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Petersohn, Dirk
 ; APPLICANT: Conradt, Marcus
 ; APPLICANT: Hofmann, Kay
 ; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

; FILE REFERENCE: HSK-0041
 ; CURRENT APPLICATION NUMBER: US/10/450,797
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: PCT/EP01/15178
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: DE 101 00 121.5
 ; PRIOR FILING DATE: 2001-01-03
 ; NUMBER OF SEQ ID NOS: 1435
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 110
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-450-797-110

Query Match 33.6%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAC 740
 Db 9 GGAGAACAC 1

RESULT 276
 US-10-450-797-284/c
 ; Sequence 284, Application US/10450797
 ; Publication No. US20040142335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Petersohn, Dirk
 ; APPLICANT: Conradt, Marcus
 ; APPLICANT: Hofmann, Kay
 ; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
 ; FILE REFERENCE: HSK-0041
 ; CURRENT APPLICATION NUMBER: US/10/450,797
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: PCT/EP01/15178
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: DE 101 00 121.5
 ; PRIOR FILING DATE: 2001-01-03
 ; NUMBER OF SEQ ID NOS: 1435
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 284
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-450-797-284

Query Match 33.6%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
 Db 9 ACAGAACAC 1

RESULT 277
 US-10-450-797-285
 ; Sequence 285, Application US/10450797
 ; Publication No. US20040142335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Petersohn, Dirk
 ; APPLICANT: Conradt, Marcus
 ; APPLICANT: Hofmann, Kay
 ; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
 ; FILE REFERENCE: HSK-0041
 ; CURRENT APPLICATION NUMBER: US/10/450,797
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: PCT/EP01/15178
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: DE 101 00 121.5
 ; PRIOR FILING DATE: 2001-01-03

; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 285
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-285

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAA 738
Db 1 CAGGAGGAA 9

RESULT 278

US-10-450-797-335/c
; Sequence 335, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 335
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-335

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACA 745
Db 10 AAGAGACA 2

RESULT 279

US-10-450-797-538
; Sequence 538, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 538
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-538

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
Db 1 GAACAAAA 9

RESULT 280

US-10-450-797-626
; Sequence 626, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 626
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-626

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 1 GGAACACAG 9

RESULT 281

US-10-450-797-662/c
; Sequence 662, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 662
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-662

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 1 AGAAACAGA 9


```
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1320
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1320

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727 TGCCAGGAG 735
Db      2 TGGCAGGAG 10
      ||| |||||
```

Search completed: October 18, 2004, 14:11:19
Job time : 1 secs

This Page Blank (uspto)

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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:05:37 ; Search time 0.001 Seconds

(without alignments)
333.432 Million cell updates/sec

Title: US-09-695-451-1

Perfect score: 22

Sequence: 1 tggcaggagaacacagaccg 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 634 seqs, 7578 residues

Total number of hits satisfying chosen parameters: 1268

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 634 summaries

Database : rge1-727.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	95.5	21	1	BD174191
C 2	21	95.5	21	1	BD185146
C 3	17	77.3	18	1	AR096376
C 4	17	77.3	18	1	BD217424
C 5	16.4	74.5	22	1	AX598452
C 6	15.4	70.0	18	1	AR175645
C 7	15.4	70.0	18	1	AR195221
C 8	15.4	70.0	18	1	AR223203
C 9	15.4	70.0	18	1	AR241422
C 10	15.4	70.0	18	1	BD014788
C 11	15.4	70.0	19	1	AX132046
C 12	15	68.2	18	1	AX286278
C 13	14.6	66.4	22	1	AX286282
C 14	14.6	66.4	22	1	AX286288
C 15	14.6	66.4	22	1	AX132045
C 16	14.4	65.5	19	1	AX132045
C 17	14.2	64.5	19	1	AX132309
C 18	14.2	64.5	21	1	AX440525
C 19	14	63.6	18	1	AX71109
C 20	13.4	60.9	18	1	AX67103
C 21	13.4	60.9	18	1	AX67105
C 22	13.4	60.9	18	1	AX67106
C 23	13.4	60.9	20	1	E26485
C 24	13.2	60.0	19	1	AX132047
C 25	13.2	60.0	19	1	AX132308
C 26	13.2	60.0	19	1	AX132310
C 27	12.8	58.2	17	1	AX499947
C 28	12.8	58.2	17	1	AX499948
C 29	12.8	58.2	19	1	AX023982
C 30	12.4	56.4	16	1	AX255710
C 31	12.4	56.4	17	1	AX076026
C 32	12.4	56.4	17	1	AX499949
C 33	12.4	56.4	17	1	AX499950

C 34	12.4	56.4	18	1	A67108
C 35	12.4	56.4	18	1	A67111
C 36	12.4	56.4	18	1	AR065607
C 37	12.2	55.5	18	1	I06264
C 38	12.2	55.5	17	1	AR292914
C 39	12	54.5	18	1	BD241241
C 40	11.8	53.6	17	1	AX499946
C 41	11.8	53.6	17	1	AX674572
C 42	11.8	53.6	17	1	AX729839
C 43	11.8	53.6	17	1	AX762877
C 44	11.8	53.6	18	1	A67102
C 45	11.8	53.6	18	1	A67104
C 46	11.4	51.8	17	1	AR190011
C 47	11.4	51.8	17	1	AR324988
C 48	11.4	51.8	17	1	AX499951
C 49	11.4	51.8	17	1	AX674143
C 50	11.4	51.8	17	1	AX732557
C 51	11.2	50.9	17	1	BD266301
C 52	11.2	50.9	17	1	E54495
C 53	11.2	50.9	17	1	AR190548
C 54	11.2	50.9	17	1	AR325471
C 55	11.2	50.9	17	1	AX227611
C 56	11.2	50.9	17	1	AX692031
C 57	11.2	50.9	17	1	AX692032
C 58	11.2	50.9	17	1	BD105092
C 59	11	50.0	15	1	A11101
C 60	11	50.0	15	1	AR362726
C 61	10.8	49.1	15	1	I61456
C 62	10.8	49.1	15	1	AX635865
C 63	10.8	49.1	15	1	BD208396
C 64	10.8	49.1	16	1	A09424
C 65	10.8	49.1	16	1	A10627
C 66	10.8	49.1	16	1	A11575
C 67	10.8	49.1	16	1	A35095
C 68	10.8	49.1	16	1	AX076025
C 69	10.4	47.3	12	1	I28559
C 70	10.4	47.3	12	1	I58721
C 71	10.4	47.3	14	1	A40588
C 72	10.4	47.3	14	1	A89112
C 73	10.4	47.3	14	1	A89603
C 74	10.4	47.3	14	1	AR061873
C 75	10.4	47.3	14	1	AR232868
C 76	10.4	47.3	14	1	AR407925
C 77	10.4	47.3	14	1	AX030163
C 78	10.4	47.3	14	1	AX316484
C 79	10.4	47.3	14	1	BD066625
C 80	10.4	47.3	14	1	BD067116
C 81	10.4	47.3	15	1	I61457
C 82	10.4	47.3	15	1	AR180064
C 83	10.4	47.3	15	1	AR180799
C 84	10.4	47.3	15	1	AX635867
C 85	10.4	47.3	16	1	A22593
C 86	10.4	47.3	16	1	AR096276
C 87	10.4	47.3	16	1	AX076029
C 88	10.4	47.3	16	1	AX255620
C 89	10.4	47.3	16	1	AX255663
C 90	10.4	47.3	16	1	AX452095
C 91	10.2	46.4	15	1	BD208458
C 92	10.2	46.4	15	1	BD208459
C 93	10	45.5	11	1	AR123024
C 94	10	45.5	11	1	AX626398
C 95	10	45.5	11	1	AR180388
C 96	10	45.5	15	1	BD208460
C 97	9.8	44.5	14	1	AX5806
C 98	9.8	44.5	14	1	A40589
C 99	9.8	44.5	14	1	A87922
C 100	9.8	44.5	14	1	A89113
C 101	9.8	44.5	14	1	A89889
C 102	9.8	44.5	14	1	AR029997
C 103	9.8	44.5	14	1	AR030009
C 104	9.8	44.5	14	1	I26228
C 105	9.8	44.5	14	1	I52188
C 106	9.8	44.5	14	1	ACCESSION:I52193

ACCESSION:A67108
ACCESSION:A67111
ACCESSION:AR065607
ACCESSION:I06264
ACCESSION:AR292914
ACCESSION:BD241241
ACCESSION:AX499946
ACCESSION:AX674572
ACCESSION:AX729839
ACCESSION:AX762877
ACCESSION:A67102
ACCESSION:A67104
ACCESSION:AR190011
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ACCESSION:AX499951
ACCESSION:AX674143
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ACCESSION:BD266301
ACCESSION:E54495
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ACCESSION:AX030163
ACCESSION:AX316484
ACCESSION:BD066625
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ACCESSION:I61457
ACCESSION:AR180064
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ACCESSION:A89889
ACCESSION:AR029997
ACCESSION:AR030009
ACCESSION:I26228
ACCESSION:I52188
ACCESSION:I52193

107	9.8	44.5	14	1	AR232869	ACCESSION:AR232869	C 180	9	40.9	11	1	AX630559	ACCESSION:AX630559
108	9.8	44.5	14	1	AX030164	ACCESSION:AX030164	C 181	9	40.9	11	1	AX632264	ACCESSION:AX632264
109	9.8	44.5	14	1	AX316485	ACCESSION:AX316485	182	9	40.9	11	1	AX632552	ACCESSION:AX632552
110	9.8	44.5	14	1	AX571850	ACCESSION:AX571850	183	9	40.9	11	1	BD242525	ACCESSION:BD242525
111	9.8	44.5	14	1	BD065435	ACCESSION:BD065435	184	9	40.9	12	1	BD242532	ACCESSION:BD242532
112	9.8	44.5	14	1	BD066626	ACCESSION:BD066626	185	9	40.9	12	1	AR217450	ACCESSION:AR217450
113	9.8	44.5	14	1	BD209300	ACCESSION:BD209300	186	9	40.9	12	1	AR217457	ACCESSION:AR217457
114	9.8	44.5	15	1	AR130724	ACCESSION:AR130724	187	9	40.9	12	1	AX766772	ACCESSION:AX766772
115	9.8	44.5	15	1	AR180392	ACCESSION:AR180392	188	9	40.9	12	1	AX766786	ACCESSION:AX766786
116	9.8	44.5	15	1	AR235561	ACCESSION:AR235561	189	9	40.9	13	1	AR364664	ACCESSION:AR364664
117	9.8	44.5	15	1	AR370348	ACCESSION:AR370348	C 190	8.8	40.0	13	1	AR123872	ACCESSION:AR123872
118	9.8	44.5	15	1	AX009449	ACCESSION:AX009449	C 191	8.8	40.0	12	1	AR123873	ACCESSION:AR123873
119	9.8	44.5	15	1	BD005884	ACCESSION:BD005884	C 192	8.8	40.0	12	1	AR123877	ACCESSION:AR123877
120	9.8	44.5	15	1	BD208397	ACCESSION:BD208397	C 193	8.8	40.0	12	1	AR178311	ACCESSION:AR178311
121	9.8	44.5	11	1	AX471642	ACCESSION:AX471642	C 194	8.8	40.0	12	1	AX323393	ACCESSION:AX323393
122	9.4	42.7	11	1	AX627643	ACCESSION:AX627643	C 195	8.8	40.0	13	1	AR021478	ACCESSION:AR021478
123	9.4	42.7	12	1	AR011923	ACCESSION:AR011923	C 196	8.8	40.0	13	1	AR061316	ACCESSION:AR061316
124	9.4	42.7	12	1	AR017794	ACCESSION:AR017794	C 197	8.8	40.0	13	1	AR100114	ACCESSION:AR100114
125	9.4	42.7	12	1	AR077199	ACCESSION:AR077199	C 198	8.8	40.0	13	1	AR100119	ACCESSION:AR100119
126	9.4	42.7	12	1	AR087821	ACCESSION:AR087821	C 199	8.8	40.0	13	1	AR175971	ACCESSION:AR175971
127	9.4	42.7	12	1	AR167798	ACCESSION:AR167798	200	8.6	39.1	13	1	BD269493	ACCESSION:BD269493
128	9.4	42.7	12	1	BD242531	ACCESSION:BD242531	201	8.6	39.1	13	1	AX035442	ACCESSION:AX035442
129	9.4	42.7	12	1	BD269489	ACCESSION:BD269489	202	8.6	39.1	13	1	AX100748	ACCESSION:AX100748
130	9.4	42.7	12	1	E29682	ACCESSION:E29682	203	8.6	39.1	13	1	AX352663	ACCESSION:AX352663
131	9.4	42.7	12	1	E38120	ACCESSION:E38120	204	8.6	39.1	13	1	AX362221	ACCESSION:AX362221
132	9.4	42.7	12	1	E38788	ACCESSION:E38788	205	8.6	39.1	13	1	AX428934	ACCESSION:AX428934
133	9.4	42.7	12	1	E64214	ACCESSION:E64214	206	8.6	39.1	13	1	AX512617	ACCESSION:AX512617
134	9.4	42.7	12	1	AR217456	ACCESSION:AR217456	207	8.6	39.1	13	1	AX522268	ACCESSION:AX522268
135	9.4	42.7	12	1	AR282763	ACCESSION:AR282763	208	8.4	38.2	10	1	AR026539	ACCESSION:AR026539
136	9.4	42.7	12	1	AX035438	ACCESSION:AX035438	209	8.4	38.2	10	1	BD238913	ACCESSION:BD238913
137	9.4	42.7	12	1	AX100751	ACCESSION:AX100751	C 210	8.4	38.2	10	1	BD239757	ACCESSION:BD239757
138	9.4	42.7	12	1	AX100751	ACCESSION:AX100751	211	8.4	38.2	10	1	BD239797	ACCESSION:BD239797
139	9.4	42.7	12	1	AX352660	ACCESSION:AX352660	C 212	8.4	38.2	10	1	E39660	ACCESSION:E39660
140	9.4	42.7	12	1	AX352661	ACCESSION:AX352661	213	8.4	38.2	10	1	AR303294	ACCESSION:AR303294
141	9.4	42.7	12	1	AX362218	ACCESSION:AX362218	C 214	8.4	38.2	10	1	AR303316	ACCESSION:AR303316
142	9.4	42.7	12	1	AX362219	ACCESSION:AX362219	C 215	8.4	38.2	10	1	AR303402	ACCESSION:AR303402
143	9.4	42.7	12	1	AX428931	ACCESSION:AX428931	C 216	8.4	38.2	10	1	AR336872	ACCESSION:AR336872
144	9.4	42.7	12	1	AX428932	ACCESSION:AX428932	C 217	8.4	38.2	10	1	AX152919	ACCESSION:AX152919
145	9.4	42.7	12	1	AX512614	ACCESSION:AX512614	C 218	8.4	38.2	10	1	AX153378	ACCESSION:AX153378
146	9.4	42.7	12	1	AX512615	ACCESSION:AX512615	C 219	8.4	38.2	10	1	AX153448	ACCESSION:AX153448
147	9.4	42.7	12	1	AX522265	ACCESSION:AX522265	220	8.4	38.2	10	1	AX035584	ACCESSION:AX035584
148	9.4	42.7	12	1	AX522266	ACCESSION:AX522266	221	8.4	38.2	10	1	BD083216	ACCESSION:BD083216
149	9.4	42.7	12	1	AX766784	ACCESSION:AX766784	222	8.4	38.2	10	1	BD166609	ACCESSION:BD166609
150	9.4	42.7	13	1	AR282758	ACCESSION:AR282758	223	8.4	38.2	10	1	BD166675	ACCESSION:BD166675
151	9.4	42.7	13	1	AR407966	ACCESSION:AR407966	224	8.4	38.2	10	1	BD166874	ACCESSION:BD166874
152	9.4	42.7	13	1	BD237463	ACCESSION:BD237463	C 225	8.4	38.2	11	1	AX470470	ACCESSION:AX470470
153	9.4	42.7	14	1	BD261338	ACCESSION:BD261338	C 226	8.4	38.2	11	1	AX470955	ACCESSION:AX470955
154	9.4	42.7	14	1	BD269502	ACCESSION:BD269502	C 227	8.4	38.2	11	1	AX470960	ACCESSION:AX470960
155	9.4	42.7	14	1	AX035451	ACCESSION:AX035451	C 228	8.4	38.2	11	1	AX471036	ACCESSION:AX471036
156	9.4	42.7	14	1	AX352673	ACCESSION:AX352673	C 229	8.4	38.2	11	1	AX471164	ACCESSION:AX471164
157	9.4	42.7	14	1	AX362231	ACCESSION:AX362231	C 230	8.4	38.2	11	1	AX623587	ACCESSION:AX623587
158	9.4	42.7	14	1	AX428944	ACCESSION:AX428944	C 231	8.4	38.2	11	1	AX623632	ACCESSION:AX623632
159	9.4	42.7	14	1	AX512628	ACCESSION:AX512628	C 232	8.4	38.2	11	1	AX624664	ACCESSION:AX624664
160	9.4	42.7	14	1	AX522279	ACCESSION:AX522279	C 233	8.4	38.2	11	1	AX624971	ACCESSION:AX624971
161	9.2	41.8	14	1	AX40498	ACCESSION:AX40498	234	8.4	38.2	11	1	AX626122	ACCESSION:AX626122
162	9.2	41.8	14	1	AR80925	ACCESSION:AR80925	235	8.4	38.2	11	1	AX627227	ACCESSION:AX627227
163	9.2	41.8	14	1	AR337778	ACCESSION:AR337778	236	8.4	38.2	11	1	AX627341	ACCESSION:AX627341
164	9.2	41.8	14	1	AX316394	ACCESSION:AX316394	C 237	8.4	38.2	11	1	AX627766	ACCESSION:AX627766
165	9.2	41.8	14	1	BD066538	ACCESSION:BD066538	C 238	8.4	38.2	11	1	AX628298	ACCESSION:AX628298
166	9.2	41.8	14	1	BD193255	ACCESSION:BD193255	C 239	8.4	38.2	11	1	AX628930	ACCESSION:AX628930
167	9.2	41.8	14	1	S5997781	ACCESSION:S5997781	C 240	8.4	38.2	11	1	AX629191	ACCESSION:AX629191
168	9	40.9	10	1	BD240369	ACCESSION:BD240369	C 241	8.4	38.2	11	1	AX630040	ACCESSION:AX630040
169	9	40.9	10	1	BD240503	ACCESSION:BD240503	C 242	8.4	38.2	11	1	AX630299	ACCESSION:AX630299
170	9	40.9	10	1	AR303296	ACCESSION:AR303296	C 243	8.4	38.2	11	1	AX631008	ACCESSION:AX631008
171	9	40.9	10	1	AR303305	ACCESSION:AR303305	C 244	8.4	38.2	11	1	AX631053	ACCESSION:AX631053
172	9	40.9	10	1	AR303339	ACCESSION:AR303339	C 245	8.4	38.2	11	1	AX632085	ACCESSION:AX632085
173	9	40.9	10	1	BD161312	ACCESSION:BD161312	C 246	8.4	38.2	11	1	AX632392	ACCESSION:AX632392
174	9	40.9	11	1	AX470590	ACCESSION:AX470590	C 247	8.4	38.2	12	1	AR123885	ACCESSION:AR123885
175	9	40.9	11	1	AX623138	ACCESSION:AX623138	248	8.4	38.2	12	1	AX328584	ACCESSION:AX328584
176	9	40.9	11	1	AX624843	ACCESSION:AX624843	249	8.4	38.2	12	1	AX328589	ACCESSION:AX328589
177	9	40.9	11	1	AX625131	ACCESSION:AX625131	250	8.4	38.2	12	1	BD132149	ACCESSION:BD132149
178	9	40.9	11	1	AX626407	ACCESSION:AX626407	251	8.4	38.2	12	1	BD132154	ACCESSION:BD132154
179	9	40.9	11	1	AX628047	ACCESSION:AX628047	252	8.4	38.2	12	1	S73118S1	ACCESSION:S73118S1

253	8	36.4	10	1	BD239119	ACCESSION:BD239119	C 326	7.8	35.5	11	1	AX629695	ACCESSION:AX629695
254	8	36.4	10	1	AR300461	ACCESSION:AR300461	C 327	7.8	35.5	11	1	AX629821	ACCESSION:AX629821
255	8	36.4	10	1	AX152111	ACCESSION:AX152111	328	7.8	35.5	11	1	AX629849	ACCESSION:AX629849
256	8	36.4	10	1	AX152162	ACCESSION:AX152162	C 329	7.8	35.5	11	1	AX630158	ACCESSION:AX630158
257	8	36.4	10	1	AX152164	ACCESSION:AX152164	C 330	7.8	35.5	11	1	AX630160	ACCESSION:AX630160
258	8	36.4	10	1	AX152170	ACCESSION:AX152170	331	7.8	35.5	11	1	AX630631	ACCESSION:AX630631
259	8	36.4	10	1	AX153406	ACCESSION:AX153406	332	7.8	35.5	11	1	AX630810	ACCESSION:AX630810
260	8	36.4	10	1	AX301382	ACCESSION:AX301382	333	7.8	35.5	11	1	AX631236	ACCESSION:AX631236
261	8	36.4	10	1	BD083241	ACCESSION:BD083241	C 334	7.8	35.5	11	1	AX631287	ACCESSION:AX631287
262	8	36.4	10	1	BD161382	ACCESSION:BD161382	C 335	7.8	35.5	11	1	AX631662	ACCESSION:AX631662
263	8	36.4	11	1	AX393135	ACCESSION:AX393135	336	7.8	35.5	11	1	AX631787	ACCESSION:AX631787
264	8	36.4	11	1	AX470875	ACCESSION:AX470875	337	7.8	35.5	11	1	AX632664	ACCESSION:AX632664
265	8	36.4	11	1	AX471137	ACCESSION:AX471137	C 338	7.8	35.5	11	1	AX632754	ACCESSION:AX632754
266	8	36.4	11	1	AX471810	ACCESSION:AX471810	C 339	7.8	35.5	11	1	AX722229	ACCESSION:AX722229
267	8	36.4	11	1	AX492050	ACCESSION:AX492050	C 340	7.8	35.5	11	1	BD124242	ACCESSION:BD124242
268	8	36.4	11	1	AX511289	ACCESSION:AX511289	341	7.8	35.5	11	1	BD174612	ACCESSION:BD174612
269	8	36.4	11	1	AX623051	ACCESSION:AX623051	342	7.8	35.5	11	1	BD174617	ACCESSION:BD174617
270	8	36.4	11	1	AX623196	ACCESSION:AX623196	343	7.8	35.5	12	1	A06060	ACCESSION:A06060
271	8	36.4	11	1	AX623555	ACCESSION:AX623555	C 344	7.8	35.5	12	1	A06061	ACCESSION:A06061
272	8	36.4	11	1	AX624933	ACCESSION:AX624933	345	7.8	35.5	12	1	A16603	ACCESSION:A16603
273	8	36.4	11	1	AX624958	ACCESSION:AX624958	346	7.8	35.5	12	1	A16604	ACCESSION:A16604
274	8	36.4	11	1	AX624999	ACCESSION:AX624999	347	7.8	35.5	12	1	A47643	ACCESSION:A47643
275	8	36.4	11	1	AX625252	ACCESSION:AX625252	C 348	7.8	35.5	12	1	A61481	ACCESSION:A61481
276	8	36.4	11	1	AX625448	ACCESSION:AX625448	349	7.8	35.5	12	1	AR027861	ACCESSION:AR027861
277	8	36.4	11	1	AX625885	ACCESSION:AX625885	350	7.8	35.5	12	1	AR030026	ACCESSION:AR030026
278	8	36.4	11	1	AX626273	ACCESSION:AX626273	351	7.8	35.5	12	1	AR030040	ACCESSION:AR030040
279	8	36.4	11	1	AX626400	ACCESSION:AX626400	352	7.8	35.5	12	1	AR030162	ACCESSION:AR030162
280	8	36.4	11	1	AX626990	ACCESSION:AX626990	C 353	7.8	35.5	12	1	AR058694	ACCESSION:AR058694
281	8	36.4	11	1	AX627679	ACCESSION:AX627679	354	7.8	35.5	12	1	BD242527	ACCESSION:BD242527
282	8	36.4	11	1	AX627723	ACCESSION:AX627723	355	7.8	35.5	12	1	BD248202	ACCESSION:BD248202
283	8	36.4	11	1	AX628113	ACCESSION:AX628113	C 356	7.8	35.5	12	1	BD263213	ACCESSION:BD263213
284	8	36.4	11	1	AX628247	ACCESSION:AX628247	C 357	7.8	35.5	12	1	BD269488	ACCESSION:BD269488
285	8	36.4	11	1	AX628626	ACCESSION:AX628626	C 358	7.8	35.5	12	1	BD269490	ACCESSION:BD269490
286	8	36.4	11	1	AX628755	ACCESSION:AX628755	C 359	7.8	35.5	12	1	E04220	ACCESSION:E04220
287	8	36.4	11	1	AX629350	ACCESSION:AX629350	360	7.8	35.5	12	1	E32720	ACCESSION:E32720
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SOURCE
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ORGANISM
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REFERENCE
1 (bases 1 to 21)
AUTHORS
HiKichi, Y., Shintani, Y. and Matsui, H.
TITLE
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JOURNAL
Patent: WO 02066049-A 37 29-AUG-2002;
TAKEDA CHEMICAL INDUSTRIES LTD, YUKIKO HIKICHI, YASUSHI SHINTANI,
HIDEKI MATSUI
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PI YUKIKO HIKICHI, YASUSHI SHINTANI, HIDEKI MATSUI PC
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QY 727 TGCCAGGAGAAACAGAACACC 747
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RESULT 2
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ACCESSION
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JP 2002356438-A/37.

ACCESSION:BD083230
ACCESSION:BD083361
ACCESSION:BD161207
ACCESSION:BD161244
ACCESSION:BD161338
ACCESSION:BD161404
ACCESSION:BD161472
ACCESSION:BD166539
ACCESSION:BD166678
ACCESSION:BD166694
ACCESSION:BD166875
ACCESSION:BD166890
ACCESSION:BD167093
ACCESSION:BD167149
ACCESSION:BD167220
ACCESSION:BD225309
ACCESSION:BD225320

ALIGNMENTS

21 bp DNA linear PAT 18-FEB-2003

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 21)
AUTHORS     Hikichi, Y., Shintani, Y. and Matsui, H.
TITLE       Cell differentiating agent
JOURNAL     Patent: JP 2002356438-A 37 13-DEC-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS Artificial Sequence
            PN JP 2002356438-A/37
            PD 13-DEC-2002
            PF 21-FEB-2002 JP 2002044741
            PI YUKIKO HIKICHI, YASUSHI SHINTANI, HIDEKI MATSUI PC
            A61K38/00, A61K31/7088, A61F15/00, A61E21/04, A61P35/00, C12N15/09// PC
            C07K14/525,
            PC C12Q1/68, A61K37/02, C12N15/00
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            FH Key
            FT source
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACAGACACC 747
DB 21 TGCCAGGAGAAACAGACACC 1
RESULT 3
LOCUS      AR096376/c
DEFINITION Sequence 47 from patent US 6007995.
ACCESSION  AR096376
VERSION     AR096376.1 GI:100251133
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Baker, B.F. and Cowsert, L.M.
TITLE       Antisense inhibition of TNFR1 expression
JOURNAL     Patent: US 6007995-A 47 28-DEC-1999;
FEATURES    Location/Qualifiers
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             /organism="unknown"
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Query Match 77.3%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 732 GGAGAAACAGACACCG 748
DB 18 GGAGAAACAGACACCG 2
RESULT 4
LOCUS      BD217424/c
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION  BD217424
VERSION     BD217424.1 GI:33027194
KEYWORDS   JP 2002519015-A/47.
SOURCE     unidentified
ORGANISM   unidentified.
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 18)
AUTHORS     Baker, B.F. and Cowsert, L.M.
TITLE       Antisense modulation of TNFR1 expression
JOURNAL     Patent: JP 2002519015-A 47 02-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS Unidentified
            PN JP 2002519015-A/47
            PD 02-JUL-2002
            PF 17-JUN-1999 JP 2000557265
            PR 26-JUN-1998 US 09/106038
            PI BRENDA F BAKER, LEX M COWSERT
            PC C12N15/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC
            C12Q1/68,
            PC C12N15/00
            CC Strandedness: Single;
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            CC Antisense modulation of TNFR1 expression
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Query Match 77.3%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 732 GGAGAAACAGACACCG 748
DB 18 GGAGAAACAGACACCG 2
RESULT 5
LOCUS      AX598452
DEFINITION Sequence 726 from Patent WO0244994.
ACCESSION  AX598452
VERSION     AX598452.1 GI:28398628
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Brower, A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
            Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
            Neri, B.P., Reimer, N.D., Roever, R.T., Skrzypczynski, Z., Ziarno, W.A.,
            Comerford, J., Stump, S. and Viegut, D.D.
            TITLE Systems and method for detection assay production and sale
            JOURNAL Patent: WO 0244994-A 726 06-JUN-2002;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES    Location/Qualifiers
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             /db_xref="taxon:32630"
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Best Local Similarity 94.4%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACAGAAC 744
DB 5 TGCCAGGAGACAGAAC 22
RESULT 6
LOCUS      AR175645/c
DEFINITION Sequence 45 from patent US 6309853.

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ACCESSION AR175645
VERSION AR175645.1 GI:117916944
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friedman,J.M., Zhang,Y. and Proenca,R.
TITLE Modulators of body weight, corresponding nucleic acids and
proteins, and diagnostic and therapeutic uses thereof
JOURNAL Patent: US 6309853-A 45 30-OCT-2001;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACACACAC 746
Db 18 CAGGAGAAACACACAC 2

RESULT 7
AR195221/c
LOCUS AR241422
DEFINITION Sequence 45 from patent US 6350730.
ACCESSION AR195221
VERSION AR195221.1 GI:20244658
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friedman,J.M., Zhang,Y. and Proenca,R.
TITLE OB polypeptides and modified forms as modulators of body weight
JOURNAL Patent: US 6350730-A 45 26-FEB-2002;
FEATURES Location/Qualifiers
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Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACACACAC 746
Db 18 CAGGAGAAACACACAC 2

RESULT 8
AR222303/c
LOCUS AR222303
DEFINITION Sequence 45 from patent US 6429290.
ACCESSION AR222303
VERSION AR222303.1 GI:23329788
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friedman,J.M., Zhang,Y. and Proenca,R.
TITLE OB polypeptides, modified forms and derivatives
JOURNAL Patent: US 6429290-A 45 06-AUG-2002;
FEATURES Location/Qualifiers
source
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Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACACACAC 746
Db 18 CAGGAGAAACACACAC 2

RESULT 9
AR241422/c
LOCUS AR241422
DEFINITION Sequence 45 from patent US 6471956.
ACCESSION AR241422
VERSION AR241422.1 GI:27287112
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friedman,J.M., Zhang,Y. and Proenca,R.
TITLE Ob polypeptides, modified forms and compositions thereto
JOURNAL Patent: US 6471956-A 45 29-OCT-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACACACAC 746
Db 18 CAGGAGAAACACACAC 2

RESULT 10
BD014788/c
LOCUS BD014788
DEFINITION Modulator of weight, corresponding nucleic acid and protein, and
diagnosis and remedy utilization thereof.
ACCESSION BD014788
VERSION BD014788.1 GI:22555571
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friedman,J.M., Zhang,Y., Proenca,R., Maffei,M., Halaas,J.L.,
Kajiwar,K. and Burley,S.K.
TITLE Modulator of weight, corresponding nucleic acid and protein, and
diagnosis and remedy utilization thereof
JOURNAL Patent: JP 2001157591-A 29 12-JUN-2001;
COMMENT THE ROCKEFELLER UNIVERSITY
OS Homo sapiens (human)
PN JP 2001157591-A/29
PD 12-JUN-2001
PF 23-SEP-2000 JP 2000301456
FR 30-NOV-1994 US 08/347563, 10-MAY-1995 US 08/438431 PR
PI JEFFERY M FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA PI
MAFFEI,
PI JEFFERY L HALAAS, KETAN KAJIWARA, STEPHEN K BURLEY PC
C12N15/09, A61K31/711, A61K38/00, A61K39/395, A61K45/00, A61K48/00, PC
A61P3/04
PC A61P3/06, A61P3/10, A61P9/12, C07K14/47, C07K16/18, C12N1/19, C12N1/
PC 21, C12N5/10,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12R1/19, C12R1/72, PC
(C12N1/19, C12R1/85), (C12N1/19, C12R1/91), (C12N1/19, C12R1/07), PC
(C12N1/21, C12R1/465), (C12N1/21, C12R1/38), (C12N5/10, C12R1/91), PC
(C12P21/02, C12R1/19), C12N15/00, A61K37/02, C12N5/00, C12N5/00, PC
(C12N5/00, C12R1/91)
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CC Strandedness: Single;
CC Topology: Linear;
CC PCR primer SWS2359 specific in sequence tag site FH key
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Query Match
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QY 730 CAGGAGAAACAGACAC 746
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Db 18 CAGGAGAAACAGACAC 2

RESULT 11
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LOCUS
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  ACCESSION
  AX132046
  VERSION
  AX132046.1 GI:14138351
  KEYWORDS
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Robbins, J.M. and Tritz, R.
  TITLE
  Ribozyme therapy for the treatment of proliferative skin and eye
  JOURNAL
  Patent: WO 0130362-A 3264 03-MAY-2001;
  IMMUSOL, INC. (US)
  FEATURES
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        /db_xref="taxon:9606"
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Query Match
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QY 732 GGAGAAACAGAACCCG 748
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Db 19 GGAGAAACAGAACCCG 3

RESULT 12
A67107/c
LOCUS
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  Sequence 274 from Patent WO9740193.
  ACCESSION
  A67107
  VERSION
  A67107.1 GI:4538478
  KEYWORDS
  unidentified
  SOURCE
  unidentified
  ORGANISM
  unidentified
  REFERENCE
  1 (bases 1 to 18)
  AUTHORS
  Stuyver, L., Rossau, R. and Maertens, G.
  TITLE
  METHOD FOR TYPING AND DETECTING HBV
  JOURNAL
  Patent: WO 9740193-A 274 30-OCT-1997;
  INNOGENETICS NV (BE)
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/db_xref="taxon:32644"

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QY 728 GCCAGGAGAAACAGA 742
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Db 18 GCCAGGAGAAACAGA 4

RESULT 13
AX286278/c
LOCUS
  DEFINITION
  Sequence 7 from Patent WO0179296.
  ACCESSION
  AX286278
  VERSION
  AX286278.1 GI:17048526
  KEYWORDS
  Homo sapiens (human)
  SOURCE
  Homo sapiens
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
  TITLE
  Human emr2, a G-protein coupled receptor from the egf-tm7 family
  JOURNAL
  Patent: WO 0179296-A 7 25-OCT-2001;
  Isis Innovation Limited (GB)
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        /mol_type="unassigned DNA"
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Query Match
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QY 727 TCCAGGAGAAACAGACACC 747
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Db 22 TCCAGGAGAAACAGACACC 2

RESULT 14
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  ACCESSION
  AX286282
  VERSION
  AX286282.1 GI:17048530
  KEYWORDS
  Homo sapiens (human)
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  Homo sapiens
  ORGANISM
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
  TITLE
  Human emr2, a G-protein coupled receptor from the egf-tm7 family
  JOURNAL
  Patent: WO 0179296-A 11 25-OCT-2001;
  Isis Innovation Limited (GB)
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Query Match
  Best Local Similarity 66.4%; Score 14.6; DB 1; Length 22;
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QY 727 TCCAGGAGAAACAGACACC 747
  |||||
Db 22 TCCAGGAGAAACAGACACC 2

RESULT 15
AX286282/c
LOCUS
  DEFINITION
  Sequence 11 from Patent WO0179296.
  ACCESSION
  AX286282
  VERSION
  AX286282.1 GI:17048530
  KEYWORDS
  Homo sapiens (human)
  SOURCE
  Homo sapiens
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
  TITLE
  Human emr2, a G-protein coupled receptor from the egf-tm7 family
  JOURNAL
  Patent: WO 0179296-A 11 25-OCT-2001;
  Isis Innovation Limited (GB)
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Query Match
  Best Local Similarity 66.4%; Score 14.6; DB 1; Length 22;
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QY 727 TCCAGGAGAAACAGACACC 747
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Db 22 TCCAGGAGAAACAGACACC 2

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RESULT 15
LOCUS AX286288 22 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 17 from Patent WO0175296.
ACCESSION AX286288
VERSION AX286288.1 GI:17048536
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lin, H.H., Gordon, D.S., McKnight, A.J. and Stacey, M.S.
TITLE Human emt2, a g-protein coupled receptor from the egf-tm7 family
JOURNAL Patent: WO 0179296-A 17 25-OCT-2001;
Isis Innovation Limited (GB)
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Query Match 66.4%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAACAGAACACC 747
Db 22 TCCAGAGACACAGAGCACC 2

RESULT 16
LOCUS AX132045 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3263 from Patent WO0130362.
ACCESSION AX132045
VERSION AX132045.1 GI:14138350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribosome therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3263 03-MAY-2001;
IMMUSOL, INC. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/Note="Cyclin B1 ribozyme binding site"
Query Match 65.5%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAACACCG 748
Db 19 GAGAGACAGAACACCG 4

RESULT 17
LOCUS AX132309 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3527 from Patent WO0130362.
ACCESSION AX132309
VERSION AX132309.1 GI:14138614
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribosome therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3527 03-MAY-2001;
IMMUSOL, INC. (US)
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/Note="Cdc25 hs ribozyme binding site"
Query Match 64.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGAACACC 747
Db 19 CCAGGAGAAACAAACACC 1

RESULT 18
LOCUS AX440525 21 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 29 from Patent WO0206529.
ACCESSION AX440525
VERSION AX440525.1 GI:21665328
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Germino, G.G., Watnick, T.J. and Phakdeekitcharoen, B.
TITLE Detection and treatment of polycystic kidney disease
JOURNAL Patent: WO 0206529-A 29 24-JAN-2002;
The Johns Hopkins University School of Medicine (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="PCR primer 5F1"
Query Match 64.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAACAC 746
Db 3 GCCAGGAGGAGCAGAACCC 21

RESULT 19
LOCUS A67109 18 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 276 from Patent WO9740193.
ACCESSION A67109
VERSION A67109.1 GI:4538480
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
AUTHORS Stuyver, L., Rossau, R. and Maertens, G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 276 30-OCT-1997;
INNOGENETICS NV (BE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      63.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACAG 5

RESULT 20
A67103/c
LOCUS      A67103      18 bp      DNA
DEFINITION Sequence 270 from Patent WO9740193.
ACCESSION  A67103
VERSION     A67103.1 GI:4538474
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
TITLE     METHOD FOR TYPING AND DETECTING HBV
JOURNAL   Patent: WO 9740193-A 270 30-OCT-1997;
          INNOGENETICS NV (BE)
FEATURES   Location/Qualifiers
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Query Match      60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 18 GCCAGGAGAAACAG 4

RESULT 21
A67105/c
LOCUS      A67105      18 bp      DNA
DEFINITION Sequence 272 from Patent WO9740193.
ACCESSION  A67105
VERSION     A67105.1 GI:4538476
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
TITLE     METHOD FOR TYPING AND DETECTING HBV
JOURNAL   Patent: WO 9740193-A 272 30-OCT-1997;
          INNOGENETICS NV (BE)
FEATURES   Location/Qualifiers
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Query Match      60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 18 GCCAGGAGAAACAG 4

RESULT 22
A67106/c
LOCUS      A67106      18 bp      DNA
DEFINITION Sequence 273 from Patent WO9740193.
ACCESSION  A67106
VERSION     A67106.1 GI:4538477
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Stuyver,L., Rossau,R. and Maertens,G.
TITLE     METHOD FOR TYPING AND DETECTING HBV
JOURNAL   Patent: WO 9740193-A 273 30-OCT-1997;
          INNOGENETICS NV (BE)
FEATURES   Location/Qualifiers
            source
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                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 18 GCCAGGAGAAACAG 4

RESULT 23
E26485/c
LOCUS      E26485      20 bp      DNA
DEFINITION Highly sensitive method for detecting lamivudine-tolerant hepatitis B virus.
ACCESSION  E26485
VERSION     E26485.1 GI:13025095
KEYWORDS   JP 199127860-A/1.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kazuaki,S. and Hiromitsu,K.
TITLE     Highly sensitive method for detecting lamivudine-tolerant hepatitis B virus
JOURNAL   Patent: JP 199127860-A 1 18-MAY-1999;
          KAZUAKI SAYAMA
COMMENT    OS Unidentified
          PN JP 199127860-A/1
          PD 18-MAY-1999
          PF 28-OCT-1997 JP 1997296042
          PR
          PT KAZUAKI SAYAMA,HIROMITSU KUMADA
          PC C12N15/09,C12Q1/70//C12N15/09,C12R1/92),C12N15/00,(C12N15/00,
          PC C12R1:92)
          CC Strandedness: Single;
          CC Topology: Linear;
          FH Key
          FT Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      60.9%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 742
Db 17 GCCAGGAGAAACGG 3

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RESULT 24
AX132047/c
LOCUS AX132047 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3265 from Patent WO0130362.
ACCESSION AX132047
VERSION AX132047.1 GI:14138952
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3265 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"
Query Match 60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGACAC 745
Db 18 GCGGGGAGAAACAGACAC 1

RESULT 25
AX132308/c
LOCUS AX132308 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3526 from Patent WO0130362.
ACCESSION AX132308
VERSION AX132308.1 GI:14138613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3526 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"
Query Match 60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGACAC 745
Db 18 GCGGGGAGAAACAGACAC 1

RESULT 26
AX132310/c
LOCUS AX132310 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3528 from Patent WO0130362.
ACCESSION AX132310
VERSION AX132310.1 GI:14138615

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KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3528 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"
Query Match 60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 729 CCAGGAGAAACAGACAC 746
Db 18 CCAGGAGAAACAGACAC 1

RESULT 27
AX499947/c
LOCUS AX499947 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 1254 from Patent EP1229046.
ACCESSION AX499947
VERSION AX499947.1 GI:23382240
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 1254 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 58.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 727 TCCGAGGAGAAACAGAC 742
Db 17 TCCGAGGAGAAACAGAC 2

RESULT 28
AX499948/c
LOCUS AX499948 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 1255 from Patent EP1229046.
ACCESSION AX499948
VERSION AX499948.1 GI:23382241
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 1255 07-AUG-2002;

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Aecomica, Inc. (US)
FEATURES
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 56.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 56;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TCCAGGAGAAACA 740
Db 14 TCCAGGTGAACA 1

RESULT 34
A67108/c
LOCUS A67108 18 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 275 from Patent WO9740193.
ACCESSION A67108
VERSION A67108.1 GI:4538479
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Stuyver, L., Rossau, R. and Maertens, G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 275 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES
    source
        1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 59;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACGG 5

RESULT 35
A67111/c
LOCUS A67111 18 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 278 from Patent WO9740193.
ACCESSION A67111
VERSION A67111.1 GI:4538482
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Stuyver, L., Rossau, R. and Maertens, G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 278 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES
    source
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            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

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Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 59;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAG 741
Db 18 GCCATGAGAAACAG 5

RESULT 36
AR065607/c
LOCUS AR065607 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5849534.
ACCESSION AR065607
VERSION AR065607.1 GI:5995823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Grotendorst, G.R. and Iida, N.
TITLE DNA encoding leukocyte derived growth factor-2 (LDGF-2)
JOURNAL Patent: US 5849534-A 6 15-DEC-1998;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 59;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAACAC 745
Db 16 GCAGAAACAGAACAC 3

RESULT 37
I06264/c
LOCUS I06264 18 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 22 from Patent EP 0319052.
ACCESSION I06264
VERSION I06264.1 GI:590255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thomas, Jnr, K.A. and Linemeyer, D.L.
TITLE Mutant acidic fibroblast growth factor
JOURNAL Patent: EP 0319052-A2 22 07-JUN-1989;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 55.5%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 64;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAACACCG 748
Db 17 GGAGAAAGTGACCACCG 1

RESULT 38
AR292914/c
LOCUS AR292914 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4649 from patent US 6537751.
ACCESSION AR292914
VERSION AR292914.1 GI:31680198
KEYWORDS

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Source	Organism	Reference	Title	Journal	Features
Homo sapiens (human)	Homo sapiens	Zhan, J.	Human testis expressed patched like protein	Patent: EP 1229046-A 1253 07-AUG-2002;	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
1					
Human testis expressed patched like protein					
Patent: EP 1229046-A 1253 07-AUG-2002;					
1					
Location/Qualifiers					
1..17					
/organism="Homo sapiens"					
/mol_type="unassigned DNA"					
/db_xref="taxon:9606"					
Query Match	53.6%;	Score 11.8;	DB 1;	Length 17;	
Best Local Similarity	86.7%;	Pred. No. 71;			
Matches 13;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	728	GCACGAGAGAAACACA 742			
DB	17	GCACGAGAGAAACACA 3			
LOCUS	AX674572	17 bp	DNA	linear	PAT 27-MAR-2003
DEFINITION	Sequence 3017 from Patent WO03004526.				
ACCESSION	AX674572				
VERSION	AX674572.1	GI:29332920			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
1					
Teleman, A., Anson, R. and Tuijinder, M.					
Sequences involved in phenomena of tumour suppression, tumour					
reversion, apoptosis and/or resistance to viruses and their use as					
medicines					
Patent: WO 03004526-A 3017 16-JAN-2003;					
1					
Molecular Engines Laboratories (FR)					
Location/Qualifiers					
1..17					
/organism="Homo sapiens"					
/mol_type="unassigned DNA"					
/db_xref="taxon:9606"					
Query Match	53.6%;	Score 11.8;	DB 1;	Length 17;	
Best Local Similarity	86.7%;	Pred. No. 71;			
Matches 13;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	730	CAGGAGAGAAACACA 744			
DB	15	CTGAGAGAGAAACAGATC 1			
LOCUS	AX729839	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 1473 from Patent WO03025175.				
ACCESSION	AX729839				
VERSION	AX729839.1	GI:30509182			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
1					
Teleman, A., Anson, R. and Tuijinder, M.					
Sequences involved in phenomena of tumour suppression, tumour					
reversion, apoptosis and/or virus resistance and their use as					
medicines					


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JOURNAL Patent: WO 03025175-A 1473 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 730 CAGGAGAACAGAC 744
Db 15 CAGGAGACAGATC 1

RESULT 43
AX762877 17 bp DNA linear PAT 25-JUN-2003
LOCUS Sequence 6198 from Patent WO03040369.
DEFINITION AX762877
ACCESSION AX762877
VERSION AX762877.1 GI:32257493
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 6198 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAACAG 741
Db 3 TCCAGGAGATCAG 17

RESULT 44
A67102/c 18 bp DNA linear PAT 29-MAR-1999
LOCUS Sequence 269 from Patent WO9740193.
DEFINITION A67102
ACCESSION A67102
VERSION A67102.1 GI:4538473
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 18)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 269 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 75;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAACAG 742
Db 18 GCCATGAGAACGGA 4

RESULT 45
A67104/c 18 bp DNA linear PAT 29-MAR-1999
LOCUS Sequence 271 from Patent WO9740193.
DEFINITION A67104
ACCESSION A67104
VERSION A67104.1 GI:4538475
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 18)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 271 30-OCT-1997;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 75;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAACAG 742
Db 18 GCCATGAGAACGGA 4

RESULT 46
AR190011 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5499 from patent US 6346398.
DEFINITION AR190011
ACCESSION AR190011
VERSION AR190011.1 GI:20235976
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5499 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGACA 745
Db 2 GAGAAATAGACA 14

RESULT 47
AR324988 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 2390 from patent US 6566127.
DEFINITION AR324988
ACCESSION AR324988
VERSION AR324988.1 GI:33710796
KEYWORDS

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2390 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 733 GAGAAACAGAAC 745
Db 2 GAGAAATAGAAC 14

RESULT 48
AX499951/c
LOCUS      AX499951
DEFINITION Sequence 1258 from Patent EP1229046.
ACCESSION  AX499951
VERSION     AX499951.1 GI:23382244
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 1258 07-AUG-2002;
            Aeonica, Inc. (US)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 727 TGCCAGGAGAAC 739
Db 13 TGCCAGGTGAAC 1

RESULT 49
AX674143/c
LOCUS      AX674143
DEFINITION Sequence 2588 from Patent WO03004526.
ACCESSION  AX674143
VERSION     AX674143.1 GI:29332491
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijinder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL     Patent: WO 03004526-A 2588 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17

SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2390 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 730 CAGGAGAACAGA 742
Db 17 CAGGAAAAACAGA 5

RESULT 50
AX732557/c
LOCUS      AX732557
DEFINITION Sequence 4191 from Patent WO03025175.
ACCESSION  AX732557
VERSION     AX732557.1 GI:30511900
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijinder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025175-A 4191 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 12; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 733 GAGAAACAGAAC 745
Db 17 GTGAAACAGAAC 5

RESULT 51
BD266301/c
LOCUS      BD266301
DEFINITION Universal arrays.
ACCESSION  BD266301
VERSION     BD266301.1 GI:33076069
KEYWORDS    JP 2002539849-A/301.
SOURCE      synthetic construct
            ORGANISM    synthetic construct
            artificial sequences.
            1 (bases 1 to 17)
REFERENCE   Fan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
            Lockhart,D.J., Ryder,T. and Sklar,P.
AUTHORS     Universal arrays
TITLE       Patent: JP 2002539849-A 301 26-NOV-2002;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
JOURNAL
COMMENT     OS Artificial Sequence
            PN JP 2002539849-A/301
            PD 26-NOV-2002
            PF 27-MAR-2000 JP 2000608794
            PR 26-MAR-1999 US 60/126473,23-JUN-1999 US 60/140359 PI
            JIAN BING PAN,JOEL N HIRSCHHORN,XIAOHUA
            HUANG,PAUL KAPLAN,ERIC
            PI S LANDER,
            PI DAVID J LOCKHART,THOMAS RYDER,PAMELA SKLAR
            PC C12Q1/68,C12M1/00,C12N15/09,C12N15/09,C12N15/09,G01N33/53, PC
            G01N33/566.

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PC      GOIN37/00.C12N15/00.C12N15/00.C12N15/00
CC      Primer
FH      Key      Location/Qualifiers
FT      source    1..17
FT      Location/Qualifiers
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                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"
Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAGAA 743
Db      16 GCCATGAGAGACGGA 1

RESULT 52
E54495/c
LOCUS      17 bp DNA linear PAT 27-AUG-2002
DEFINITION Heat-resistant lysine biosynthesis enzyme gene of thermophilic
            coryneform bacterium.
ACCESSION E54495
VERSION    E54495.1 GI:22553552
KEYWORDS   JP 2001120270-A/19.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Iraya, M., Kimura, E., Kawara, Y. and Sugimoto, S.
TITLE      Heat-resistant lysine biosynthesis enzyme gene of thermophilic
            coryneform bacterium
JOURNAL    Patent: JP 2001120270-A 19 08-MAY-2001;
            AJINOMOTO CO INC
COMMENT    OS Artificial Sequence
            PN JP 2001120270-A/19
            PD 08-MAY-2001
            PF 01-NOV-1999 JP 1999311148
            PI MINORU ITOYA, EIICHIRO KIMURA, YOSHIO KAWARA, SHINICHI SUGIMOTO PC
            C12N15/09// (C12N15/09, C12R1:15), C12N15/00, (C12N15/00, C12R1:15) CC
            Description of Artificial Sequence: Primer for LA cloning of CC
            lysA
FH      Key      Location/Qualifiers
FEATURES
    source        1..17
                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"
Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAGAA 743
Db      17 GCCACGAGGATCAGAA 2

RESULT 53
AR190548/c
LOCUS      17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6036 from patent US 6346398.
ACCESSION AR190548
VERSION    AR190548.1 GI:20236513
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

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TITLE      Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6346398-A 6036 12-FEB-2002;
FEATURES
    source        1..17
                  /organism="unknown"
                  /mol_type="unassigned DNA"
Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAGAA 743
Db      16 GCCAGGAGACACGTA 1

RESULT 54
AR325471/c
LOCUS      17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2873 from patent US 6566127.
ACCESSION AR325471
VERSION    AR325471.1 GI:33711279
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE      Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 2873 20-MAY-2003;
FEATURES
    source        1..17
                  /organism="unknown"
                  /mol_type="unassigned RNA"
Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAGAA 743
Db      16 GCCAGGAGACACGTA 1

RESULT 55
AX227611
LOCUS      17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 983 from Patent WO0157206.
ACCESSION AX227611
VERSION    AX227611.1 GI:15556752
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
TITLE      Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
JOURNAL    Patent: WO 0157206-A 983 09-AUG-2001;
            RIBOZYNE PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
    source        1..17
                  /organism="synthetic construct"
                  /mol_type="unassigned RNA"
                  /db_xref="taxon:32630"
Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      731 AGCAGAAACAGAACAC 746

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Db          ||||| ||||| ||||| |||||
2 AGGAGAAACAATAAC 17

RESULT 56
AX692031/c
LOCUS      AX692031      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 4763 from Patent EPI281758.
ACCESSION  AX692031
VERSION     AX692031.1 GI:29414975
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens

REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    mdz12
PATENT:    EP 1281758-A 4763 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES   source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGAA 743
||| ||||| ||||| |||||
Db 17 GCCAGGAGAAACAGGA 2

RESULT 57
AX692032/c
LOCUS      AX692032      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 4764 from Patent EPI281758.
ACCESSION  AX692032
VERSION     AX692032.1 GI:29414976
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens

REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    mdz12
PATENT:    EP 1281758-A 4764 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES   source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGAA 743
||| ||||| ||||| |||||
Db 16 GCCAGGAGAAACAGGA 1

RESULT 58
BD105092
LOCUS      BD105092      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD105092

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VERSION     BD105092.1 GI:22650666
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE   1 (bases 1 to 17)
AUTHORS     Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
TITLE      Kit and method for determining HLA type
JOURNAL     Patent: WO 0192572-A 1196 06-DEC-2001;
            NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS Artificial Sequence
            PN WO 0192572-A/1196
            PD 06-DEC-2001
            PF 01-JUN-2001 WO 2001JP004662
            PR 01-JUN-2000 JP 00P 164798
            PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
            MATSUMURA,
            PT SHOGO MORIYA, MICHIO NISHIDA
            PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
            CC Description of Artificial Sequence:capture
            FH Key
            FT source
            1..17
            /organism="Artificial Sequence".
            /Location/Qualifiers

FEATURES   source
            1..17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 729 CCAGGAGAAACAGAAC 744
||| ||||| ||||| |||||
Db 1 CCGGAGATACAGATC 16

RESULT 59
A11101
LOCUS      A11101      15 bp      DNA      linear      PAT 03-DEC-1993
DEFINITION Oligonucleotide U23.
ACCESSION  A11101
VERSION     A11101.1 GI:490951
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE   1 (bases 1 to 15)
AUTHORS     Ikehara,M. and Kida,M.
TITLE      Synthetic gene for human lysozyme
JOURNAL     Patent: EP 0181634-A 45 21-MAY-1986;
            Takeda Chemical Industries, Ltd
FEATURES   source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      50.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGA 742
||| ||||| ||||| |||||
Db 2 GGAGAAACAGA 12

RESULT 60
AR362726

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LOCUS       AR362726               15 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION   Sequence 60 from patent US 5182195.
ACCESSION    AR362726
VERSION      AR362726.1  GI:34423106
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Nakahama,K., Kaisho,Y. and Yoshimura,K.
TITLE        Method for increasing gene expression using protease deficient
            yeasts
JOURNAL      Patent: US 5182195-A 60 26-JAN-1993;
FEATURES     Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="genomic DNA"
Query Match      50.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAC 742
Db 2 GGAGAAACAGAC 12

RESULT 61
I61456/c
LOCUS       I61456               15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION   Sequence 10 from patent US 5658780.
ACCESSION    I61456
VERSION      I61456.1  GI:2479404
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE        Real a targeted ribozymes
JOURNAL      Patent: US 5658780-A 10 19-AUG-1997;
FEATURES     Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAC 744
Db 14 AGGAGAAACAGATC 1

RESULT 62
AX635865/c
LOCUS       AX635865             15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION   Sequence 3004 from Patent EPI260586.
ACCESSION    AX635865
VERSION      AX635865.1  GI:28471479
KEYWORDS     unidentified
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1
AUTHORS      Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE        Method and reagent for inhibiting the expression of disease related
            genes

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JOURNAL      Patent: EP 1260586-A 3004 27-NOV-2002;
FEATURES     Location/Qualifiers
            source          1..15
                        /organism="unidentified"
                        /mol_type="unassigned RNA"
                        /db_xref="taxon:32644"
Query Match      49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAC 744
Db 14 AGGAGAAACAGATC 1

RESULT 63
BD208396/c
LOCUS       BD208396             15 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION   Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION    BD208396
VERSION      BD208396.1  GI:33018166
KEYWORDS     JP 2002512791-A/1986.
SOURCE       unidentified
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE        Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
JOURNAL      Patent: JP 2002512791-A 1986 08-MAY-2002;
COMMENT      RIBOZYME PHARMACEUTICALS INC
            OS Hepatitis virus (hepatitis C virus)
            PN JP 2002512791-A/1986
            PD 08-MAY-2002
            PF 26-APR-1999 JP 2000545991
            PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
            PS 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
            LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
            PAVCO,
            PI DENNIS MACEJAK
            PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
            PC A61K37/66,
            PC C12N15/00
            CC Enzymatic nucleic acid treatment of diseases or conditions CC
            related to
            CC hepatitis C virus infection.
            FH Key
            FT source          1..15
                        /organism='Hepatitis virus (hepatitis C FT
                        virus)';
            Location/Qualifiers
            source          1..15
                        /organism="unidentified"
                        /mol_type="genomic RNA"
                        /db_xref="taxon:32644"
Query Match      49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGAAACACCG 748
Db 15 GAACAGTACACTG 2

RESULT 64
A09424/c
LOCUS       A09424
DEFINITION   Oligonucleotide (a6).
ACCESSION    A09424

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VERSION      A09424.1 GI:490529
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Ueda,I., Niwa,M., Saitoh,Y., Sato,S. and Yamada,H.
TITLE        Process for production of somatostatin
JOURNAL      Patent: EP 0197558-A 30 15-OCT-1986;
              FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

Query Match
Best Local Similarity 49.1%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACGAGAACACC 747
Db 16 AGAACGAGAACACC 3

RESULT 67
A35095/c
LOCUS       A35095 Synthetic IGF-I gene oligo. 16 bp DNA linear PAT 06-DEC-1996
DEFINITION A35095 Synthetic IGF-I gene oligo.
ACCESSION  A35095
VERSION    A35095.1 GI:1926754
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1 (bases 1 to 16)
AUTHORS    Ueda,I., Niwa,M., Sato,S., Saitoh,Y. and Kusunoki,C.
TITLE      Process for production of insulin-like growth factor I and plasmid
JOURNAL    Patent: EP 0219814-A 45 29-APR-1987;
              FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES   Location/Qualifiers
            source
              1..16
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match
Best Local Similarity 49.1%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACGAGAACACC 747
Db 16 AGAACGAGAACACC 3

RESULT 68
AX076025/c
LOCUS       AX076025 Sequence 1 from Patent WO0104358. 16 bp DNA linear PAT 06-FEB-2001
DEFINITION AX076025 Sequence 1 from Patent WO0104358.
ACCESSION  AX076025
VERSION    AX076025.1 GI:12710678
KEYWORDS   Hepatitis B virus
SOURCE     Hepatitis B virus
ORGANISM   Hepatitis B virus
REFERENCE  1
AUTHORS     Stuyver,L., Maertens,G. and van Geyt,C.
TITLE       Detection of anti-hepatitis b drug resistance
JOURNAL     Patent: WO 0104358-A 1 18-JAN-2001;
              INNOGENETICS N.V. (BE)
FEATURES    Location/Qualifiers
            source
              1..16
              /organism="Hepatitis B virus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:10407"

Query Match
Best Local Similarity 49.1%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAG 741
Db 14 GCCAGGAGAACAG 1

VERSION      A10627.1 GI:490755
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
TITLE        Process for production of gamma-interferon
JOURNAL      Patent: EP 0176916-A 12 09-APR-1986;
              FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

Query Match
Best Local Similarity 49.1%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACGAGAACACC 747
Db 16 AGAACGAGAACACC 3

RESULT 65
A10627/c
LOCUS       A10627 Oligonucleotide (A6). 16 bp DNA linear PAT 02-DEC-1993
DEFINITION A10627 Oligonucleotide (A6).
ACCESSION  A10627
VERSION    A10627.1 GI:490755
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 16)
AUTHORS    Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
TITLE      Process for production of gamma-interferon
JOURNAL    Patent: EP 0176916-A 12 09-APR-1986;
              FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES   Location/Qualifiers
            source
              1..16
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match
Best Local Similarity 49.1%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACGAGAACACC 747
Db 16 AGAACGAGAACACC 3

RESULT 66
A11575/c
LOCUS       A11575 Oligonucleotide 'a6'. 16 bp DNA linear PAT 16-NOV-1993
DEFINITION A11575 Oligonucleotide 'a6'.
ACCESSION  A11575
VERSION    A11575.1 GI:491117
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 16)
AUTHORS    Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
TITLE      59 Valine insulin-like growth factor I and process for production thereof
JOURNAL    Patent: EP 0158892-A 71 23-OCT-1985;
              FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES   Location/Qualifiers
            source
              1..16

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RESULT 69
LOCUS       128559             12 bp      DNA          linear      PAT 06-FEB-1997
DEFINITION   Sequence 12 from patent US 5571937.
ACCESSION    128559
VERSION      128559.1  GI:1819335
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS     Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE       Complementary DNA and toxins
JOURNAL     Patent: US 5571937-A 12 05-NOV-1996;
FEATURES    Location/Qualifiers
             source
             1..12
             /organism="unknown"
             /mol_type="unassigned DNA"
Query Match      47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAGA 742
Db      1 AGGAGAAACAGA 12
|||||
|||||

RESULT 70
LOCUS       158721             12 bp      DNA          linear      PAT 07-OCT-1997
DEFINITION   Sequence 12 from patent US 5652350.
ACCESSION    158721
VERSION      158721.1  GI:2477959
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS     Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE       Complementary DNA and toxins
JOURNAL     Patent: US 5652350-A 12 29-JUL-1997;
FEATURES    Location/Qualifiers
             source
             1..12
             /organism="unknown"
             /mol_type="unassigned DNA"
Query Match      47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAGA 742
Db      1 AGGAGAAACAGA 12
|||||
|||||

RESULT 71
LOCUS       A40588             14 bp      DNA          linear      PAT 05-MAR-1997
DEFINITION   Sequence 125 from Patent WO9425578.
ACCESSION    A40588
VERSION      A40588.1  GI:2296623
KEYWORDS     unidentified
SOURCE       unidentified
ORGANISM     unidentified
REFERENCE    1 (bases 1 to 14)
AUTHORS     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE       EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL     Patent: WO 9425578-A 125 10-NOV-1994;
            BIOGNOSTIK GES (DE)

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FEATURES    Location/Qualifiers
             source
             1..14
             /organism="unidentified"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32644"
Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAGA 742
Db      1 AGGAGAAACAGA 12
|||||
|||||

RESULT 72
LOCUS       A89112             14 bp      DNA          linear      PAT 22-JAN-2000
DEFINITION   Sequence 1260 from Patent WO9833904.
ACCESSION    A89112
VERSION      A89112.1  GI:6737682
KEYWORDS     unidentified
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1260 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
             source
             1..14
             /organism="unidentified"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32644"
Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAGA 742
Db      1 AGGAGAAACAGA 12
|||||
|||||

RESULT 73
LOCUS       A89603             14 bp      DNA          linear      PAT 22-JAN-2000
DEFINITION   Sequence 1751 from Patent WO9833904.
ACCESSION    A89603
VERSION      A89603.1  GI:6738173
KEYWORDS     unidentified
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1751 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
             source
             1..14
             /organism="unidentified"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32644"
Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      736 AAACAGAACACC 747
Db      12 AAACAGAACACC 1
|||||
|||||

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RESULT 74
LOCUS       AR061873               14 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION   Sequence 4 from patent US 5843661.
ACCESSION   AR061873
VERSION     AR061873.1 GI:5989564
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Rothmund,P.W.K.
TITLE      Method for construction universal DNA based molecular turing
machine
JOURNAL    Patent: US 5843661-A 4 01-DEC-1998;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 746
Db 2 GAAACAGTACAC 13

RESULT 75
LOCUS       AR232868               14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION   Sequence 125 from patent US 6455689.
ACCESSION   AR232868
VERSION     AR232868.1 GI:27275206
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 125 24-SEP-2002;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAGACAGA 12

RESULT 76
LOCUS       AR407925/c              14 bp      RNA      linear      PAT 18-DEC-2003
DEFINITION   Sequence 18 from patent US 6632057.
ACCESSION   AR407925
VERSION     AR407925.1 GI:40157912
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Fauchet,C.R.J.

```

```

TITLE      Fixing unit with an end imprint in a threaded terminal portion
JOURNAL    Patent: US 6632057-A 18 14-OCT-2003;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 14 AGCAGAAACAGA 3

RESULT 77
LOCUS       AX030163               14 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION   Sequence 125 from Patent EP1008649.
ACCESSION   AX030163
VERSION     AX030163.1 GI:10190380
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS    Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
            and Schlingensiepen,R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 125 14-JUN-2000;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 1 AGGAGAGACAGA 12

RESULT 78
LOCUS       AX316484               14 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION   Sequence 125 from Patent EP1160319.
ACCESSION   AX316484
VERSION     AX316484.1 GI:17899657
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS    Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL    Patent: EP 1160319-A 125 05-DEC-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"

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Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 79
BD066625
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066625
VERSION BD066625.1 GI:22612228
KEYWORDS JP 2001511000-A/1260.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1260 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1260
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
FT Location/Qualifiers
1..14 /organism='Unknown'

FEATURES
source
1..14 Location/Qualifiers
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 80
BD067116/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD067116
VERSION BD067116.1 GI:22612719
KEYWORDS JP 2001511000-A/1751.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1751 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1751
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 81
BD067116/c
LOCUS 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD067116
VERSION BD067116.1 GI:22612719
KEYWORDS JP 2001511000-A/1751.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1751 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1751
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
FT Location/Qualifiers
1..14 /organism='Unknown'

FEATURES
source
1..14 Location/Qualifiers
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 1 AGGAGAACAGCA 12

RESULT 82
ARI80064
LOCUS 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 132 from patent US 6333152.
ACCESSION ARI80064
VERSION ARI80064.1 GI:20222097
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 132 25-DEC-2001;
FEATURES
source
1..15 Location/Qualifiers
/organism='unassigned DNA'
/mol_type='unassigned DNA'

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGCA 742
Db 13 AGGGGAAACAGCA 2

RESULT 82
ARI80064
LOCUS 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 132 from patent US 6333152.
ACCESSION ARI80064
VERSION ARI80064.1 GI:20222097
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 132 25-DEC-2001;
FEATURES
source
1..15 Location/Qualifiers
/organism='unassigned DNA'
/mol_type='unassigned DNA'

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAGGAAA 738
Db 3 TCCAGGAGGAAA 14

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RESULT 83
ARI180799
LOCUS       ARI180799             15 bp    DNA             linear    PAT 20-APR-2002
DEFINITION   Sequence 867 from patent US 6331152.
ACCESSION   ARI180799
VERSION     ARI180799.1  GI:20222832
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE       Gene expression profiles in normal and cancer cells
JOURNAL     Patent: US 6331152-A 867 25-DEC-2001;
FEATURES
SOURCE      1..15
            |||||||
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 738
Db 3 TGCCAGGAGAA 14

RESULT 84
AX635867/c
LOCUS       AX635867             15 bp    RNA             linear    PAT 21-FEB-2003
DEFINITION   Sequence 3006 from Patent EP1260586.
ACCESSION   AX635867
VERSION     AX635867.1  GI:28471481
KEYWORDS
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
JOURNAL     Genes
PATENT      EP 1260586-A 3006 27-NOV-2002;
RIBOZYME    PHARMACEUTICALS, INC. (US)
FEATURES
SOURCE      1..15
            |||||||
            /organism="unidentified"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32644"

Query Match      47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 13 AGGAGAAACAGA 2

RESULT 85
A22593
LOCUS       A22593             16 bp    DNA             linear    PAT 24-OCT-1994
DEFINITION   Oligonucleotide.
ACCESSION   A22593
VERSION     A22593.1  GI:641563
KEYWORDS
SOURCE      Petunia x hybrida
ORGANISM    Petunia x hybrida

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Petunia.

REFERENCE   1 (bases 1 to 16)
AUTHORS
JOURNAL
FEATURES
SOURCE      Patent: WO 9218625-A 4 29-OCT-1992;
            Location/Qualifiers
            1..16
            /organism="Petunia x hybrida"
            /mol_type="unassigned DNA"
            /db_xref="taxon:4102"

Query Match      47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 4 AGGAGAAACAGA 15

RESULT 86
AR096276
LOCUS       AR096276             16 bp    DNA             linear    PAT 08-SEP-2000
DEFINITION   Sequence 4 from patent US 6005167.
ACCESSION   AR096276
VERSION     AR096276.1  GI:10024937
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Van Tunen,A.Johannes., Van Der Meer,I.Maria. and
            Mol,J.Nicolaas.Maria..
TITLE       Male-sterile plants, method for obtaining male-sterile plants and
            recombinant DNA for use therein
JOURNAL     Patent: US 6005167-A 4 21-DEC-1999;
FEATURES
SOURCE      Location/Qualifiers
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 4 AGGAGAAACAGA 15

RESULT 87
AX076029/c
LOCUS       AX076029             16 bp    DNA             linear    PAT 06-FEB-2001
DEFINITION   Sequence 5 from Patent WO0104358.
ACCESSION   AX076029
VERSION     AX076029.1  GI:12710682
KEYWORDS
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1
AUTHORS     Stuyver,L., Maertens,G. and van Geyt,C.
TITLE       Detection of anti-hepatitis b drug resistance
JOURNAL     Patent: WO 0104358-A 5 18-JAN-2001;
            INNOGENETICS N.V. (BE)
FEATURES
SOURCE      Location/Qualifiers
            1..16
            /organism="Hepatitis B virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10407"

Query Match      47.3%; Score 10.4; DB 1; Length 16;

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Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAC 739
DB 13 GCCATGAGAAC 2

RESULT 88
AX255620
LOCUS AX255620
DEFINITION Sequence 41 from Patent WO0170982.
ACCESSION AX255620
VERSION AX255620.1 GI:16074676
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Beger,C., Barber,J. and Wong-Staal,F.
TITLE Brca-1 regulators and methods of use
JOURNAL Patent: WO 0170982-A 41 27-SEP-2001;
Immusol Incorporated (US) ; Beger, Carmela (DE)
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 5 AAAGAGAACACC 16

RESULT 89
AX255663
LOCUS AX255663
DEFINITION Sequence 84 from Patent WO0170982.
ACCESSION AX255663
VERSION AX255663.1 GI:16074719
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Beger,C., Barber,J. and Wong-Staal,F.
TITLE Brca-1 regulators and methods of use
JOURNAL Patent: WO 0170982-A 84 27-SEP-2001;
Immusol Incorporated (US) ; Beger, Carmela (DE)
FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
DB 5 AAAGAGAACACC 16

RESULT 90
AX452095/c
LOCUS AX452095
DEFINITION Sequence 2 from Patent EP1211326.
ACCESSION AX452095.1 GI:21712097
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blair,E.D., Snowden,B.W. and Ward,C.L.
TITLE Diagnostic method
JOURNAL Patent: EP 1211326-A 2 05-JUN-2002;
GLAXO GROUP LIMITED (GB)
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
DB 16 GGGGAAACAGAA 5

RESULT 91
BD208458/c
LOCUS BD208458
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208458
VERSION BD208458.1 GI:33018228
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2048 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2048
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
CC hepatitis C virus infection.
PH Key
FT source
1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      729 CCAGGAGAAACAGAA 743
Db      15 CCAGGAGAAAGGAAAA 1

RESULT 92
BD208459/c
LOCUS   BD208459
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD208459
VERSION
BD208459.1 GI:33018229
KEYWORDS
JP 2002512791-A/2049.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Blatt L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL
Patent: JP 2002512791-A 2049 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2049
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT virus) ;
/organism='Hepatitis virus (hepatitis C FT
virus)' ;
Location/Qualifiers
source
1..15
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAGA 742
Db      15 GCCAGGAGAGAGGAAA 1

RESULT 93
AR123024
LOCUS   AR123024
DEFINITION
Sequence 15 from patent US 6168943.
ACCESSION
AR123024
VERSION
AR123024.1 GI:14107990
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Rose, J.K.
TITLE
Methods for making modified recombinant vesiculoviruses
JOURNAL
Patent: US 6168943-A 15 02-JAN-2001;
LOCATION/Qualifiers
source
1..11

QY      729 CCAGGAGAAACAGAA 743
Db      15 CCAGGAGAAAGGAAAA 1

RESULT 92
BD208459/c
LOCUS   BD208459
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD208459
VERSION
BD208459.1 GI:33018229
KEYWORDS
JP 2002512791-A/2049.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Blatt L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL
Patent: JP 2002512791-A 2049 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2049
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT virus) ;
/organism='Hepatitis virus (hepatitis C FT
virus)' ;
Location/Qualifiers
source
1..15
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      728 GCCAGGAGAAACAGA 742
Db      15 GCCAGGAGAGAGGAAA 1

RESULT 93
AR123024
LOCUS   AR123024
DEFINITION
Sequence 15 from patent US 6168943.
ACCESSION
AR123024
VERSION
AR123024.1 GI:14107990
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Rose, J.K.
TITLE
Methods for making modified recombinant vesiculoviruses
JOURNAL
Patent: US 6168943-A 15 02-JAN-2001;
LOCATION/Qualifiers
source
1..11

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAAAC 739
Db      2 CAGGAGAAAC 11

RESULT 94
AX626398
LOCUS   AX626398
DEFINITION
Sequence 3439 from Patent WO02053774.
ACCESSION
AX626398
VERSION
AX626398.1 GI:28454436
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Petersohn, D., Conradt, M. and Hofmann, K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 3439 11-JUN-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
LOCATION/Qualifiers
source
1..11
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 45.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      732 GGAGAAACAG 741
Db      1 GGAGAAACAG 10

RESULT 95
AR180388
LOCUS   AR180388
DEFINITION
Sequence 456 from patent US 6333152.
ACCESSION
AR180388
VERSION
AR180388.1 GI:20222421
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.
TITLE
Gene expression profiles in normal and cancer cells
JOURNAL
Patent: US 6333152-A 456 25-DEC-2001;
LOCATION/Qualifiers
source
1..15
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      732 GGAGAAACAG 741
Db      5 GGAGAAACAG 14

RESULT 96
BD208460/c

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LOCUS BD208460 15 bp RNA linear PAT 17-JUL-2003
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
 ACCESSION BD208460
 VERSION BD208460.1 GI:33018230
 KEYWORDS JP 2002512791-A/2050.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Blatt, L., McSwiggen, J. A., Roberts, E., Pavco, P. A., and Macejak, D.
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
 JOURNAL RIBOZYME PHARMACEUTICALS INC
 COMMENT Patent: JP 2002512791-A 2050 08-MAY-2002;
 OS Hepatitis virus (hepatitis C virus)
 PN JP 2002512791-A/2050
 PD 08-MAY-2002
 PF 26-APR-1999 JP 2000545991
 PR 27-APR-1998 US 60/083217, 19-SEP-1998 US 60/100842 PR
 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
 PAVCO,
 PI DENNIS MACEJAK
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
 PC A61K37/66,
 PC C12N15/00
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC hepatitis C virus infection.
 FH Key Location/Qualifiers
 FT source 1..15
 FT virus', /organism='Hepatitis virus (hepatitis C FT
 virus)',
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 source
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 /organism='unidentified'
 /mol_type='genomic RNA'
 /db_xref='taxon:32644'
 Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAA 737
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 DB 13 GCCAGGAGAA 4
 RESULT 97
 A25806
 LOCUS A25806 14 bp DNA linear PAT 14-MAR-1995
 DEFINITION Polynucleotide 14CS.
 ACCESSION A25806
 VERSION A25806.1 GI:904774
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Patent: FR 2680520-A 13 26-FEB-1993;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1..14
 /organism='synthetic construct'
 /mol_type='unassigned DNA'
 /db_xref='taxon:32630'
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACAGACA 745
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DB 1 GACAAACAGACA 13
 |||||
 RESULT 98
 A40589
 LOCUS A40589 14 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 126 from Patent WO9425578.
 ACCESSION A40589
 VERSION A40589.1 GI:2296624
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS
 TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
 EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
 JOURNAL Patent: WO 9425578-A 126 10-NOV-1994;
 BIOGNOSTIK GES (DE)
 FEATURES
 source
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 Location/Qualifiers
 /organism='unidentified'
 /mol_type='unassigned DNA'
 /db_xref='taxon:32644'
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAAACA 740
 |||||
 DB 2 GCAAGGAGAGCA 14
 |||||
 RESULT 99
 A87922
 LOCUS A87922 14 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 70 from Patent WO9833904.
 ACCESSION A87922
 VERSION A87922.1 GI:6736492
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Brysch, W. and Schlingsien, K.
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 JOURNAL Patent: WO 9833904-A 70 06-AUG-1998;
 BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
 FEATURES
 source
 1..14
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='unassigned DNA'
 /db_xref='taxon:32644'
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAG 741
 |||||
 DB 1 CCATGAGAGCAG 13
 |||||
 RESULT 100
 A89113
 LOCUS A89113 14 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 1261 from Patent WO9833904.
 ACCESSION A89113
 VERSION A89113.1 GI:6737683
 KEYWORDS
 SOURCE unidentified

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ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingsiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1261 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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        1..14
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACCA 740
Db 2 GCAAGGAGAGCA 14

RESULT 101
LOCUS A89889 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 70 from Patent EP0856579.
ACCESSION A89889
VERSION A89889.1 GI:6738403
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingsiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 70 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAG 741
Db 1 CCATGAGAGCAG 13

RESULT 102
LOCUS AR029997 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 186 from patent US 5861244.
ACCESSION AR029997
VERSION AR029997.1 GI:5943211
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 186 19-JAN-1999;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 743
Db 13 AGGAGAGCAGCA 1

RESULT 103
LOCUS AR030009 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 198 from patent US 5861244.
ACCESSION AR030009
VERSION AR030009.1 GI:5943223
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 198 19-JAN-1999;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 743
Db 13 AGGAGAGCAGCA 1

RESULT 104
LOCUS I26228 14 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5556955.
ACCESSION I26228
VERSION I26228.1 GI:1606098
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Vergnaud,G.
TITLE Process for detection of new polymorphic loci in a DNA sequence,
nucleotide sequences forming hybridization probes and their
applications
JOURNAL Patent: US 5556955-A 13 17-SEP-1996;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACAGAACCA 745
Db 1 GACAAACAGAGCA 13

RESULT 105
LOCUS I52188/c 14 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5646031.
ACCESSION I52188
VERSION I52188.1 GI:2473389
KEYWORDS
SOURCE Unknown.

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QY	728 GCCAGGAGAACA 740 DDB 2 GCAAGGAAGCA 14
RESULT 108	
LOCUS AX030164	14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 126 from Patent EP1008649.	
ACCESSION AX030164	
VERSION AX030164.1 GI:10190381	
KEYWORDS Homo sapiens (human)	
SOURCE Homo sapiens	
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE 1 Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H. and Schlingensiepen,R. Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-beta(tgf-b2) Patent: EP 1008649-A 126 14-JUN-2000; BIOGNOSTIK GES (DE)	
AUTHORS Location/Qualifiers	
JOURNAL 1..14	
FEATURES /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
Query Match 44.5%; Score 9.8; DB 1; Length 14;	
Best Local Similarity 84.6%; Pred.No.1.3e+02;	
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 728 GCCAGGAGAACA 740 DDB 2 GCAAGGAAGCA 14	
RESULT 109	
LOCUS AX316485	14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 126 from Patent EP1160319.	
ACCESSION AX316485	
VERSION AX316485.1 GI:17899658	
KEYWORDS unidentified	
SOURCE unclassified.	
ORGANISM 1	
REFERENCE Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H., Schlingensiepen,R. and Bogdahn,U. Antisense-oligonucleotides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta) Patent: EP 1160319-A 126 05-DEC-2001; BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)	
AUTHORS Location/Qualifiers	
TITLE 1..14	
JOURNAL /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" /note="Description of unknown: unknown"	
FEATURES Query Match 44.5%; Score 9.8; DB 1; Length 14;	
Best Local Similarity 84.6%; Pred.No.1.3e+02;	
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 728 GCCAGGAGAACA 740 DDB 2 GCAAGGAAGCA 14	
RESULT 110	
AX571850	

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LOCUS      AX571850                14 bp      DNA      linear      PAT 29-MAY-2003
DEFINITION Sequence 9 from Patent WO02077274.
ACCESSION  AX571850
VERSION    AX571850.1  GI:26003984
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Blanche, F. and Cameron, B.
TITLE      Methods for purifying and detecting double stranded dna target
            sequences by triple helix interaction
JOURNAL    Patent: WO 02077274-A 9 03-OCT-2002;
            Aventis Pharma S.A. (FR)
FEATURES   source
            1..14
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 2 AGGAGAGAGAGAA 14

RESULT 111
BD065435
LOCUS      BD065435                14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065435
VERSION    BD065435.1  GI:22611038
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
            1 (bases 1 to 14)
REFERENCE  1
AUTHORS    Schlingensiefen, K.H. and Brysch, W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 70 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
            PN JP 2001511000-A/70
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
            PC C12N15/11, C07H21/04, A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source 1..14
            /organism="Unknown"

FEATURES   source
            1..14
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAGAGCA 740
Db 2 GCAAGGAGAGAGCA 14

RESULT 113
BD209300/c
LOCUS      BD209300/c              14 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION  BD209300
VERSION    BD209300.1  GI:33019070
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
            1 (bases 1 to 14)
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE      Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
JOURNAL    Patent: JP 2002512791-A 2890 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
            OS Hepatitis virus (hepatitis C virus)
            PN JP 2002512791-A/2890
            PD 08-MAY-2002
            PF 26-APR-1999 JP 2000545991
            PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
            25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
            LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
            PAVCO.
            PI DENNIS MACEJAK
            PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
            A61K37/66,
            CC Enzymatic nucleic acid treatment of diseases or conditions
            related to
            hepatitis C virus infection.
            FH Key Location/Qualifiers
            FT source 1..14

Query Match      44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAGAGAG 741
Db 1 CCATGAGAGAGAG 13

RESULT 112
BD066626

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LOCUS      BD066626                14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066626
VERSION    BD066626.1  GI:22612229
KEYWORDS   JP 2001511000-A/1261.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
            1 (bases 1 to 14)
REFERENCE  1
AUTHORS    Schlingensiefen, K.H. and Brysch, W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1261 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
            PN JP 2001511000-A/1261
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
            PC C12N15/11, C07H21/04, A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source 1..14
            /organism="Unknown"

FEATURES   source
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            /organism="unidentified"
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            /db_xref="taxon:32644"

Query Match      44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAGAGCA 740
Db 2 GCAAGGAGAGAGCA 14

RESULT 113
BD209300/c
LOCUS      BD209300/c              14 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION  BD209300
VERSION    BD209300.1  GI:33019070
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
            1 (bases 1 to 14)
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE      Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
JOURNAL    Patent: JP 2002512791-A 2890 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
            OS Hepatitis virus (hepatitis C virus)
            PN JP 2002512791-A/2890
            PD 08-MAY-2002
            PF 26-APR-1999 JP 2000545991
            PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
            25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
            LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
            PAVCO.
            PI DENNIS MACEJAK
            PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
            A61K37/66,
            CC Enzymatic nucleic acid treatment of diseases or conditions
            related to
            hepatitis C virus infection.
            FH Key Location/Qualifiers
            FT source 1..14

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FT      /organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
source
1. .14
/organism="unidentified"
/db_type="genomic RNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      732 GGAGAAACAGAAC 744
Db      13 GGTGAAACAGTAC 1

RESULT 114
AR130724/c
LOCUS      AR130724      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6190866.
ACCESSION  AR130724
VERSION     AR130724.1 GI:14119049
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Nielsen,P.E. and Good,L.
TITLE      Methods of bacterial gene function determination using peptide
nucleic acids
JOURNAL    Patent: US 6190866-A 11 20-FEB-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      731 AGGAGAAACAGAA 743
Db      15 AGGAGAAAGAGTA 3

RESULT 115
AR180392/c
LOCUS      AR180392      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 460 from patent US 6333152.
ACCESSION  AR180392
VERSION     AR180392.1 GI:20222425
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Vogelstein,B., Kinler,K.W., Zhang,L. and Zhou,W.
TITLE      Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 6333152-A 460 25-DEC-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      728 GCCAGGAGAACAA 740
Db      15 GCCAGCAGAAACA 3

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RESULT 116
AR235561
LOCUS      AR235561      15 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 60 from patent US 6461810.
ACCESSION  AR235561
VERSION     AR235561.1 GI:27278782
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Fresco,J.R. and Johnson,M.D.
TITLE      Triplex in-situ hybridization
JOURNAL    Patent: US 6461810-A 60 08-OCT-2002;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="genomic DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      731 AGGAGAAACAGAA 743
Db      2 AGGTGAAAAGAA 14

RESULT 117
AR370348/c
LOCUS      AR370348      15 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 11 from patent US 6300318.
ACCESSION  AR370348
VERSION     AR370348.1 GI:34606876
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Nielsen,P.E. and Good,L.
TITLE      Antibacterial and antibiotic methods using peptide nucleic acids
and pharmaceutical compositions therefor
JOURNAL    Patent: US 6300318-A 11 09-OCT-2001;
FEATURES   Location/Qualifiers
source     1. .15
/mol_type="genomic DNA"

Query Match
Best Local Similarity 44.5%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      731 AGGAGAAACAGAA 743
Db      15 AGGAGAAAGAGTA 3

RESULT 118
AX009449/c
LOCUS      AX009449      15 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9961662.
ACCESSION  AX009449
VERSION     AX009449.1 GI:9996735
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS    Shchepinov,M.S. and Southern,E.M.
TITLE      Polynucleotide multimers and their use in hybridisation assays
JOURNAL    Patent: WO 9961662-A 2 02-DEC-1999;
           SHCHEPINOV MIKHAIL SERGEEVICH (GB); SOUTHERN EDWIN MELLOR (GB);

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ISIS INNOVATION (GB)
FEATURES
  source
    Location/Qualifiers
      1..15
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Oligonucleotide"

Query Match
  44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity
  84.6%; Pred. No. 1.4e+02;
Matches
  11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAA 743
Db 14 AAGAGAAAGAGAA 2

RESULT 119
BD005884/c
LOCUS
DEFINITION Novel probes for the detection of Mycobacteria.
ACCESSION BD005884
VERSION BD005884.1 GI:18634255
KEYWORDS JP 2001501825-A/95.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE
  1 (bases 1 to 15)
  Stender, H., Lund, K. and Mollerup, T.A.
  Novel probes for the detection of Mycobacteria
  Patent: JP 2001501825-A 95 13-FEB-2001,
  DAKO AS
COMMENT
  OS Unidentified
  PN JP 2001501825-A/95
  PD 13-FEB-2001
  PF 03-OCT-1997 JP 1998517095
  PR 04-OCT-1996 DK 1096/96, 18-OCT-1996 DK 1156/96 PR
  05-MAY-1997 DK 0512/97
  PI HENRIK STENDER, KARE LUND, TINA ANDRESEN MOLLERUP PC
  C12Q1/68, C07K14/00
  CC Strandedness: Single;
  CC Topology: Linear;
  FH Key Location/Qualifiers
  FT source 1..15
  /organism="Unidentified".
  /db_xref="taxon:32644".

FEATURES
  source
    Location/Qualifiers
      1..15
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644".

Query Match
  44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity
  84.6%; Pred. No. 1.4e+02;
Matches
  11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAAC 744
Db 13 GGTGAACAGTAC 1

RESULT 121
AX471642/c
LOCUS
DEFINITION Sequence 1219 from Patent WO02053773.
ACCESSION AX471642
VERSION AX471642.1 GI:22206767
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Hofmann, K., Conradt, M. and Petersohn, D.
  Method for determining skin stress or skin ageing in vitro
  Patent: WO 02053773-A 1219 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606".

Query Match
  42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity
  90.9%; Pred. No. 1.2e+02;
Matches
  10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAAACAGAAC 744
Db 11 AGAAACAGATC 1

RESULT 122
AX627643/c
LOCUS
DEFINITION Sequence 4684 from Patent WO02053774.

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Enzymatic nucleic acid treatment of diseases or conditions related
to Hepatitis C virus infection
Patent: JP 2002512791-A 1987 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/1987
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO, DENNIS MACEJAK
PI C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
  hepatitis C virus infection.
  FH Key Location/Qualifiers
  FT source 1..15
  /organism="Hepatitis virus (hepatitis C FT
  virus)".
  /db_xref="taxon:32644".

FEATURES
  source
    Location/Qualifiers
      1..15
      /organism="unidentified"
      /mol_type="genomic RNA"
      /db_xref="taxon:32644".

Query Match
  44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity
  84.6%; Pred. No. 1.4e+02;
Matches
  11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAAC 744
Db 13 GGTGAACAGTAC 1

RESULT 121
AX471642/c
LOCUS
DEFINITION Sequence 1219 from Patent WO02053773.
ACCESSION AX471642
VERSION AX471642.1 GI:22206767
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Hofmann, K., Conradt, M. and Petersohn, D.
  Method for determining skin stress or skin ageing in vitro
  Patent: WO 02053773-A 1219 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606".

Query Match
  42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity
  90.9%; Pred. No. 1.2e+02;
Matches
  10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAAACAGAAC 744
Db 11 AGAAACAGATC 1

RESULT 122
AX627643/c
LOCUS
DEFINITION Sequence 4684 from Patent WO02053774.

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Query Match	42.7%;	Score 9.4;	DB 1;	Length 12;
Best Local Similarity	90.9%;	Pred. No. 1.3e+02;		
Matches	10;	Conservative 0;	Mismatches 1;	Indels 0;
QY	728	GCCAGGAGAAA 738		
DB	12	GCCAGGAGAGA 2		
RESULT 125				
LOCUS	AR077199/c		12 bp	DNA
DEFINITION	Sequence 15 from patent US 5962228.			linear
ACCESSION	AR077199			
VERSION	AR077199.1	GI:10003945		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 12)			
TITLE	Brenner, S.			
JOURNAL	DNA extension and analysis with rolling primers			
FEATURES	Patent: US 5962228-A 15 05-OCT-1999;			
source	Location/Qualifiers			
	1..12			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	42.7%;	Score 9.4;	DB 1;	Length 12;
Best Local Similarity	90.9%;	Pred. No. 1.3e+02;		
Matches	10;	Conservative 0;	Mismatches 1;	Indels 0;
QY	728	GCCAGGAGAAA 738		
DB	12	GCCAGGAGAGA 2		
RESULT 126				
LOCUS	AR087821		12 bp	DNA
DEFINITION	Sequence 14 from patent US 5989810.			linear
ACCESSION	AR087821			
VERSION	AR087821.1	GI:10014584		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 12)			
TITLE	Planagan, W.M. and Crabtree, G.R.			
JOURNAL	Screening methods for immunosuppressive agents			
FEATURES	Patent: US 5989810-A 14 23-NOV-1999;			
source	Location/Qualifiers			
	1..12			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	42.7%;	Score 9.4;	DB 1;	Length 12;
Best Local Similarity	90.9%;	Pred. No. 1.3e+02;		
Matches	10;	Conservative 0;	Mismatches 1;	Indels 0;
QY	730	CAGGAGAAACA 740		
DB	1	CAGGAGAAAAA 11		
RESULT 127				
LOCUS	AR167798		12 bp	DNA
DEFINITION	Sequence 162 from patent US 6287769.			linear
ACCESSION	AR167798			
VERSION	AR167798.1	GI:17903601		
KEYWORDS				

```

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Inoue,T.
TITLE        Method of amplifying DNA fragment, apparatus for amplifying DNA
              fragment, method of assaying microorganisms, method of analyzing
              microorganisms and method of assaying contaminant
JOURNAL      Patent: US 6287769-A 162 11-SEP-2001;
FEATURES     Location/Qualifiers
              source
              1..12
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 2 AGGAGAAACGG 12

RESULT 128
LOCUS       BD242531 12 bp DNA linear PAT 17-JUL-2003
DEFINITION  A system for cell based screening.
ACCESSION   BD242531
VERSION     BD242531.1 GI:33052301
KEYWORDS    JP 2002528136-A/37.
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Guiliano,K.A., Bright,G., Olson,K. and Tencza,S.B.
TITLE        A system for cell based screening
JOURNAL      Patent: JP 2002528136-A 37 03-SEP-2002;
COMMENT      CELLOMICS INC
OS           Artificial Sequence
PN           JP 2002528136-A/37
PD           03-SEP-2002
PF           29-OCT-1999 JP 2000579780
PR           30-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI
KENNETH A GUILIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI
TENCZA
PC          C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/
PC          37,G01N33/15,
PC          G01N33/50,C12N15/00,C12N5/00
CC          Description of Artificial Sequence: Caspase-8 substrate CC
              recognition
              sequence
              Location/Qualifiers
              FH Key
              FT source
              1..12
              /organism="Artificial Sequence".
              Location/Qualifiers
              1..12
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
DB 1 GTAGAAACAGA 11

RESULT 129
LOCUS       BD269489/c 12 bp RNA linear PAT 17-JUL-2003
DEFINITION  Stable recombinant influenza virus free from helper virus.

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ACCESSION   BD269489
VERSION     BD269489.1 GI:33079257
KEYWORDS    JP 2002537844-A/13.
SOURCE      synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
              1 (bases 1 to 12)
REFERENCE    Hobom,G., Flick,R., Menke,A. and Azzeah,M.
              Stable recombinant influenza virus free from helper virus
              Patent: JP 2002537844-A 13 12-NOV-2002;
              ARTEMIS PHARMACEUTICALS GMBH
JOURNAL
COMMENT      OS Artificial Sequence
              PN JP 2002537844-A/13
              PD 12-NOV-2002
              PF 03-MAR-2000 JP 2000603407
              PR 06-MAR-1999 EP 99104519.6
              PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEAH PC
              C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
              A61K35/12.
              PC (C12N7/00,C12R1:93),C12N15/00
              CC Description of Artificial Sequence: Modified influenza A 3'
              sequence
              CC (pHL1104 and 1920)
              FH Key
              FT source
              1..12
              Location/Qualifiers
              /organism="Artificial Sequence".
              Location/Qualifiers
              1..12
              /organism="synthetic construct"
              /mol_type="genomic RNA"
              /db_xref="taxon:32630"

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 12 AGTGAACACAG 2

RESULT 130
LOCUS       E29682
DEFINITION  Method for amplifying DNA fragment, method for estimating state of
              microorganism existing and method for estimating state of
              microorganism existing and method for estimating state of waste
              Patent: JP 1999276176-A 162 12-OCT-1999;
              SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
              FORESTRY AND FISHERIES
              OS Unidentified
              PN JP 1999276176-A/162
              PD 12-OCT-1999
              PF 31-MAR-1998 JP 1998087652
              PR KOICHI INOUE
              PI C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
              Strandedness: Single;
              FH Key
              FT source
              1..12
              Location/Qualifiers
              /organism="Unidentified".
              Location/Qualifiers
              1..12
              /organism="unidentified"
              source

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 2 AGGAGAAACGG 12
|||||

RESULT 131
E38120/c
LOCUS          12 bp      RNA      linear      PAT 18-JUN-2001
DEFINITION    DNA elongation and analysis with the use of rolling primer.
ACCESSION     E38120
VERSION       J38120.1 GI:13027155
KEYWORDS      JP 199151092-A/15.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 12)
AUTHORS       Sydney,B.
TITLE         DNA elongation and analysis with the use of rolling primer
JOURNAL       LYNX THERAPEUTICS INC
COMMENT       OS Artificial Sequence
              PN JP 199151092-A/15
              PF 08-JUN-1999
              PD 24-AUG-1998 JP 1998237840
              PR 22-AUG-1997 US 08/916.120
              PC C12N15/09,C12Q1/68,C12N15/00
              CC
              FH Key Location/Qualifiers
              FT source 1..12
              /organism="synthetic construct"
              /mol_type="genomic RNA"
              /db_xref="taxon:32630"

FEATURES
source
    Query Match      42.7%; Score 9.4; DB 1; Length 12;
    Best Local Similarity 90.9%; Pred. No. 1.3e+02;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

    QY 731 AGGAGAAACAG 741
    DB 2 AGGAGAAACGG 12
    |||||

RESULT 132
E38788
LOCUS          12 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION    Method and device for amplifying DNA fragment.
ACCESSION     E38788
VERSION       E38788.1 GI:18621450
KEYWORDS      JP 2000270867-A/162.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 12)
AUTHORS       Inoue,K.
TITLE         Method and device for amplifying DNA fragment
JOURNAL       SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
COMMENT       OS Unidentified
              PN JP 2000270867-A/162
              PD 03-OCT-2000
              PF 19-MAR-1999 JP 1999076844

/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 12 GCCAGGAGAGA 2
|||||

RESULT 133
E64214
LOCUS          12 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION    Method for amplifying DNA fragment, amplification apparatus of DNA
              fragment, method for assaying a group of microorganisms, method
              for analyzing a group of microorganisms, and method for assaying
              contaminating substance.
ACCESSION     E64214
VERSION       E64214.1 GI:13019618
KEYWORDS      JP 1999341989-A/162.
SOURCE        synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE     1 (bases 1 to 12)
AUTHORS       Koichi,I.
TITLE         Method for amplifying DNA fragment, amplification apparatus of DNA
              fragment, method for assaying a group of microorganisms, method for
              analyzing a group of microorganisms, and method for assaying
              contaminating substance
              Patent: JP 1999341989-A 162 14-DEC-1999;
              SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
              FORESTRY AND FISHERIES
              OS Artificial Sequence
              PN JP 1999341989-A/162
              PD 14-DEC-1999
              PF 16-MAR-1999 JP 1999069694
              PR
              PI KOICHI INOUE
              PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
              CC
              FH Key Location/Qualifiers
              FT source 1..12
              /organism="Artificial Sequence".

FEATURES
source
    Query Match      42.7%; Score 9.4; DB 1; Length 12;
    Best Local Similarity 90.9%; Pred. No. 1.3e+02;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

    QY 731 AGGAGAAACAG 741
    DB 2 AGGAGAAACGG 12
    |||||

RESULT 134
AR217456

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LOCUS       AR217456               12 bp      DNA              linear      PAT 25-SEP-2002
DEFINITION   Sequence 73 from patent US 6416959.
ACCESSION    AR217456
VERSION      AR217456.1   GI:23317149
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS     Giuliano,K. and Kapur,R.
TITLE       System for cell-based screening
JOURNAL     Patent: US 6416959-A 73 09-JUL-2002;
FEATURES     Location/Qualifiers
             source
               1..12
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      732 GGAGAAACAG 742
        |||||||
Db      1 GTAGAAACAG 11

RESULT 135
LOCUS       AR282763               12 bp      RNA              linear      PAT 10-APR-2003
DEFINITION   Sequence 9 from patent US 6524588.
ACCESSION    AR282763
VERSION      AR282763.1   GI:29719542
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 12)
AUTHORS     Hobom,G., Neumann,G. and Menke,A.
TITLE       Attenuated vaccination and gene-transfer virus, a method to make
             the virus and a pharmaceutical composition comprising the virus
JOURNAL     Patent: US 6524588-A 9 25-FEB-2003;
FEATURES     Location/Qualifiers
             source
               1..12
               /organism="unknown"
               /mol_type="genomic RNA"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||||
Db      12 AGTAGAAACAG 2

RESULT 136
LOCUS       AX035438               12 bp      RNA              linear      PAT 15-NOV-2000
DEFINITION   Sequence 13 from Patent EP1035209.
ACCESSION    AX035438
VERSION      AX035438.1   GI:11191080
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS     Azzey,M., Hobom,G., Menke,A. and Flick,R.
TITLE       Stable recombinant influenza viruses free of helper viruses
JOURNAL     Patent: EP 1035209-A 13 13-SEP-2000;
FEATURES     ARTHEMIS PHARMACEUTICALS GMBH (DE)
             Location/Qualifiers
             source
               1..12
               /organism="synthetic construct"

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Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||||
Db      12 AGTAGAAACAG 2

RESULT 137
LOCUS       AX100750/c              12 bp      RNA              linear      PAT 10-APR-2001
DEFINITION   Sequence 7 from Patent WO0122083.
ACCESSION    AX100750
VERSION      AX100750.1   GI:13619696
KEYWORDS     .
SOURCE       Influenza A virus
ORGANISM     Influenza A virus
REFERENCE    1
AUTHORS     Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE       Method for identifying mhc-restricted antigens
JOURNAL     Patent: WO 0122083-A 7 29-MAR-2001;
             GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
             Pharmaceuticals GmbH (DE)
FEATURES     Location/Qualifiers
             source
               1..12
               /organism="Influenza A virus"
               /mol_type="unassigned RNA"
               /db_xref="taxon:11320"
             misc_feature
               1..12
               /note="3'-terminale Nukleotidsequenz"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAAACAG 741
        |||||||
Db      12 AGGAGAACACAG 2

RESULT 138
LOCUS       AX100751/c              12 bp      RNA              linear      PAT 10-APR-2001
DEFINITION   Sequence 8 from Patent WO0122083.
ACCESSION    AX100751
VERSION      AX100751.1   GI:13619697
KEYWORDS     .
SOURCE       Influenza A virus
ORGANISM     Influenza A virus
REFERENCE    1
AUTHORS     Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE       Method for identifying mhc-restricted antigens
JOURNAL     Patent: WO 0122083-A 8 29-MAR-2001;
             GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
             Pharmaceuticals GmbH (DE)
FEATURES     Location/Qualifiers
             source
               1..12
               /organism="Influenza A virus"
               /mol_type="unassigned RNA"
               /db_xref="taxon:11320"
             misc_feature
               1..12
               /note="3'-terminale Nukleotidsequenz"

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Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 139
AX352660/c
LOCUS      12 bp      RNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 4 from Patent EP1174514.
ACCESSION  AX352660
VERSION     AX352660.1 GI:18617790
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE      Recombinant influenza viruses with bicistronic vrnas coding for two
           Genes in tandem arrangement
JOURNAL    Patent: EP 1174514-A 4 23-JAN-2002;
           ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES   source
           1..12
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Modified influenza A 5'-sequence (pHL1104 and
           pHL1920)"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 140
AX352661/c
LOCUS      12 bp      RNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent EP1174514.
ACCESSION  AX352661
VERSION     AX352661.1 GI:18617791
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE      Recombinant influenza viruses with bicistronic vrnas coding for two
           Genes in tandem arrangement
JOURNAL    Patent: EP 1174514-A 5 23-JAN-2002;
           ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES   source
           1..12
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Modified influenza A 3'-sequence (pHL1948)"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAACAG 2

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RESULT 141
AX362218/c
LOCUS      12 bp      RNA      linear      PAT 15-FEB-2002
DEFINITION Sequence 4 from Patent WO0208434.
ACCESSION  AX362218
VERSION     AX362218.1 GI:18694556
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE      Recombinant influenza viruses with bicistronic vrnas coding for two
           Genes in tandem arrangement
JOURNAL    Patent: WO 0208434-A 4 31-JAN-2002;
           ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES   source
           1..12
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Modified influenza A 3'-sequence (pHL1104 and
           pHL1920)"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 731 AGGAGAAACAG 741
Db 12 AGTAGAACAG 2

RESULT 142
AX362219/c
LOCUS      12 bp      RNA      linear      PAT 15-FEB-2002
DEFINITION Sequence 5 from Patent WO0208434.
ACCESSION  AX362219
VERSION     AX362219.1 GI:18694557
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE      Recombinant influenza viruses with bicistronic vrnas coding for two
           Genes in tandem arrangement
JOURNAL    Patent: WO 0208434-A 5 31-JAN-2002;
           ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES   source
           1..12
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Modified influenza A 3'-sequence (pHL1948)"

Query Match      42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAACAG 2

RESULT 143
AX428931/c
LOCUS      12 bp      RNA      linear      PAT 21-JUN-2002
DEFINITION Sequence 4 from Patent EP1201760.
ACCESSION  AX428931
VERSION     AX428931.1 GI:21540315
KEYWORDS   .

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Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
Db 12 AGTAGAACAG 2

RESULT 148
AX522266/c
LOCUS
DEFINITION Sequence 6 from Patent WO02064757.
ACCESSION AX522266
VERSION AX522266.1 GI:24411220
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational capacities
JOURNAL ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source 1..12
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza A 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
Db 12 AGGAGAACAG 2

RESULT 149
AX766784
LOCUS
DEFINITION Sequence 73 from Patent EP1314980.
ACCESSION AX766784
VERSION AX766784.1 GI:32260536
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Giuliano, K.A. and Kapur, R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 73 28-MAY-2003;
Cellomics, Inc. (US)
FEATURES
source 1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Capase-8 substrate recognition sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAACAG 742
Db 1 GTAGAACAG 11

RESULT 150
AR282758/c
LOCUS

Sequence 4 from patent US 6524588.
ACCESSION AR282758
VERSION AR282758.1 GI:29719537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Hobom, G., Neumann, G. and Menke, A.
TITLE Attenuated vaccination and gene-transfer virus, a method to make the virus and a pharmaceutical composition comprising the virus
JOURNAL Patent: US 6524588-A 4 25-FEB-2003;
FEATURES
source 1..13
/organism="unknown"
/mol_type="genomic RNA"

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
Db 13 AGTAGAACAG 3

RESULT 151
AR407966/c
LOCUS
DEFINITION Sequence 59 from patent US 6632057.
ACCESSION AR407966
VERSION AR407966.1 GI:40157953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Fauchet, C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 59 14-OCT-2003;
FEATURES
source 1..13
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
Db 11 AGCAGAACAG 1

RESULT 152
BD237463
LOCUS
DEFINITION Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.
ACCESSION BD237463
VERSION BD237463.1 GI:33047233
KEYWORDS JP 2002534434-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Dale, R.M.K., Gattton, S.L. and Arrow, A.
TITLE Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof
JOURNAL Patent: JP 2002534434-A 1 15-OCT-2002;
ChigOS ETC INC
COMMENT OS Artificial Sequence
PN JP 2002534434-A/1

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PD 15-OCT-2002
PF 16-DEC-1999 JP 2000592300
PR 30-DEC-1998 US 09/223498,19-JUL-1999 US 09/356069 PI
RODERIC M K DALE,STEVEN L GATTON,AMY ARROW
PC C07H21/00,A61K9/127,A61K31/7088,A61K47/44,A61K48/00,
PC A61P3/00,
PC A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
PC C12N5/10,
PC C12N15/09,C12N15/00,C12N5/00
CC Nucleic acid having blocked terminals modified with an acid-
stable
CC skeleton and therapeutic method thereof
CC key Location/Qualifiers
FH key 1..14
FT source
FEATURES
source
Location/Qualifiers
1..14
/organism="Artificial Sequence"
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737
DB 3 TGTCCAGGAGAA 13

RESULT 153
BD263138
LOCUS
DEFINITION Phosphodiesterase inhibitors for therapeutic use.
ACCESSION BD263138
VERSION BD263138.1 GI:33072906
KEYWORDS JP 2002534086-A/32.
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 14)
AUTHORS Dale,R.M.K., Arrow,A. and Thompson,T.
TITLE Phosphodiesterase inhibitors for therapeutic use
JOURNAL Patent: JP 2002534086-A 32 15-OCT-2002;
COMMENT ORIGOS ETC INC
OS Artificial Sequence
PN JP 2002534086-A/32
PD 15-OCT-2002
PF 15-DEC-1999 JP 2000592411
PR 30-DEC-1998 US 09/223498,29-JUL-1999 US 09/364626 PI
RODERIC M K DALE,AMY ARROW,TERRY THOMPSON
PC C12N15/09,A61K31/7088,A61K48/00,A61P/00,A61P1/04,A61P3/10,PC
A61P9/00,
PC A61P9/10,A61P11/00,A61P11/06,A61P13/16,A61P17/04,PC
A61P17/06,
PC A61P19/02,A61P25/00,A61P25/24,A61P25/28,A61P27/14,A61P27/16,
PC A61P29/00,
PC A61P31/18,A61P33/06,A61P35/00,A61P37/06,A61P43/00,C12N15/00 CC
Synthesized oligonucleotide
FH Key Location/Qualifiers
FT source 1..14
/organism="Artificial Sequence"
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAA 737

```

```

DB 3 TGTCCAGGAGAA 13

RESULT 154
BD269502/c
LOCUS
DEFINITION Stable recombinant influenza virus free from helper virus.
ACCESSION BD269502
VERSION BD269502.1 GI:33079270
KEYWORDS JP 2002537844-A/26.
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 14)
AUTHORS Hobom,G., Flick,R., Menke,A. and Azzev,M.
TITLE Stable recombinant influenza virus free from helper virus
JOURNAL Patent: JP 2002537844-A 26 12-NOV-2002;
COMMENT ARTEMIS PHARMACEUTICALS GMBH
OS Artificial Sequence
PN JP 2002537844-A/26
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519,6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEZ PC
C12N15/09,A61K39/145,A61K48/00,A61P1/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12P1:93),C12N15/00
CC Description of Artificial Sequence: Modified influenza C 3'
CC sequence
FH Key Location/Qualifiers
FT source 1..14
/organism="Artificial Sequence"
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
DB 14 AGTAGAACAG 4

RESULT 155
AX035451/c
LOCUS
DEFINITION Sequence 26 from Patent EP1035209.
ACCESSION AX035451
VERSION AX035451.1 GI:11191093
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Azzev,M., Hobom,G., Menke,A. and Flick,R.
TITLE Stable recombinant influenza viruses free of helper viruses
JOURNAL Patent: EP 1035209-A 26 13-SEP-2000;
COMMENT ARTEMIS PHARMACEUTICALS GMBH (DE)
OS Artificial Sequence
PN 1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Modified influenza C 3' sequence"
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 156
AX352673/c
LOCUS 14 bp RNA linear PAT 06-FEB-2002
DEFINITION Sequence 17 from Patent EP1174514.
ACCESSION AX352673
VERSION AX352673.1 GI:18617803
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom, G., Menke, A. and Meyer-Rogge, S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
JOURNAL genes in tandem arrangement
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 157
AX362231/c
LOCUS 14 bp RNA linear PAT 15-FEB-2002
DEFINITION Sequence 17 from Patent WO0208434.
ACCESSION AX362231
VERSION AX362231.1 GI:18694569
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom, G., Menke, A. and Meyer-Rogge, S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
JOURNAL genes in tandem arrangement
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 158
AX428944/c
LOCUS 14 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 17 from Patent EP1201760.
ACCESSION AX428944
VERSION AX428944.1 GI:21540328
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schuler, G.D., Hobom, G., Steinkasserer, A.D., Strobel, I.D. and
Grassmann, R.
TITLE Influenza virus vector for human dendritic cells
JOURNAL Patent: EP 1201760-A 17 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 159
AX512628/c
LOCUS 14 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 19 from Patent EP1233059.
ACCESSION AX512628
VERSION AX512628.1 GI:23503851
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational
JOURNAL capacities
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza C 3'-sequence"

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 14 AGTAGAAACAG 4

RESULT 160
AX522279/c
LOCUS 14 bp RNA linear PAT 24-OCT-2002
DEFINITION Sequence 19 from Patent WO02064757.
ACCESSION AX522279
VERSION AX522279.1 GI:24411233
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hobom, G. and Menke, A.

```

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TITLE      Influenza viruses with enhanced transcriptional and replicational
            capacities
JOURNAL    Patent: WO 02064757-A 19 22-AUG-2002;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Modified influenza C 3'-sequence"

Query Match      42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      731 AGGAGAACAG 741
Db      14 AGTAGAACAG 4

RESULT 161
LOCUS      A40498          14 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 35 from Patent WO9425578.
ACCESSION  A40498
VERSION     A40498.1 GI:2296533
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 14)
AUTHORS    Brysch,W. and Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
            Antisense-oligonucleotides for transforming growth factor-.beta.
            (TGF-.beta.)
JOURNAL    Patent: US 6455689-A 35 24-SEP-2002;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 162
LOCUS      A89025          14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1173 from Patent WO9833904.
ACCESSION  A89025
VERSION     A89025.1 GI:6737595
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 14)
AUTHORS    Brysch,W. and Schlingensiepen,K.
            Antisense-oligonucleotide preparation method
            AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL    Patent: WO 9833904-A 1173 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      41.8%; Score 9.2; DB 1; Length 14;

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Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 163
LOCUS      AR232778          14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 35 from patent US 6455689.
ACCESSION  AR232778
VERSION     AR232778.1 GI:27275116
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
            Antisense-oligonucleotides for transforming growth factor-.beta.
            (TGF-.beta.)
JOURNAL    Patent: US 6455689-A 35 24-SEP-2002;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 164
LOCUS      AX316394          14 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 35 from Patent EPl160319.
ACCESSION  AX316394
VERSION     AX316394.1 GI:17899567
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
            Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL    Patent: EP 1160319-A 35 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"

Query Match      41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      730 CAGGAGAACAGAA 743
Db      1 CATGAGAGCAGGA 14

RESULT 165
BD066538

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LOCUS BD066538 14 bp DNA linear PAT 27-AUG-2002
 DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD066538
 VERSION BD066538.1 GI:22612141
 KEYWORDS JP 2001511000-A/1173.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Schlingensiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 1173 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 COMMENT OS Unknown
 PN JP 2001511000-A/1173
 PD 07-AUG-2001
 PE 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
 PC C12N15/11, C07H21/04, A61K31/70
 CC An antisense oligonucleotide preparation method FH Key
 LOCATION/Qualifiers
 FT source 1. .14
 FT Location/Qualifiers
 FEATURES
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 1. .14
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 1.6e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 730 CAGGAGAACAGAA 743
 DB 1 CATGAGAGCAGGA 14
 RESULT 166
 BD199355/C
 LOCUS BD199355 14 bp RNA linear PAT 17-JUL-2003
 DEFINITION Method and reagent for treating diseases or conditions concerning
 molecule participating in vasculogenic response.
 ACCESSION BD199355
 VERSION BD199355.1 GI:33009125
 KEYWORDS JP 2002509721-A/2381.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
 TITLE Method and reagent for treating diseases or conditions concerning
 molecule participating in vasculogenic response
 JOURNAL Patent: JP 2002509721-A 2381 02-APR-2002;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002509721-A/2381
 PD 02-APR-2002
 PE 24-MAR-1999 JP 2000541291
 PR 27-MAR-1998 US 60/079678
 PI FAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
 PI JAMES A MCSWIGGEN
 PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
 A61P29/00,
 PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
 C12N5/00
 CC Method and reagent for treating diseases or conditions CC
 concerning molecule
 CC participating in vasculogenic response
 FH Key Location/Qualifiers

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 /mol_type="genomic RNA"
 /db_xref="taxon:9606"
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 Best Local Similarity 78.6%; Pred. No. 1.6e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 731 AGGAGAACAGAAC 744
 DB 14 AGAGGAGACAGCAC 1
 RESULT 167
 S59977S1/c
 LOCUS S59977S1 14 bp mRNA linear ROD 11-OCT-2002
 DEFINITION GM-CSF-granulocyte-macrophage colony-stimulating factor [mice,
 WEHI-231 cell line, mRNA Partial, 14 nt, segment 1 of 2].
 ACCESSION S59977
 VERSION S59977.1 GI:237044
 KEYWORDS
 SEGMENT 1 of 2
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Leslie,K.B., Lee,F. and Schrader,J.W.
 TITLE Intracisternal A-type particle-mediated activations of cytokine
 genes in a murine myelomonocytic leukemia: generation of functional
 cytokine mRNAs by retroviral splicing events
 JOURNAL Mol. Cell. Biol. 11 (11), 5562-5570 (1991)
 MEDLINE 92017836
 PUBMED 1922064
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gibbsq 59977] from the original journal article.
 COMMENT This sequence comes from fig6b.
 spliced transcript.
 FEATURES
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
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 Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 1.6e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 733 GAGAAACAGAACAC 746
 DB 14 GAGAGAGAGAAC 1
 RESULT 168
 BD240369
 LOCUS BD240369 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240369
 VERSION BD240369.1 GI:33050139
 KEYWORDS JP 2002534056-A/1787.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Roberts,B.L. and Shankara,S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1787 15-OCT-2002;


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Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 30 08-APR-2003;
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Query Match      40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
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Db 1 GAGAAACAG 9

RESULT 172
AR303339/c
LOCUS AR303339 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 64 from patent US 6544736.
ACCESSION AR303339
VERSION AR303339.1 GI:31692115
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 64 08-APR-2003;
FEATURES
    source
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        /organism="unknown"
        /mol_type="genomic DNA"
Query Match      40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
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Db 10 GAGAAACAG 2

RESULT 173
BD161312/c
LOCUS BD161312 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161312
VERSION BD161312.1 GI:27867070
KEYWORDS JP 2002186482-A/134.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 10)
Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 134 02-JUL-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/134
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source
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    Location/Qualifiers

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    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
Query Match      40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 AGAACACCG 748
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Db 10 AGAACACCG 2

RESULT 174
AX470590
LOCUS AX470590 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 167 from Patent WO02053773.
ACCESSION AX470590
VERSION AX470590.1 GI:22205715
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 167 11-JUL-2002;
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
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Db 3 CCAGGAGAA 11

RESULT 175
AX623138/c
LOCUS AX623138 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 179 from Patent WO02053774.
ACCESSION AX623138
VERSION AX623138.1 GI:28451079
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 179 11-JUL-2002;
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 736 AAACAGAAC 744
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Db 10 AAACAGAAC 2

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Db          9 AAACAGAAC 1

RESULT 176
AX624843/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 1884 from Patent WO02053774.
ACCESSION  AX624843
VERSION     AX624843.1  GI:28452784
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1884 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE      1. .11
            /organism="Homo sapiens"
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Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      734 AGAAGACAGA 742
Db      11 AGAAGACAGA 3

RESULT 179
AX628047
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5088 from Patent WO02053774.
ACCESSION  AX628047
VERSION     AX628047.1  GI:28456085
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5088 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE      1. .11
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            /mol_type="unassigned DNA"
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Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      739 CAGAACACCC 747
Db      3 CAGAACACCC 11

RESULT 180
AX630559/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7600 from Patent WO02053774.
ACCESSION  AX630559
VERSION     AX630559.1  GI:28458597
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7600 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE      1. .11
            /organism="Homo sapiens"

Db          9 AAACAGAAC 1

RESULT 177
AX625131
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2172 from Patent WO02053774.
ACCESSION  AX625131
VERSION     AX625131.1  GI:28453072
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2172 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE      1. .11
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            /mol_type="unassigned DNA"
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Query Match      40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      729 CCAGAGAGAA 737
Db      3 CCAGAGAGAA 11

RESULT 178
AX626407/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3448 from Patent WO02053774.
ACCESSION  AX626407
VERSION     AX626407.1  GI:28454445
KEYWORDS
SOURCE      Homo sapiens (human)

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Query Match	40.9%;	Score 9;	DB 1;	Length 11;	
Best Local Similarity	100.0%;	Pred. No. 1.4e+02;			
Matches	9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	736	AAACAGAAC 744			
Db	9	AAACAGAAC 1			
RESULT 181					
AX632264/c					
LOCUS	AX632264	11 bp	DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 9306 from Patent WO02053774.				
ACCESSION	AX632264				
VERSION	AX632264.1	GI:28467879			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.				
TITLE	Method for determining homeostasis of the skin				
JOURNAL	Patent: WO 02053774-A 9306 11-JUL-2002;				
	Henkel Kommanditgesellschaft auf Aktien (DE)				
FEATURES	Location/Qualifiers				
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	/db_xref="taxon:9606"				
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Best Local Similarity	100.0%;	Pred. No. 1.4e+02;			
Matches	9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	738	ACAGAACAC 746			
Db	9	ACAGAACAC 1			
RESULT 182					
AX632552					
LOCUS	AX632552	11 bp	DNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 9594 from Patent WO02053774.				
ACCESSION	AX632552				
VERSION	AX632552.1	GI:28468167			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.				
TITLE	Method for determining homeostasis of the skin				
JOURNAL	Patent: WO 02053774-A 9594 11-JUL-2002;				
	Henkel Kommanditgesellschaft auf Aktien (DE)				
FEATURES	Location/Qualifiers				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
Query Match	40.9%;	Score 9;	DB 1;	Length 11;	
Best Local Similarity	100.0%;	Pred. No. 1.4e+02;			
Matches	9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	729	CCAGAGAA 737			
Db	3	CCAGAGAA 11			

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CC sequence recognition
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FEATURES
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            1..12 /organism="synthetic construct"
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Query Match
Best Local Similarity 40.9%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 185
LOCUS AR217450 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 61 from patent US 6416959.
ACCESSION AR217450
VERSION AR217450.1 GI:23317143
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Giuliano,K. and Kapur,R.
TITLE System for cell-based screening
JOURNAL Patent: US 6416959-A 61 09-JUL-2002;
FEATURES
    source
        Location/Qualifiers
            1..12 /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 40.9%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 186
LOCUS AR217457 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 75 from patent US 6416959.
ACCESSION AR217457
VERSION AR217457.1 GI:23317150
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Giuliano,K. and Kapur,R.
TITLE System for cell-based screening
JOURNAL Patent: US 6416959-A 75 09-JUL-2002;
FEATURES
    source
        Location/Qualifiers
            1..12 /organism="unknown"
            /mol_type="genomic DNA"

Query Match
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 187
LOCUS AX766772 12 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 61 from Patent EPI314980.
ACCESSION AX766772
VERSION AX766772.1 GI:32260530
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Giuliano,K.A. and Kapur,R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 61 28-MAY-2003;
CELLONICS, Inc. (US)
FEATURES
    source
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            1..12 /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="procaspase-3 substrate recognition sequence"

Query Match
Best Local Similarity 40.9%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 188
LOCUS AX766786 12 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 75 from Patent EPI314980.
ACCESSION AX766786
VERSION AX766786.1 GI:32260537
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Giuliano,K.A. and Kapur,R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 75 28-MAY-2003;
CELLONICS, Inc. (US)
FEATURES
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            /db_xref="taxon:32630"
            /note="procaspase-8 substrate recognition sequence"

Query Match
Best Local Similarity 40.9%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGA 742
Db 3 AGAAACAGA 11

RESULT 189
LOCUS AR364664 13 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 3 from patent US 5395927.
ACCESSION AR364664
VERSION AR364664.1 GI:34427588
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Bock, A., Binder, F., and Muller, F.
TITLE DNA-fragment having the cyclodextrin glycosyltransferase gene
JOURNAL Patent: US 5395927-A 3 07-MAR-1995;
FEATURES Location/Qualifiers
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1. .13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 40.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 735 GAAACAGAA 743
Db 3 GAAACAGAA 11
RESULT 190
ARI23872/c
LOCUS ARI23872 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6171821.
ACCESSION ARI23872
VERSION ARI23872.1 GI:14109233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Korneluk, R.G., Holcik, M., and Liston, P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 5 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 734 AGAAACAGAA 745
Db 12 AGAAACAGAA 1
RESULT 191
ARI23873
LOCUS ARI23873 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6171821.
ACCESSION ARI23873
VERSION ARI23873.1 GI:14109234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Korneluk, R.G., Holcik, M., and Liston, P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 6 09-JAN-2001;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 734 AGAAACAGAA 745
Db 12 AGAAACAGAA 1

Db 1 AAAAGAGAAC 12
RESULT 192
ARI23877/c
LOCUS ARI23877 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6171821.
ACCESSION ARI23877
VERSION ARI23877.1 GI:14109238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Korneluk, R.G., Holcik, M., and Liston, P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 10 09-JAN-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 734 AGAAACAGAA 745
Db 12 AAAAGAGAAC 1
RESULT 193
ARI78311/c
LOCUS ARI78311 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 28 from patent US 6319672.
ACCESSION ARI78311
VERSION ARI78311.1 GI:20219449
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F., and Cameron, B.
TITLE Purification of a triple helix formation with an immobilized oligonucleotide
JOURNAL Patent: US 6319672-A 28 20-NOV-2001;
FEATURES Location/Qualifiers
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAACAGA 742
Db 12 AGGAGAACAGA 1
RESULT 194
AX323393/c
LOCUS AX323393 12 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 28 from Patent WO0192511.
ACCESSION AX323393
VERSION AX323393.1 GI:18094155
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Crouzet, J., Scherman, D., Wils, P., Blanche, F., and Cameron, B.
TITLE Purification of a triple helix formation with an immobilized

```

oligonucleotide
Patent: WO 0192511-A 28 06-DEC-2001;
Aventis Pharma (FR)
FEATURES
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="caxon:32630"
            /note="synthetic oligonucleotide"
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    Best Local Similarity 40.0%; Score 8.8; DB 1; Length 12;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGA 742
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Db 12 AGGAAAAAAGA 1

RESULT 195
AR021478/c
LOCUS
DEFINITION Sequence 8 from patent US 5789651.
ACCESSION AR021478
VERSION AR021478.1 GI:3976093
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 5789651-A 8 04-AUG-1998;
FEATURES
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            /mol_type="unassigned DNA"
Query Match
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    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGCAGACCA 745
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Db 13 AGAAGCAGACCA 2

RESULT 196
AR061316/c
LOCUS
DEFINITION Sequence 8 from patent US 5843652.
ACCESSION AR061316
VERSION AR061316.1 GI:5989007
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 5843652-A 8 01-DEC-1998;
FEATURES
    source
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            /mol_type="unassigned DNA"
Query Match
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    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGCAGACCA 745
    ||||| |||||
Db 13 AGAAGCAGACCA 2

RESULT 197
AR100114/c
LOCUS
DEFINITION Sequence 9 from patent US 6080550.
ACCESSION AR100114
VERSION AR100114.1 GI:12810562
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 6080550-A 9 27-JUN-2000;
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            /mol_type="unassigned DNA"
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Db 13 AGAAGCAGACCA 2

RESULT 198
AR100119/c
LOCUS
DEFINITION Sequence 14 from patent US 6080550.
ACCESSION AR100119
VERSION AR100119.1 GI:12810567
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 13)
AUTHORS Woychik,R.P.
TITLE Isolation and characterization of Agouti: a diabetes/obesity
related gene
JOURNAL Patent: US 6080550-A 14 27-JUN-2000;
FEATURES
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            /mol_type="unassigned DNA"
Query Match
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    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGCAGACCA 745
    ||||| |||||
Db 13 AGAAGCAGACCA 2

RESULT 199
AR175971/c
LOCUS
DEFINITION Sequence 23 from patent US 6310034.
ACCESSION AR175971
VERSION AR175971.1 GI:17917270
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 13)

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AUTHORS      Woychik,R.P., Bultman,S.J. and Michaud,E.J.
TITLE        Agouti polypeptide compositions
JOURNAL      Patent: US 6310034-A 23 30-OCT-2001;
FEATURES     Location/Qualifiers
source       1..13
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGCAGACCA 745
Db 13 AGAAGCAGACCA 2

RESULT 200
LOCUS      BD269493                13 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Stable recombinant influenza virus free from helper virus.
ACCESSION  BD269493
VERSION     BD269493.1 GI:33079261
KEYWORDS   JP 2002537844-A/17.
SOURCE     Influenza B virus
ORGANISM   Influenza B virus
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B
1 (bases 1 to 13)
Hobom,G., Flick,R., Menke,A. and AzzeH,M.
Stable recombinant influenza virus free from helper virus
TITLE      Patent: JP 2002537844-A 17 12-NOV-2002;
JOURNAL    ARTEMIS PHARMACEUTICALS GMBH
COMMENT    OS Influenza B virus
PN JP 2002537844-A/17
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519.6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEH PC
C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
A61K35/12
PC C12N7/00,C12P1/93,C12N15/00
CC Stable recombinant influenza virus free from helper virus FH
Key        Location/Qualifiers
FT source  1..13
            /organism='Influenza B virus'.
            /mol_type='genomic RNA'
            /db_xref='taxon:11520'

FEATURES     source
source       1..13
            /organism="Influenza B virus"
            /mol_type="genomic RNA"
            /db_xref="taxon:11520"

Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 201
LOCUS      AX035442                13 bp      RNA      linear      PAT 15-NOV-2000
DEFINITION Sequence 17 from Patent EP1035209.
ACCESSION  AX035442
VERSION     AX035442.1 GI:11191084
KEYWORDS   Influenza B virus
SOURCE     Influenza B virus
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
1
Hobom,G., Menke,A. and Meyer-Rogge,S.
Recombinant influenza viruses with bicistronic vrnas coding for two
genes in tandem arrangement
Patent: EP 1174514-A 7 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
JOURNAL
FEATURES     source
source       1..13
            /organism="Influenza B virus"

AUTHORS      AzzeH,M., Hobom,G., Menke,A. and Flick,R.
TITLE        Stable recombinant influenza viruses free of helper viruses
JOURNAL      Patent: EP 1035209-A 17 13-SEP-2000;
FEATURES     Location/Qualifiers
source       1..13
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Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 202
LOCUS      AX100748                13 bp      RNA      linear      PAT 10-APR-2001
DEFINITION Sequence 5 from Patent WO0122083.
ACCESSION  AX100748
VERSION     AX100748.1 GI:13619694
KEYWORDS   Influenza B virus
SOURCE     Influenza B virus
ORGANISM   Influenza B virus
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
1
Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
Method for identifying mhc-restricted antigens
Patent: WO 0122083-A 5 29-MAR-2001;
GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
Pharmaceuticals GmbH (DE)
JOURNAL
FEATURES     source
source       1..13
            /organism="Influenza B virus"
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            /db_xref="taxon:11520"
            misc_feature 1..13
                        /note="5'-Konservierte Region des Wildtyp-Influenzavirus"

Query Match      39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 1 AGTAGWAACAR 11

RESULT 203
LOCUS      AX352663                13 bp      RNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 7 from Patent EP1174514.
ACCESSION  AX352663
VERSION     AX352663.1 GI:18617793
KEYWORDS   Influenza B virus
SOURCE     Influenza B virus
ORGANISM   Influenza B virus
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
1
Hobom,G., Menke,A. and Meyer-Rogge,S.
Recombinant influenza viruses with bicistronic vrnas coding for two
genes in tandem arrangement
Patent: EP 1174514-A 7 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
JOURNAL
FEATURES     source
source       1..13
            /organism="Influenza B virus"
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/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAG 741
Db 1 AGTAGWAACAR 11

RESULT 204
AX362221
LOCUS AX362221 13 bp RNA linear PAT 15-FEB-2002
DEFINITION Sequence 7 from Patent WO0208434.
ACCESSION AX362221
VERSION AX362221.1 GI:18694559
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Hobom, G., Menke, A. and Meyer-Rogge, S.
TITLE Recombinant Influenza viruses with bicistronic vrnas coding for two
genes in tandem arrangement
JOURNAL Patent: WO 0208434-A 7 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAG 741
Db 1 AGTAGWAACAR 11

RESULT 205
AX428934
LOCUS AX428934 13 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 7 from Patent EP1201760.
ACCESSION AX428934
VERSION AX428934.1 GI:21540318
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Schuler, G.D., Hobom, G., Steinkasserer, A.D., Strobel, I.D. and
Grassmann, R.
TITLE Influenza virus vector for human dendritic cells
JOURNAL Patent: EP 1201760-A 7 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAG 741
Db 1 AGTAGWAACAR 11

RESULT 206
AX512617
LOCUS AX512617 13 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 8 from Patent EP1233059.
ACCESSION AX512617
VERSION AX512617.1 GI:23503840
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational
capacities
JOURNAL Patent: EP 1233059-A 8 21-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAG 741
Db 1 AGTAGWAACAR 11

RESULT 207
AX522268
LOCUS AX522268 13 bp RNA linear PAT 24-OCT-2002
DEFINITION Sequence 8 from Patent WO02064757.
ACCESSION AX522268
VERSION AX522268.1 GI:24411222
KEYWORDS
SOURCE
ORGANISM
Influenza B virus
Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
REFERENCE
1.
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational
capacities
JOURNAL Patent: WO 02064757-A 8 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
source
1. .13
/organism="Influenza B virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11520"

Query Match
Best Local Similarity 39.1%; Score 8.6; DB 1; Length 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAG 741
Db 1 AGTAGWAACAR 11

RESULT 208
AR026539
LOCUS AR026539 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5856103.
ACCESSION AR026539
VERSION AR026539.1 GI:5937379

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KEYWORDS	Unknown.	Query Match	38.2%; Score 8.4; DB 1; Length 10;	
SOURCE	Unknown.	Best Local Similarity	90.0%; Pred. No. 1.7e+02;	
ORGANISM	Unclassified.	Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
REFERENCE	1 (bases 1 to 10)			
AUTHORS	Gray,D.M. and Clark,C.L.			
TITLE	Method for selectively ranking sequences for antisense targeting			
JOURNAL	Patent: US 5856103-A 2 05-JAN-1999;			
FEATURES	Location/Qualifiers			
source	1..10			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	38.2%; Score 8.4; DB 1; Length 10;			
Best Local Similarity	90.0%; Pred. No. 1.7e+02;			
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	727 TGCACGAGA 736			
Db	1 TGCCCCGAGA 10			
RESULT 209				
BD238913/C				
LOCUS	BD238913	10 bp	DNA	linear
DEFINITION	Preparation and use of superior vaccines.			
ACCESSION	BD238913			
VERSION	BD238913.1 GI:33048683			
KEYWORDS	JP 2002534056-A/331.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 10)				
REFERENCE	Roberts,B.L. and Shankara,S.			
AUTHORS	Preparation and use of superior vaccines			
TITLE	Patent: JP 2002534056-A 331 15-OCT-2002;			
JOURNAL	GENZYME CORP			
COMMENT	OS Homo sapiens (human)			
	PN JP 2002534056-A/331			
	PD 15-OCT-2002			
	PF 18-JUN-1999 JP 2000554749			
	PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR			
	19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR			
	19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR			
	19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR			
	19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR			
	19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR			
	19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR			
	19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR			
	19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR			
	19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR			
	19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR			
	19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR			
	19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR			
	19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR			
	08-DEC-1998 US 60/111715			
	PI BRUCE L ROBERTS,SRINIVAS SHANKARA			
	PC C12N15/09,C12N15/09,A61P35/00,A61P37/04,C12N1/15, PC			
	C12N1/19,			
	PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC			
	G01N37/00,			
	PC C12N15/00,C12N5/00,C12N15/00			
	CC Preparation and use of superior vaccines			
	PH Key Location/Qualifiers			
	FT source 1..10			
	FT /organism='Homo sapiens (human)'			
FEATURES	Location/Qualifiers			
source	1..10			
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	/db_xref="taxon:9606"			
Query Match	38.2%; Score 8.4; DB 1; Length 10;			
Best Local Similarity	90.0%; Pred. No. 1.7e+02;			
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	727 TGCCAGAGA 736			
Db	1 TGCCAGAGA 10			
RESULT 211				
BD239797				
LOCUS	BD239797	10 bp	DNA	linear
DEFINITION	Preparation and use of superior vaccines.			

ACCESSION BD239797
 VERSION BD239797.1 GI:33049567
 KEYWORDS JP 2002534056-A/1215
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 10)
 REFERENCE Roberts,B.L. and Shankara,S.
 AUTHORS Preparation and use of superior vaccines
 TITLE Patent: JP 2002534056-A 1215 15-OCT-2002;
 JOURNAL GENZYME CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002534056-A/1215
 PD 15-OCT-2002
 PF 18-JUN-1999 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
 19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
 19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
 19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
 19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
 19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
 19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
 19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
 19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
 19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS,SRINIVAS SHANKARA
 PC C12N15/09,C12N15/09,A61K39/00,A61P37/04,C12N1/15, PC
 C12N1/19
 PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
 G01N37/00,
 CC C12N15/00,C12N5/00,C12N15/00
 CC Preparation and use of superior vaccines
 FH Key Location/Qualifiers
 FT source 1..10
 /organism='Homo sapiens (human)'.
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 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'
 Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred.No.1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 729 CCAGGAGGAAA 738
 Db 1 CCAGGAGGAAA 10
 RESULT 212
 E39660/c
 LOCUS AR303316/c
 DEFINITION Genes with human dendritic cell expression.
 ACCESSION E39660
 VERSION E39660.1 GI:18621751
 KEYWORDS JP 2000279181-A/193.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 10)
 REFERENCE Hashimoto,S., Matsushima,X. and Suzuki,T.
 AUTHORS Genes with human dendritic cell expression
 TITLE Patent: JP 2000279181-A 193 10-OCT-2000;
 JOURNAL SCIENCE & TECH AGENCY
 COMMENT OS Homo sapiens (human)

PN JP 2000279181-A/193
 PD 10-OCT-2000
 PF 01-APR-1999 JP 1999095481
 PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
 C12N15/09,C07K14/475,C07K16/18,C12N15/00
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 FH Key Location/Qualifiers
 FT source 1..10
 /organism='Homo sapiens (human)'.
 FEATURES source
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 Location/Qualifiers
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 /mol_type='genomic DNA'
 /db_xref='taxon:9606'
 Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred.No.1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAAACA 740
 Db 10 AGGAGAAACA 1
 RESULT 213
 AR303294
 LOCUS AR303294
 DEFINITION Sequence 19 from patent US 6544736.
 ACCESSION AR303294
 VERSION AR303294.1 GI:31692070
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 19 08-APR-2003;
 FEATURES source
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 Location/Qualifiers
 /organism='unknown'
 /mol_type='genomic DNA'
 Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred.No.1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 730 CAGGAGAAAC 739
 Db 1 CTGAGAGAAAC 10
 RESULT 214
 AR303316/c
 LOCUS AR303316
 DEFINITION Sequence 41 from patent US 6544736.
 ACCESSION AR303316
 VERSION AR303316.1 GI:31692092
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 41 08-APR-2003;
 FEATURES source
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 Location/Qualifiers
 /organism='unknown'
 /mol_type='genomic DNA'

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGAGAAAC 739
 Db 10 CTGAGAAAC 1

RESULT 215
 AR303402/c 10 bp DNA PAT 12-JUN-2003
 LOCUS Sequence 127 from patent US 6544736.
 DEFINITION AR303402
 ACCESSION AR303402.1 GI:31692178
 VERSION AR303402.1
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
 TITLE Method for synthesizing cDNA from mRNA sample
 JOURNAL Patent: US 6544736-A 127 08-APR-2003;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
 Db 10 GAGAACACAGA 1

RESULT 216
 AR336872/c 10 bp DNA PAT 17-AUG-2003
 LOCUS Sequence 47 from patent US 6566130.
 DEFINITION AR336872
 ACCESSION AR336872
 VERSION AR336872.1 GI:33722722
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
 TITLE Androgen-regulated gene expressed in prostate tissue
 JOURNAL Patent: US 6566130-A 47 20-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
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Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
 Db 10 AGGATAACA 1

RESULT 217
 AX152919 10 bp DNA PAT 22-JUN-2001
 LOCUS Sequence 834 from Patent WO0138577.
 DEFINITION AX152919
 ACCESSION AX152919
 VERSION AX152919.1 GI:14534570

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 834 31-MAY-2001;
 The Johns Hopkins University (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
 Db 1 CCAGGAGGAA 10

RESULT 218
 AX153378/c 10 bp DNA PAT 22-JUN-2001
 LOCUS Sequence 1293 from Patent WO0138577.
 DEFINITION AX153378
 ACCESSION AX153378
 VERSION AX153378.1 GI:14535029
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1293 31-MAY-2001;
 The Johns Hopkins University (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
 Db 10 AGGATAACA 1

RESULT 219
 AX153448/c 10 bp DNA PAT 22-JUN-2001
 LOCUS Sequence 1363 from Patent WO0138577.
 DEFINITION AX153448
 ACCESSION AX153448
 VERSION AX153448.1 GI:14535099
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1363 31-MAY-2001;
 The Johns Hopkins University (US)
 FEATURES Location/Qualifiers

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source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAACAGCA 742
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Db 10 GATAACAGCA 1

RESULT 220
LOCUS AX302584 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 102 from Patent WO0175177.
ACCESSION AX302584
VERSION AX302584.1 GI:17383111
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Morin, P. J., Sherman-Baust, C. A., Pizer, E. S. and Hough, C. D.
COMMENT Tumor markers in ovarian cancer
PATENT: WO 01/5177-A 102 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 744
    |||||
Db 1 GAAACTGAAC 10

RESULT 221
LOCUS BD083216 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083216
VERSION BD083216.1 GI:22628826
KEYWORDS JP 2001327293-A/137.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
COMMENT Human matured/activated dendritic cell expression genes
PATENT: JP 2001327293-A 137 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/137
PD 27-NOV-2001
PF KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
PI NAGAI
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/09, C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FEATURES
source
1..10
/organism="Homo sapiens"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
    |||||
Db 1 TGCCAGGACA 10

RESULT 223
LOCUS BD166675 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166675
VERSION BD166675.1 GI:27872487
KEYWORDS JP 2002209591-A/220.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 220 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/220
PD 30-JUL-2002

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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAAC 739
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Db 1 CAGGTGAAC 10

RESULT 222
LOCUS BD166609 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166609
VERSION BD166609.1 GI:27872421
KEYWORDS JP 2002209591-A/154.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
JOURNAL Human liver disease-expressing genes
COMMENT Patent: JP 2002209591-A 154 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/154
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGA 736
    |||||
Db 1 TGCCAGGACA 10

RESULT 223
LOCUS BD166675 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166675
VERSION BD166675.1 GI:27872487
KEYWORDS JP 2002209591-A/220.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
JOURNAL Human liver disease-expressing genes
COMMENT Patent: JP 2002209591-A 220 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/220
PD 30-JUL-2002

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PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
    /organism='Homo sapiens (human)'.
    Location/Qualifiers
FEATURES
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        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
    Query Match 38.2%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.7e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 744
    |||||
    1 GAAACTGAAC 10

RESULT 224
BD166874
LOCUS BD166874 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166874
VERSION BD166874.1 GI:37872686
KEYWORDS JP 2002209591-A/419.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 419 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/419
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
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    Location/Qualifiers
FEATURES
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    1..10
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        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
    Query Match 38.2%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.7e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 744
    |||||
    1 GAAACTGAAC 10

RESULT 225
AX470470/c
LOCUS AX470470 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 47 from Patent WO02053773.
ACCESSION AX470470

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VERSION AX470470.1 GI:22205595
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 47 11-JUL-2002;
    HENKEL KGAA (DE)
FEATURES
    source
    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
    Query Match 38.2%; Score 8.4; DB 1; Length 11;
    Best Local Similarity 90.0%; Pred. No. 1.8e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGA 742
    |||||
    10 GATAAACAGA 1

RESULT 226
AX470955/c
LOCUS AX470955 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 532 from Patent WO02053773.
ACCESSION AX470955
VERSION AX470955.1 GI:22206080
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 532 11-JUL-2002;
    HENKEL KGAA (DE)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
    Query Match 38.2%; Score 8.4; DB 1; Length 11;
    Best Local Similarity 90.0%; Pred. No. 1.8e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAAC 745
    |||||
    10 AATCAGAAC 1

RESULT 227
AX470960/c
LOCUS AX470960 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 537 from Patent WO02053773.
ACCESSION AX470960
VERSION AX470960.1 GI:22206085
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 537 11-JUL-2002;
    HENKEL KGAA (DE)

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FEATURES             Location/Qualifiers
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACCG 748
Db 1 CGAACACCG 10

RESULT 228
AX471036/c
LOCUS AX471036 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 613 from Patent WO02053773.
ACCESSION AX471036
VERSION AX471036.1 GI:22206161
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 613 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
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    1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACAGAA 743
Db 10 AGAACAGAA 1

RESULT 229
AX471164
LOCUS AX471164 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 741 from Patent WO02053773.
ACCESSION AX471164
VERSION AX471164.1 GI:22206289
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 741 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
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    1..11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAA 738
Db 10 CCAGGAGAA 1

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Db 1 CCAGGAGAA 10

RESULT 230
AX623587/c
LOCUS AX623587 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 628 from Patent WO02053774.
ACCESSION AX623587
VERSION AX623587.1 GI:28451528
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 628 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAA 745
Db 10 AATCAGAA 1

RESULT 231
AX623632
LOCUS AX623632 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 673 from Patent WO02053774.
ACCESSION AX623632
VERSION AX623632.1 GI:28451573
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 673 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 38.2%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAC 746
Db 2 AACAGAACAC 11

RESULT 232
AX624664/c
LOCUS AX624664 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1705 from Patent WO02053774.
ACCESSION AX624664
VERSION AX624664.1 GI:28452605
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1705 11-JUL-2002; (DE)
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      734 AGAACAGAA 743
Db      10 AGAAAAAGAA 1

RESULT 233
LOCUS      AX624971      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2012 from Patent WO02053774.
ACCESSION  AX624971
VERSION     AX624971.1 GI:28452912
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2012 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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              1..11
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Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      736 AACACAGAAC 745
Db      2 AACAAAAACA 11

RESULT 234
AX626122
LOCUS      AX626122      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3163 from Patent WO02053774.
ACCESSION  AX626122
VERSION     AX626122.1 GI:28454160
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3163 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      739 CAGAACACG 748
Db      1 CGGAACACG 10

RESULT 235
AX627227
LOCUS      AX627227      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4268 from Patent WO02053774.
ACCESSION  AX627227
VERSION     AX627227.1 GI:28455265
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4268 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      729 CCAGGAGAA 738
Db      2 CCAGGGGAAA 11

RESULT 236
AX627341
LOCUS      AX627341      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4382 from Patent WO02053774.
ACCESSION  AX627341
VERSION     AX627341.1 GI:28455379
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4382 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      728 GCACGAGAA 737
Db      1 GTCAGGAGAA 10

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RESULT 237
AX627766/c
LOCUS AX627766 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4807 from Patent WO02053774.
TITLE
ACCESSION AX627766
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 4807 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 729 CCAGGAGAAA 738
Db 11 CCAGGAGAAA 2
RESULT 238
AX628298
LOCUS AX628298 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5339 from Patent WO02053774.
TITLE
ACCESSION AX628298
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 5339 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAACAG 741
Db 1 GGAGAACAG 10
RESULT 239
AX628930/c
LOCUS AX628930 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5971 from Patent WO02053774.
TITLE
ACCESSION AX628930
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 5971 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGA 742
Db 10 GATAAACAGA 1
RESULT 240
AX629191/c
LOCUS AX629191 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6232 from Patent WO02053774.
TITLE
ACCESSION AX629191
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 6232 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 743
Db 11 AAAAACAGAA 2
RESULT 241
AX630040/c
LOCUS AX630040 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7081 from Patent WO02053774.
TITLE
ACCESSION AX630040
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conrad,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 7081 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

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/ db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
Db 11 CCAGCAGAAA 2

RESULT 242
AX630299
LOCUS AX630299 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7340 from Patent WO02053774.
ACCESSION AX630299
VERSION AX630299.1 GI:28458337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7340 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAA 738
Db 1 CCAGGAGAAA 10

RESULT 243
AX631008/c
LOCUS AX631008 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8049 from Patent WO02053774.
ACCESSION AX631008
VERSION AX631008.1 GI:28459050
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8049 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACACAGAAA 745
Db 10 AATCAGAAA 1

RESULT 244
AX631053
LOCUS AX631053 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8094 from Patent WO02053774.
ACCESSION AX631053
VERSION AX631053.1 GI:28459095
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8094 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
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Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGACAC 746
Db 2 AACAGACGC 11

RESULT 245
AX632085/c
LOCUS AX632085 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9127 from Patent WO02053774.
ACCESSION AX632085
VERSION AX632085.1 GI:28467700
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9127 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
Db 10 AGAAACAGAA 1

RESULT 246
AX632392
LOCUS AX632392 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9434 from Patent WO02053774.
ACCESSION AX632392
VERSION AX632392.1 GI:28468007
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9434 11-JUN-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
SOURCE Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAGACA 745
Db 2 AACAGAGACA 11

RESULT 247
LOCUS ARI23885/c 12 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6171821.
ACCESSION ARI23885
VERSION ARI23885.1 GI:14109246
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1
AUTHORS Korneluk,R.G., Holcik,M. and Liston,P.
TITLE XIAP IRES and uses thereof
JOURNAL Patent: US 6171821-A 18 09-JAN-2001;
FEATURES Location/Qualifiers
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAGACA 745
Db 10 AACAGAGACA 1

RESULT 248
AX328584
LOCUS AX328584 12 bp DNA linear PAT 08-JAN-2002
DEFINITION Sequence 81 from Patent EP1164203.
ACCESSION AX328584
VERSION AX328584.1 GI:18101783
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 81 19-DEC-2001;
FEATURES Location/Qualifiers
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Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 249
AX328589
LOCUS AX328589 12 bp DNA linear PAT 08-JAN-2002
DEFINITION Sequence 86 from Patent EP1164203.
ACCESSION AX328589
VERSION AX328589.1 GI:18101788
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 86 19-DEC-2001;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
Db 2 GCCAGGAGAA 11

RESULT 250
BD132149
LOCUS BD132149 12 bp DNA linear PAT 18-SEP-2002
DEFINITION Dna diagnosis method based on mass spectrometry.
ACCESSION BD132149
VERSION BD132149.1 GI:23227094
KEYWORDS JP 2002507883-A/81.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koester,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE Dna diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 81 12-MAR-2002;
COMMENT SEQUENOM INC
PN JP 2002507883-A/81
PD 12-MAR-2002
PR 06-NOV-1997 JP 1998521832
PF 06-NOV-1996 US 08/744481, 06-NOV-1996 US 08/746036 PR
06-NOV-1996 US 08/746055, 06-NOV-1996 US 08/744590 PR
23-JAN-1997 US 08/786988, 23-JAN-1997 US 08/787639 PR
19-SEP-1997 US 08/933792, 08-OCT-1997 US 08/947801 PI HUBERT
KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI GUOBIING
XIANG,
PI DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
C12Q1/68,C07H21/00,C07F9/24
CC Strandedness: Single;
CC Topology: Unknown;
FH Key Location/Qualifiers
1. .12
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source

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Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
|||||
Db 2 GCCAGGAGAA 11

RESULT 251
BD132154
LOCUS
DEFINITION DNA diagnosis method based on mass spectrometry.
ACCESSION BD132154
VERSION BD132154.1 GI:23227059
KEYWORDS JP 2002507883-A/86.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE DNA diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 86 12-MAR-2002;
SEQUENCE INC
COMMENT PN JP 2002507883-A/86
PD 12-MAR-2002
PR 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR
08-NOV-1996 US 08/746055,06-NOV-1996 US 08/744590 PR
23-JAN-1997 US 08/786988,23-JAN-1997 US 08/787639 PR
19-SEP-1997 US 08/933792,08-OCT-1997 US 08/947801 PI
KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI GUORING
XIANG.
PI DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
C12Q1/68,C07H21/00,C07F9/24
CC Strandedness: Single;
CC Topology: Unknown;
FH Key Location/Qualifiers.

FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737
|||||
Db 2 GCCAGGAGAA 11

RESULT 252
S73118S1
LOCUS
DEFINITION dystrophin {intragenic deletion} [human, Genomic Mutant, 12 nt,
segment 1 of 2].
ACCESSION S73118
VERSION S73118.1 GI:241100
SEGMENT
SOURCE i of 2
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12)
AUTHORS Love,D.R., Flint,T.J., Genet,S.A., Middleton-Price,H.R. and
Davies,K.E.
TITLE Becker muscular dystrophy patient with a large intragenic
dystrophin deletion: implications for functional minigenes and gene
therapy

J. Med. Genet. 28 (12), 860-864 (1991)
92099269
MEDLINE 1757963
PUBMED
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This sequence comes from 2.
Location/Qualifiers
1..12
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAC 746
|||||
Db 2 AACAGATCAC 11

RESULT 253
BD239119
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239119
VERSION BD239119.1 GI:33048889
KEYWORDS JP 2002534056-A/537.
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.I. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 537 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/537
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/00,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19
PC C12N1/21,C12N5/10,C01N33/15,C01N33/50,C01N33/53,C01N33/566, PC
GOIN37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 36.4%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	741 GAACACCG 748 		
Db	1 GAACACCG 8		
RESULT 254			
LOCUS	AR300461/c		
DEFINITION	Sequence 15 from patent US 6537784.	10 bp	DNA
ACCESSION	AR300461		
VERSION	AR300461.1 GI:31687903		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 10)		
AUTHORS	Tatake,R.J., Marlin,S.D. and Barton,R.W.		
TITLE	Self-regulated apoptosis of inflammatory cells by gene therapy		
JOURNAL	Patent: US 6537784-A 15 25-MAR-2003;		
FEATURES	Location/Qualifiers		
source	1..10		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match 36.4%; Score 8; DB 1; Length 10;			
Best Local Similarity 100.0%; Pred. No. 2e+02;			
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	732 GGAGAAC 739 		
Db	10 GGAGAAC 3		
RESULT 255			
LOCUS	AX152111		
DEFINITION	Sequence 26 from Patent WO0138577.	10 bp	DNA
ACCESSION	AX152111		
VERSION	AX152111.1 GI:14533762		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.		
TITLE	Human transcriptomes		
JOURNAL	Patent: WO 0138577-A 26 31-MAY-2001;		
FEATURES	The Johns Hopkins University (US)		
source	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match 36.4%; Score 8; DB 1; Length 10;			
Best Local Similarity 100.0%; Pred. No. 2e+02;			
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	740 AGAACACC 747 		
Db	1 AGAACACC 8		
RESULT 256			
LOCUS	AX152162		
DEFINITION	Sequence 77 from Patent WO0138577.	10 bp	DNA
ACCESSION	AX152162		
VERSION	AX152162.1 GI:14533813		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.		
TITLE	Human transcriptomes		
JOURNAL	Patent: WO 0138577-A 26 31-MAY-2001;		
FEATURES	The Johns Hopkins University (US)		
source	Location/Qualifiers		
	1..10		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match 36.4%; Score 8; DB 1; Length 10;			
Best Local Similarity 100.0%; Pred. No. 2e+02;			
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	740 AGAACACC 747 		
Db	1 AGAACACC 8		
RESULT 257			
LOCUS	AX152164		
DEFINITION	Sequence 79 from Patent WO0138577.	10 bp	DNA
ACCESSION	AX152164		
VERSION	AX152164.1 GI:14533815		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.		
TITLE	Human transcriptomes		
JOURNAL	Patent: WO 0138577-A 79 31-MAY-2001;		
FEATURES	The Johns Hopkins University (US)		
source	Location/Qualifiers		
	1..10		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match 36.4%; Score 8; DB 1; Length 10;			
Best Local Similarity 100.0%; Pred. No. 2e+02;			
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	736 AAACAGAA 743 		
Db	3 AAACAGAA 10		
RESULT 258			
LOCUS	AX152170		
DEFINITION	Sequence 85 from Patent WO0138577.	10 bp	DNA
ACCESSION	AX152170		
VERSION	AX152170.1 GI:14533821		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.		
TITLE	Human transcriptomes		
JOURNAL	Patent: WO 0138577-A 85 31-MAY-2001;		
FEATURES	The Johns Hopkins University (US)		
	Location/Qualifiers		

Qy 728 GCCAGGAG 735


```
AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: EP 1225233-A 27 24-JUL-2002;
             Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="TAG sequence Hs23579"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 268
AX623051
LOCUS      AX623051
DEFINITION Sequence 92 from Patent WO02053774.
ACCESSION  AX623051
VERSION     AX623051.1 GI:28450992
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 92 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 269
AX623051
LOCUS      AX623051
DEFINITION Sequence 92 from Patent WO02053774.
ACCESSION  AX623051
VERSION     AX623051.1 GI:28450992
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 92 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: WO 02059558-A 27 01-AUG-2002;
             Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="TAG sequence Hs23579"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 268
AX623051
LOCUS      AX623051
DEFINITION Sequence 27 from Patent WO02059558.
ACCESSION  AX623051
VERSION     AX623051.1 GI:23392166
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE    1
AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: WO 02059558-A 27 01-AUG-2002;
             Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="TAG sequence Hs23579"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 269
AX623051
LOCUS      AX623051
DEFINITION Sequence 92 from Patent WO02053774.
ACCESSION  AX623051
VERSION     AX623051.1 GI:28450992
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 92 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

AUTHORS      van der Kuyl, A.C. and Cornelissen, M.
TITLE        Means and methods for treatment evaluation
JOURNAL      Patent: EP 1225233-A 27 24-JUL-2002;
             Amsterdam Support Diagnostics B.V. (NL)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="TAG sequence Hs23579"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 CAGGAGAA 737
Db      4 CAGGAGAA 11

RESULT 270
AX623196/c
LOCUS      AX623196/c
DEFINITION Sequence 237 from Patent WO02053774.
ACCESSION  AX623196
VERSION     AX623196.1 GI:28451137
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 237 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
Db      11 GCCAGGAG 4

RESULT 271
AX623555/c
LOCUS      AX623555/c
DEFINITION Sequence 596 from Patent WO02053774.
ACCESSION  AX623555
VERSION     AX623555.1 GI:28451496
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn, D., Conradt, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 596 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
            source
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      729 CCAGGAGA 736
Db      8 CCAGGAGA 1

RESULT 272
AX624933
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LOCUS       AX624933               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 1974 from Patent WO02053774.
ACCESSION    AX624933
VERSION      AX624933.1  GI:28452874
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 1974 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      736 AAACAGAA 743
      11
      |||||
Db      3 AAACAGAA 10

RESULT 273
AX624958/c
LOCUS       AX624958               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 1999 from Patent WO02053774.
ACCESSION    AX624958
VERSION      AX624958.1  GI:28452899
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 1999 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      736 AAACAGAA 743
      11
      |||||
Db      11 AAACAGAA 4

RESULT 274
AX624999/c
LOCUS       AX624999               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2040 from Patent WO02053774.
ACCESSION    AX624999
VERSION      AX624999.1  GI:28452940
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.

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TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2040 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      8
      |||||
Db      8 GCCAGGAG 1

RESULT 275
AX625252
LOCUS       AX625252               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2293 from Patent WO02053774.
ACCESSION    AX625252
VERSION      AX625252.1  GI:28453193
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2293 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      1
      |||||
Db      1 GCCAGGAG 8

RESULT 276
AX625448
LOCUS       AX625448               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2489 from Patent WO02053774.
ACCESSION    AX625448
VERSION      AX625448.1  GI:28453389
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2489 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      1
      |||||
Db      1 GCCAGGAG 8

RESULT 277
AX625448
LOCUS       AX625448               11 bp    DNA             linear      PAT 21-FEB-2003
DEFINITION   Sequence 2489 from Patent WO02053774.
ACCESSION    AX625448
VERSION      AX625448.1  GI:28453389
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2489 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             1..11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      728 GCCAGGAG 735
      1
      |||||
Db      1 GCCAGGAG 8

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Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      741 GACACCG 748
Db      1 GAACACCG 8

RESULT 277
AX625885/c
LOCUS      AX625885      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION      Sequence 2926 from Patent WO02053774.
ACCESSION      AX625885
VERSION      AX625885.1      GI:28453923
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2926 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity      100.0%; Pred. No. 2.1e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      728 GCCAGGAG 735
Db      3 GCCAGGAG 10

RESULT 280
AX626990/c
LOCUS      AX626990      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION      Sequence 4031 from Patent WO02053774.
ACCESSION      AX626990
VERSION      AX626990.1      GI:28455028
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4031 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      36.4%; Score 8; DB 1; Length 11;
Best Local Similarity      100.0%; Pred. No. 2.1e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      732 GGAGAAAC 739
Db      10 GGAGAAAC 3

RESULT 281
AX627679
LOCUS      AX627679      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION      Sequence 4720 from Patent WO02053774.
ACCESSION      AX627679
VERSION      AX627679.1      GI:28455717
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4720 11-JUL-2002;

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FEATURES
  source
    Henkel Kommanditgesellschaft auf Aktien (DE)
    Location/Qualifiers
    1. .11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGAA 737
Db 1 CAGGAGAA 8

RESULT 282
AX627723
LOCUS
  DEFINITION
    Sequence 4764 from Patent WO02053774.
  ACCESSION
    AX627723
  VERSION
    AX627723.1 GI:28455761
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    AUTHORS
      Petersohn,D., Conradt,M. and Hofmann,K.
    TITLE
      Method for determining homeostasis of the skin
    JOURNAL
      Patent: WO 02053774-A 4764 11-JUL-2002;
      Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
    source
      1. .11
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
Db 3 CAGAACAC 10

RESULT 283
AX628113
LOCUS
  DEFINITION
    Sequence 5154 from Patent WO02053774.
  ACCESSION
    AX628113
  VERSION
    AX628113.1 GI:28456151
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    AUTHORS
      Petersohn,D., Conradt,M. and Hofmann,K.
    TITLE
      Method for determining homeostasis of the skin
    JOURNAL
      Patent: WO 02053774-A 5154 11-JUL-2002;
      Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
    source
      1. .11
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 CAGAACAC 740
Db 1 CAGAACAC 8

RESULT 284
AX628247/c
LOCUS
  DEFINITION
    Sequence 5288 from Patent WO02053774.
  ACCESSION
    AX628247
  VERSION
    AX628247.1 GI:28456285
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    AUTHORS
      Petersohn,D., Conradt,M. and Hofmann,K.
    TITLE
      Method for determining homeostasis of the skin
    JOURNAL
      Patent: WO 02053774-A 5288 11-JUL-2002;
      Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
    source
      1. .11
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACAC 746
Db 8 CAGAACAC 1

RESULT 285
AX628626/c
LOCUS
  DEFINITION
    Sequence 5667 from Patent WO02053774.
  ACCESSION
    AX628626
  VERSION
    AX628626.1 GI:28456664
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    AUTHORS
      Petersohn,D., Conradt,M. and Hofmann,K.
    TITLE
      Method for determining homeostasis of the skin
    JOURNAL
      Patent: WO 02053774-A 5667 11-JUL-2002;
      Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
    source
      1. .11
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AAACAGAA 743
Db 9 AAACAGAA 2

RESULT 286
AX628755/c
LOCUS
  DEFINITION
    Sequence 5796 from Patent WO02053774.
  ACCESSION
    AX628755
  VERSION
    AX628755.1 GI:28456793

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KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5796 11-JUL-2002; (DE) Henkel Kommanditgesellschaft auf Aktien (DE)
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	36.4%; Score 8; DB 1; Length 11;
Best Local Similarity	100.0%; Pred.No. 2.le+02;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	732 GGAGAAAC 739
Dd	11 GGAGAAAC 4
RESULT 287	
AX629350/c	
LOCUS	AX629350 11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 6391 from Patent WO02053774.
ACCESSION	AX629350
VERSION	AX629350.1 GI:28457388
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 6391 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers 1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	36.4%; Score 8; DB 1; Length 11;
Best Local Similarity	100.0%; Pred.No. 2.le+02;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	728 GCCAGGAG 735
Dd	10 GCCAGGAG 3
RESULT 288	
AX629616/c	
LOCUS	AX629616 11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 6657 from Patent WO02053774.
ACCESSION	AX629616
VERSION	AX629616.1 GI:28457654
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 02053774-A 6657 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers


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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAG 735
    |||||
Db 1 GCCAGGAG 8

RESULT 296
AR029821/c
LOCUS
DEFINITION Sequence 10 from patent US 5861244.
ACCESSION AR029821
VERSION AR029821.1 GI:5943035
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 10 19-JAN-1999;
FEATURES
    source
        Location/Qualifiers
            1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 738
    |||||
Db 8 AGGAGAAAC 1

RESULT 297
I43337
LOCUS
DEFINITION Sequence 5 from patent US 5631148.
ACCESSION I43337
VERSION I43337.1 GI:2468581
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Urdea, M.S.
TITLE Ribozymes with product ejection by strand displacement
JOURNAL Patent: US 5631148-A 5 20-MAY-1997;
FEATURES
    source
        Location/Qualifiers
            1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 36.4%; Score 8; DB 1; Length 12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
    |||||
Db 4 ANGAGAAAC 12

RESULT 298
AR029900
LOCUS
DEFINITION Sequence 89 from patent US 5861244.
ACCESSION AR029900
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VERSION AR029900.1 GI:5943114
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 89 19-JAN-1999;
FEATURES
    source
        Location/Qualifiers
            1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
    |||||
Db 1 AGGAGAGAAAG 11

RESULT 299
AR070933/c
LOCUS
DEFINITION Sequence 14 from patent US 5908972.
ACCESSION AR070933
VERSION AR070933.1 GI:7221821
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Houtz, R.L.
TITLE Isolated spinach ribulose-1,5-bisphosphate carboxylase/oxygenase
JOURNAL Patent: US 5908972-A 14 01-JUN-1999;
FEATURES
    source
        Location/Qualifiers
            1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
    |||||
Db 11 GAGAAAAAAA 1

RESULT 300
AR157632/c
LOCUS
DEFINITION Sequence 14 from patent US 6245541.
ACCESSION AR157632
VERSION AR157632.1 GI:16218594
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Houtz, R.L.
TITLE Isolated spinach ribulose-1,5-bisphosphate carboxylase/oxygenase
JOURNAL Patent: US 6245541-A 14 12-JUN-2001;
FEATURES
    source
        Location/Qualifiers
            1..11
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<p>AX393119.1 GI:19701169</p> <p>VERSION KEYWORDS SOURCE ORGANISM</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>REFERENCE AUTHORS TITLE JOURNAL</p> <p>St Croix, B., Kinzler, K.W. and Vogelstein, B. Endothelial cell expression patterns Patent: WO 0210217-A 49 07-FEB-2002; The Johns Hopkins University (US)</p> <p>FEATURES source</p> <p>1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p> <p>QY 727 TGCCAGGAGAA 737 Db 1 TGCCAGGTGCA 11</p> <p>RESULT 304 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>AX470720 Sequence 297 from Patent WO02053773. AX470720 AX470720.1 GI:22205845 Homo sapiens (human) Homo sapiens</p> <p>REFERENCE AUTHORS TITLE JOURNAL</p> <p>Hofmann, K., Conradt, M. and Petersohn, D. Method for determining skin stress or skin ageing in vitro Patent: WO 02053773-A 297 11-JUL-2002; HENKEL KGAA (DE)</p> <p>FEATURES source</p> <p>1..11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p> <p>Query Match Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p> <p>QY 727 TGCCAGGAGAA 737 Db 1 TGCCAGAGAT 1</p> <p>RESULT 305 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>AX471467 Sequence 1044 from Patent WO02053773. AX471467 AX471467.1 GI:22206592 Homo sapiens (human) Homo sapiens</p> <p>REFERENCE AUTHORS TITLE JOURNAL</p> <p>Hofmann, K., Conradt, M. and Petersohn, D. Method for determining skin stress or skin ageing in vitro Patent: WO 02053773-A 1044 11-JUL-2002; HENKEL KGAA (DE)</p>	<p>/organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p> <p>QY 733 GAGAAACAGAA 743 Db 11 GAGAAACAAAA 1</p> <p>RESULT 301 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>AR164474 Sequence 8 from patent US 6274134. AR164474 AR164474.1 GI:16237515 Unknown. Unclassified.</p> <p>REFERENCE AUTHORS TITLE JOURNAL</p> <p>Beckner, M.E., Krutzsch, H.C. and Liotta, L.A. Human cell adhesion protein AAMP-1 and uses thereof Patent: US 6274134-A 8 14-AUG-2001; Location/Qualifiers</p> <p>FEATURES source</p> <p>1..11 /organism="unknown" /mol_type="unassigned DNA"</p> <p>Query Match Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p> <p>QY 731 AGGAGAACAG 741 Db 1 AGGAGAACAG 11</p> <p>RESULT 302 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>AR301492/c Sequence 73 from patent US 6538173. AR301492 AR301492.1 GI:31689294 Unknown. Unclassified.</p> <p>REFERENCE AUTHORS TITLE JOURNAL</p> <p>Heber-Katz, E. Compositions and methods for wound healing Patent: US 6538173-A 73 25-MAR-2003; Location/Qualifiers</p> <p>FEATURES source</p> <p>1..11 /organism="unknown" /mol_type="genomic DNA"</p> <p>Query Match Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p> <p>QY 732 GGAGAACAGA 742 Db 11 GGAGAACCGA 1</p> <p>RESULT 303 LOCUS DEFINITION ACCESSION</p> <p>AX393119 Sequence 49 from Patent WO0210217. AX393119</p>	<p>PAT 17-OCT-2001</p> <p>PAT 12-JUN-2003</p> <p>PAT 23-MAR-2002</p>
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FEATURES             Location/Qualifiers
  source              1..11
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

Query Match          35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACACAGA 742
Db 11 GGGGATACAGA 1

RESULT 306
AX623210
LOCUS                11 bp DNA linear PAT 21-FEB-2003
DEFINITION           Sequence 251 from Patent WO02053774.
ACCESSION            AX623210
VERSION              AX623210.1 GI:28451151
KEYWORDS
SOURCE               Homo sapiens (human)
ORGANISM             Homo sapiens
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS             Petersohn,D., Conradt,M. and Hofmann,K.
TITLE               Method for determining homeostasis of the skin
JOURNAL             Patent: WO 02053774-A 251 11-JUL-2002;
                    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
  source              1..11
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

Query Match          35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGAACACA 745
Db 1 GAACAGAACAAA 11

RESULT 309
AX623866/C
LOCUS                11 bp DNA linear PAT 21-FEB-2003
DEFINITION           Sequence 907 from Patent WO02053774.
ACCESSION            AX623866
VERSION              AX623866.1 GI:28451807
KEYWORDS
SOURCE               Homo sapiens (human)
ORGANISM             Homo sapiens
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS             Petersohn,D., Conradt,M. and Hofmann,K.
TITLE               Method for determining homeostasis of the skin
JOURNAL             Patent: WO 02053774-A 907 11-JUL-2002;
                    Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
  source              1..11
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

Query Match          35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACACAGAA 743
Db 11 GAGAACACAAA 11

RESULT 310
AX624241/C
LOCUS                11 bp DNA linear PAT 21-FEB-2003
DEFINITION           Sequence 1282 from Patent WO02053774.
ACCESSION            AX624241
VERSION              AX624241.1 GI:28452182
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1282 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGACAGAAC 744
DB      11 AAAAGAGAGAAC 1

RESULT 311
LOCUS      AX624366              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 1407 from Patent WO02053774.
ACCESSION  AX624366
VERSION     AX624366.1 GI:28452307
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1407 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      733 GAGAGACAGAA 743
DB      1 GAGAGACAGAA 11

RESULT 312
LOCUS      AX625243              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 2284 from Patent WO02053774.
ACCESSION  AX625243
VERSION     AX625243.1 GI:28453184
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2284 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11

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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGACAGAAC 744
DB      1 AGCACCAGAAC 11

RESULT 313
LOCUS      AX625333              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 2374 from Patent WO02053774.
ACCESSION  AX625333
VERSION     AX625333.1 GI:28453274
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2374 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAACAGAA 742
DB      11 GGTGTACAGAA 1

RESULT 314
LOCUS      AX626135              11 bp      DNA              linear      PAT 21-FEB-2003
DEFINITION Sequence 3176 from Patent WO02053774.
ACCESSION  AX626135
VERSION     AX626135.1 GI:28454173
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3176 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGACAGAAC 744
DB      11 AGAACCAGAGC 1

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RESULT 315
AX626314
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3355 from Patent WO02053774.
ACCESSION AX626314
VERSION    AX626314.1 GI:28454352
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3355 11-JUL-2002; (DE)
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      738 ACAGAACACCG 748
      |||||
Db      1 ACAGAGCACAG 11

RESULT 316
AX626528
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3569 from Patent WO02053774.
ACCESSION AX626528
VERSION    AX626528.1 GI:28454566
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3569 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      736 AAACAGAACAC 746
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Db      1 AAACATACAC 11

RESULT 317
AX626853/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3894 from Patent WO02053774.
ACCESSION AX626853
VERSION    AX626853.1 GI:28454891
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3894 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      734 AGAACAGAAC 744
      |||||
Db      1 AGAATCAGCAC 11

RESULT 318
AX627269
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4310 from Patent WO02053774.
ACCESSION AX627269
VERSION    AX627269.1 GI:28455307
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 4310 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      735 GAAACAGAAC 745
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Db      1 GAACGAGAAAA 11

RESULT 319
AX627481
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4522 from Patent WO02053774.
ACCESSION AX627481
VERSION    AX627481.1 GI:28455519
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 4522 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   source
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/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 1 GCACGAGAAA 11

RESULT 320
AX628291/c
LOCUS AX628291 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5332 from Patent WO02053774.
ACCESSION AX628291
VERSION AX628291.1 GI:28456329
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5332 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCACGAGAAA 737
DB 11 TGCAAGAGTA 1

RESULT 321
AX628354/c
LOCUS AX628354 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5395 from Patent WO02053774.
ACCESSION AX628354
VERSION AX628354.1 GI:28456392
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5395 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACAA 745
DB 11 GAAACCAACAA 1

RESULT 324
AX628943/c
LOCUS AX628943 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5984 from Patent WO02053774.
ACCESSION AX628943
VERSION AX628943.1 GI:28456981
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5984 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAAC 744
Db 11 ACAAGAGAAC 1

RESULT 325
LOCUS AX629425 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6466 from Patent WO02053774.
ACCESSION AX629425
VERSION AX629425.1 GI:28457463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6466 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 1 AAACAAATCAC 11

RESULT 326
LOCUS AX629695/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6736 from Patent WO02053774.
ACCESSION AX629695
VERSION AX629695.1 GI:28457733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6736 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACAC 747
Db 11 AACAAACAGC 1

RESULT 327
LOCUS AX629821/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6862 from Patent WO02053774.
ACCESSION AX629821
VERSION AX629821.1 GI:28457859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6862 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
1. .11
Location/Qualifiers
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
Db 11 AGGAGGACAG 1

RESULT 328
LOCUS AX629849 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6890 from Patent WO02053774.
ACCESSION AX629849
VERSION AX629849.1 GI:28457887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6890 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
1. .11
Location/Qualifiers
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 738
Db 1 GCCAGGTGAA 11

RESULT 329
LOCUS AX630158/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6900 from Patent WO02053774.
ACCESSION AX630158
VERSION AX630158.1 GI:28457900
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
```



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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 745
   |||||
Db 1 GAAACAGAAC 11

RESULT 334
AX631287/c
LOCUS AX631287 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8329 from Patent WO02053774.
ACCESSION AX631287
VERSION AX631287.1 GI:28459333
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8329 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACAGAA 743
   |||||
Db 11 GAGAACAAAA 1

RESULT 335
AX631662/c
LOCUS AX631662 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8704 from Patent WO02053774.
ACCESSION AX631662
VERSION AX631662.1 GI:28459769
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8704 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGAAC 744
   |||||
Db 11 AGAACAGAAC 1

RESULT 336
AX631787
LOCUS AX631787 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8829 from Patent WO02053774.

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ACCESSION AX631787
VERSION AX631787.1 GI:28459894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8829 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAACAGAA 743
   |||||
Db 1 GAGAACAGAA 11

RESULT 337
AX632664
LOCUS AX632664 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9706 from Patent WO02053774.
ACCESSION AX632664
VERSION AX632664.1 GI:28468279
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9706 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGAAC 744
   |||||
Db 1 AGAACAGAAC 11

RESULT 338
AX632754/c
LOCUS AX632754 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9796 from Patent WO02053774.
ACCESSION AX632754
VERSION AX632754.1 GI:28468369
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9796 11-JUL-2002;

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Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
 Location/Qualifiers
 1. .11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 35.5%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 2.3e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 742

Db 11 GGTGTAACAG 1

RESULT 339

AX772229/c

LOCUS AX772229 11 bp DNA linear PAT 02-JUL-2003

DEFINITION Sequence 19 from Patent WO03042407.

ACCESSION AX772229

VERSION AX772229.1 GI:32438802

KEYWORDS Drosophila melanogaster (fruit fly)

SOURCE Drosophila melanogaster

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS Dickson,B., Berger,J., Suzuki,T. and Knoblich,J.

TITLE Method for identifying therapeutic targets by use of genetic

screens in drosophila melanogaster

PATENT. WO 03042407-A 19 22-MAY-2003;

JOURNAL BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)

FEATURES

source
 Location/Qualifiers
 1. .11
 /organism="Drosophila melanogaster"
 /mol_type="unassigned DNA"
 /db_xref="taxon:7227"

Query Match

Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746

Db 11 AAACAAAAAC 1

RESULT 340

BD124242/c

LOCUS BD124242 11 bp DNA linear PAT 18-SEP-2002

DEFINITION Compositions and method for healing wound.

ACCESSION BD124242

VERSION BD124242.1 GI:23219187

KEYWORDS JP 2002503460-A/73.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 11)

Katz,E.H.

Compositions and method for healing wound

PATENT: JP 2002503460-A 73 05-FEB-2002;

THE WISTAR INSTITUTE

OS Mus musculus (mouse)

PN JP 2002503460-A/73

PD 05-FEB-2002

PF 12-FEB-1999 JP 2000331545

PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR

28-SEP-1998 US 60/102051

PI ELLEN HEBER KATZ

PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC

C12N5/00

CC Compositions and method for healing wound

FH Key Location/Qualifiers

FT source 1. .11

FT /organism="Mus musculus (mouse)"

FEATURES Location/Qualifiers

source 1. .11

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

Query Match 35.5%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 2.3e+02;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 742

Db 11 GCAGAAACCGA 1

RESULT 341

BD174612

LOCUS BD174612

DEFINITION Modified promoter.

ACCESSION BD174612

VERSION BD174612.1 GI:29120302

KEYWORDS JP 200272466-A/1.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 11)

AUTHORS Mizubuchi,H., Fushimi,N. and Miyoshi,S.

TITLE Modified promoter

JOURNAL Patent: JP 200272466-A 1 24-SEP-2002;

SHOWA SANGYO CO LTD DIRECTOR GENERAL OF NATIONAL INSTITUTE OF

COMMENT OS Artificial Sequence

PN JP 200272466-A/1

PD 24-SEP-2002

PF 15-MAR-2001 JP 2001074780

PI HIROYUKI MIZUBUCHI, NAOYA FUSHIMI, SHINSUKE MIYOSHI PC

C12N15/09,C12N1/21,C12P21/02//(C12N1/21,C12R1/07),(C12N1/21, PC

C12R1/01)

PC (C12N1/21,C12R1/19),C12N15/00

CC Modified promoter

FH Key Location/Qualifiers

FT source 1. .11

FT /organism="Artificial Sequence".

FEATURES Location/Qualifiers

source 1. .11

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match

Best Local Similarity 35.5%; Score 7.8; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741

Db 1 AGGAGTACCAG 11

RESULT 342

BD174617

LOCUS BD174617

DEFINITION Modified promoter.

ACCESSION BD174617

VERSION BD174617.1 GI:29120307

KEYWORDS JP 200272466-A/6.

SOURCE synthetic construct

ORGANISM artificial sequences.

linear PAT 18-MAR-2003

11 bp DNA

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REFERENCE 1 (bases 1 to 11)
AUTHORS Mizubuchi,H., Fushimi,N. and Miyoshi,S.
TITLE Modified promoter
JOURNAL Patent: JP 200272466-A 6 24-SEP-2002;
COMMENT SHOWA SANGYO CO LTD
OS Artificial Sequence
PN JP 200272466-A/6
PD 24-SEP-2002
PF 15-MAR-2001 JP 2001074780
PI HIROYUKI MIZUBUCHI,NAOYA FUSHIMI,SHINSUKE MIYOSHI PC
C12N15/09,C12N1/21,C12P21/02/(C12N1/21,C12R1:07), (C12N1/21, PC
C12R1:01),
PC (C12N1/21,C12R1:19),C12N15/00
CC Modified promoter
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
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/organism="Artificial Sequence".
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
|||||
DB 1 AGGAGGAGCAG 11
|||||
RESULT 343
A06060
LOCUS 12 bp DNA linear PAT 25-MAY-1993
DEFINITION Synthetic primer 579-590.
ACCESSION A06060
VERSION A06060.1 GI:411192
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hudson,P.J., Haley,J.D., Niall,H.D. and Shine,J.
TITLE Molecular cloning and characterization of the gene sequence coding
for porcine relaxin
JOURNAL Patent: EP 0086649-A 10 24-AUG-1993;
HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
|||||
DB 2 GAAGCAGAGA 12
|||||
RESULT 344
A06061/c
LOCUS 12 bp DNA linear PAT 25-MAY-1993
DEFINITION Synthetic primer 579-590 (Reverse complement).
ACCESSION A06061
VERSION A06061.1 GI:411193
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
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REFERENCE 1 (bases 1 to 12)
AUTHORS Hudson,P.J., Haley,J.D., Niall,H.D. and Shine,J.
TITLE Molecular cloning and characterization of the gene sequence coding
for porcine relaxin
JOURNAL Patent: EP 0086649-A 11 24-AUG-1993;
HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
|||||
DB 11 GAAGCAGAGA 1
|||||
RESULT 345
A16603
LOCUS 12 bp DNA linear PAT 29-SEP-1994
DEFINITION Nucleotide sequence 11 from patent number AU562012.
ACCESSION A16603
VERSION A16603.1 GI:641064
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS
JOURNAL Patent: AU 562012-B 11 28-MAY-1987;
FEATURES
source
1..12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
|||||
DB 2 GAAGCAGAGA 12
|||||
RESULT 346
A16604/c
LOCUS 12 bp DNA linear PAT 29-SEP-1994
DEFINITION Nucleotide sequence 12 from patent number AU562012.
ACCESSION A16604
VERSION A16604.1 GI:641065
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS
JOURNAL Patent: AU 562012-B 12 28-MAY-1987;
FEATURES
source
1..12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 735 GAAACAGAACCA 745
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Db      11 GAAGCAGAGA 1
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RESULT 347
A47643
LOCUS      A47643
DEFINITION Sequence 3 from Patent EP0692555.
ACCESSION  A47643
VERSION    A47643.1 GI:2301584
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Colore,S. and Pirotzky,E.
TITLE     Oligonucleotides to inhibit the role of isoprenyl protein
          transferases
JOURNAL    Patent: EP 0692535-A 3 17-JAN-1996;
          SOD CONSEILS RECH APPLIC (FR)
COMMENT    Other publication CN 1124142 960612
          Other publication CZ 950168 960515
          Other publication BR 9503015 960504
          Other publication NZ 727398 960426
          Other publication HU 72133 960328
          Other publication JP 8051985 960227
          Other publication FR 2721930 960105
          Other publication FR 2721827 960105
          Other publication FI 953170 951230
          Other publication SE 9502259 951230
          Other publication PL 309384 960108
          Other publication NO 952601 960102
          Other publication AU 2329995 960111
          Other publication CA 2152233 951230
          Other publication GB 2290791 960110.
          Location/Qualifiers
FEATURES   source
            1..12
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      731 AGGAGAACAG 741
Db      2 AGGAGTAGCAG 12
|||||
RESULT 348
A61481/c
LOCUS      A61481
DEFINITION Sequence 50 from Patent WO9710332.
ACCESSION  A61481
VERSION    A61481.1 GI:3715876
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1
AUTHORS   Schmidt,G.
TITLE     CHIMERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION
          OF ANTISENSE BINDING SITES
JOURNAL    Patent: WO 9710332-A 50 20-MAR-1997;
          BRAX GENOMICS LTD (GB)
FEATURES   Location/Qualifiers
            1..12
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
            35.5%; Score 7.8; DB 1; Length 12;

Db      11 GAAGCAGAGA 1
|||||

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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      734 AGAAGCAGAAC 744
Db      12 AGGAGAGAGAC 2
|||||
RESULT 349
AR027861
LOCUS      AR027861
DEFINITION Sequence 3 from patent US 5856461.
ACCESSION  AR027861
VERSION    AR027861.1 GI:5938681
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Colore,S. and Pirotzky,E.
TITLE     Oligonucleotides to inhibit the expression of isoprenyl protein
          transferases
JOURNAL    Patent: US 5856461-A 3 05-JAN-1999;
          Location/Qualifiers
FEATURES   source
            1..12
            /organism="unassigned DNA"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.8%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      731 AGGAGAACAG 741
Db      2 AGGAGTAGCAG 12
|||||
RESULT 350
AR030026
LOCUS      AR030026
DEFINITION Sequence 215 from patent US 5861244.
ACCESSION  AR030026
VERSION    AR030026.1 GI:5943240
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Wang,C.-G. and Hepburn,A.G.
TITLE     Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 215 19-JAN-1999;
          Location/Qualifiers
FEATURES   source
            1..12
            /organism="unassigned DNA"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.8%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      733 GAGAAACAGAA 743
Db      1 GAGGAAAAGAA 11
|||||
RESULT 351
AR030040
LOCUS      AR030040
DEFINITION Sequence 229 from patent US 5861244.
ACCESSION  AR030040
VERSION    AR030040.1 GI:5943254
KEYWORDS   Unknown.
SOURCE     Unknown.

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ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 12)
AUTHORS      Wang C.-G. and Hepburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 229 19-JAN-1999;
FEATURES      Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match   35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
Db 1 GAGATAGAGAA 11

RESULT 352
LOCUS      AR030162
DEFINITION Sequence 351 from patent US 5861244.
ACCESSION  AR030162
VERSION     AR030162.1 GI:5943376
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Wang C.-G. and Hepburn, A.G.
TITLE     Genetic sequence assay using DNA triple strand formation
JOURNAL   Patent: US 5861244-A 351 19-JAN-1999;
FEATURES  Location/Qualifiers
         1..12
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match   35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
Db 2 GAGGAGAGAA 12

RESULT 353
LOCUS      AR058694/c
DEFINITION Sequence 271 from patent US 5837832.
ACCESSION  AR058694
VERSION     AR058694.1 GI:5984271
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Chee, M., Cronin, M.T., Fodor, S.P.A., Huang, X.X., Hubbell, E.A.,
           Lipshutz, R.J., Lloban, P.E., Morris, M.S. and Sheldon, E.L.
TITLE     Arrays of nucleic acid probes on biological chips
JOURNAL   Patent: US 5837832-A 271 17-NOV-1998;
FEATURES  Location/Qualifiers
         1..12
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match   35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 742
Db 1 GTAGAAATAGA 11

RESULT 354
LOCUS      BD242527
DEFINITION A system for cell based screening.
ACCESSION  BD242527
VERSION     BD242527.1 GI:33052297
KEYWORDS   JP 2002528136-A/33.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
           1 (bases 1 to 12)
REFERENCE  1 (bases 1 to 12)
AUTHORS   Guiliano, K.A., Bright, G., Olson, K. and Tencza, S.B.
TITLE     A system for cell based screening
JOURNAL   Patent: JP 2002528136-A 33 03-SEP-2002;
COMMENT    CELLOMICS INC
           OS Artificial Sequence
           PN JP 2002528136-A/33
           PD 03-SEP-2002
           PF 23-OCT-1999 JP 2000579780
           PR 30-OCT-1998 US 60/106308, 26-MAY-1999 US 60/136078 PI
           KENNETH A GUILIANO, GARY BRIGHT, KEITH OLSON, SARAH BURROUGHS PI
           TENCZA
           PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12Q1/
           37, G01N33/15,
           PC G01N33/50, C12N15/00, C12N5/00
           CC Description of Artificial Sequence: Caspase-6 substrate CC
           recognition
           CC sequence
           FH Key
           FT source
           FT source
           Location/Qualifiers
         1..12
         /organism="synthetic construct"
         /mol_type="genomic DNA"
         /db_xref="taxon:32630"

Query Match   35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 742
Db 1 GTAGAAATAGA 11

RESULT 355
LOCUS      BD248202
DEFINITION Short-chain oligonucleotide for inhibiting VEGF expression.
ACCESSION  BD248202
VERSION     BD248202.1 GI:33057972
KEYWORDS   JP 2002524038-A/21.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
           1 (bases 1 to 12)
REFERENCE  1 (bases 1 to 12)
AUTHORS   Uhlmann, E., Peyman, A., Bitonti, A. and Woessner, R.
TITLE     Short-chain oligonucleotide for inhibiting VEGF expression
JOURNAL   Patent: JP 2002524038-A 21 06-AUG-2002;
COMMENT    AVENTIS PHARMA DEUTSCHLAND GMBH
           OS Artificial Sequence
           PN JP 2002524038-A/21
           PD 06-AUG-2002
           PF 29-JUL-1999 JP 2000563768
           PR 07-AUG-1998 EP 98114853 9
           PI EUGEN UHLMANN, ANUSCHIRVAN PEYMAN, ALAN BITONTI, RICHARD WOESSNER
           PC C12N15/09, A61K31/711, A61K31/712, A61K31/715, A61K31/7125 PC
           , A61K48/00, A61P9/00,

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Db 12 GGGAAGCAGA 2
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RESULT 354
LOCUS      BD242527
DEFINITION A system for cell based screening.
ACCESSION  BD242527
VERSION     BD242527.1 GI:33052297
KEYWORDS   JP 2002528136-A/33.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
           1 (bases 1 to 12)
REFERENCE  1 (bases 1 to 12)
AUTHORS   Guiliano, K.A., Bright, G., Olson, K. and Tencza, S.B.
TITLE     A system for cell based screening
JOURNAL   Patent: JP 2002528136-A 33 03-SEP-2002;
COMMENT    CELLOMICS INC
           OS Artificial Sequence
           PN JP 2002528136-A/33
           PD 03-SEP-2002
           PF 23-OCT-1999 JP 2000579780
           PR 30-OCT-1998 US 60/106308, 26-MAY-1999 US 60/136078 PI
           KENNETH A GUILIANO, GARY BRIGHT, KEITH OLSON, SARAH BURROUGHS PI
           TENCZA
           PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12Q1/
           37, G01N33/15,
           PC G01N33/50, C12N15/00, C12N5/00
           CC Description of Artificial Sequence: Caspase-6 substrate CC
           recognition
           CC sequence
           FH Key
           FT source
           FT source
           Location/Qualifiers
         1..12
         /organism="synthetic construct"
         /mol_type="genomic DNA"
         /db_xref="taxon:32630"

Query Match   35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 742
Db 1 GTAGAAATAGA 11

RESULT 355
LOCUS      BD248202
DEFINITION Short-chain oligonucleotide for inhibiting VEGF expression.
ACCESSION  BD248202
VERSION     BD248202.1 GI:33057972
KEYWORDS   JP 2002524038-A/21.
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
           1 (bases 1 to 12)
REFERENCE  1 (bases 1 to 12)
AUTHORS   Uhlmann, E., Peyman, A., Bitonti, A. and Woessner, R.
TITLE     Short-chain oligonucleotide for inhibiting VEGF expression
JOURNAL   Patent: JP 2002524038-A 21 06-AUG-2002;
COMMENT    AVENTIS PHARMA DEUTSCHLAND GMBH
           OS Artificial Sequence
           PN JP 2002524038-A/21
           PD 06-AUG-2002
           PF 29-JUL-1999 JP 2000563768
           PR 07-AUG-1998 EP 98114853 9
           PI EUGEN UHLMANN, ANUSCHIRVAN PEYMAN, ALAN BITONTI, RICHARD WOESSNER
           PC C12N15/09, A61K31/711, A61K31/712, A61K31/715, A61K31/7125 PC
           , A61K48/00, A61P9/00,

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PC A61P13/12,A61P17/16,A61P27/02,A61P29/00,A61P35/00,A61P43/00,
PC C12N15/00
CC Description of Artificial Sequence: Antisense FH Key
FT Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
FT /organism='Artificial Sequence'.
FEATURES
source
1..12
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 1 GACAGCAGAAA 11

RESULT 356
BD263213/c
LOCUS
DEFINITION
ACCESSION BD263213
VERSION
KEYWORDS JP 2002536346-A/26.
SOURCE
ORGANISM
artificial construct
artificial sequences
1 (bases 1 to 12)
REFERENCE
PASTERNAK,G.R. and Bai,J.
AUTHORS
TITLE
JOURNAL
METHOD of treating cancer by restoration of pp32 function
PATENT: JP 2002536346-A 26 29-OCT-2002;
COMMENT
OS Artificial Sequence
PN JP 2002536346-A/26
PD 29-OCT-2002
PF 03-FEB-2000 JP 2000596971
PR 03-FEB-1999 US 60/118667
PI GARY R PASTERNAK,JINING BAI
PC A61K48/00,A61K31/7115,A61K45/00,A61P35/00,C12Q1/42,G01N33/15,
PC G01N33/50//
PC C12N15/09,C12N15/00
CC recognition sequence
FH Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.
FEATURES
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1..12
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAGAAA 745
DB 12 GAAAAAGAGAAA 2

RESULT 357
BD269488/c
LOCUS
DEFINITION
ACCESSION BD269488
VERSION
KEYWORDS JP 2002537844-A/12.
SOURCE
ORGANISM
Stable recombinant influenza virus free from helper virus.
PAT 17-JUL-2003
12 bp RNA linear

```

```

Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
1 (bases 1 to 12)
AUTHORS
Hobom,G., Flick,R., Menke,A. and Azzeah,M.
TITLE
JOURNAL
Stable recombinant influenza virus free from helper virus
PATENT: JP 2002537844-A 12 12-NOV-2002;
COMMENT
OS INFLUENZA C VIRUS
PN JP 2002537844-A/12
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519.6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEAH PC
C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12R1:93),C12N15/00
CC Stable recombinant influenza virus free from helper virus FH
Key Location/Qualifiers
FT source 1..12
FT /organism='Influenza C virus'.
FEATURES
source
1..12
Location/Qualifiers
/organism='Influenza C virus'
/mol_type='genomic RNA'
/db_xref='taxon:11552'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
DB 12 AGCAGAGCAG 2

RESULT 358
BD269490/c
LOCUS
DEFINITION
ACCESSION BD269490
VERSION
KEYWORDS JP 2002537844-A/14.
SOURCE
ORGANISM
synthetic construct
artificial sequences.
1 (bases 1 to 12)
REFERENCE
Hobom,G., Flick,R., Menke,A. and Azzeah,M.
AUTHORS
TITLE
JOURNAL
Stable recombinant influenza virus free from helper virus
PATENT: JP 2002537844-A 14 12-NOV-2002;
COMMENT
OS ARTHEMIS PHARMACEUTICALS GMBH
PN JP 2002537844-A/14
PD 12-NOV-2002
PF 03-MAR-2000 JP 2000603407
PR 06-MAR-1999 EP 99104519.6
PI GERD HOBOM,RAMON FLICK,ANETTE MENKE,MAYSA AZZEAH PC
C12N15/09,A61K39/145,A61K48/00,A61P31/16,C12N7/00,C12P21/02// PC
A61K35/12,
PC (C12N7/00,C12R1:93),C12N15/00
CC Description of Artificial Sequence: Modified influenza A 3'
sequence
CC (PHL1948)
CC Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.
FEATURES
source
1..12
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;

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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741
 |||||
 12 AGGAGAACAG 2

Db

RESULT 359
 E04220/c
 LOCUS 5'-region of satellite RNA. 12 bp RNA linear PAT 29-SEP-1997
 DEFINITION
 ACCESSION E04220
 VERSION E04220.1 GI:5708497
 KEYWORDS JP 1993003789-A/1.
 SOURCE Cucurbit mosaic virus (cucumber mosaic cucumovirus)
 ORGANISM Cucurbit mosaic virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; Cucumovirus.

REFERENCE 1 (bases 1 to 12)
 AUTHORS Kominato,M., Sato,S. and Sayama,H.
 TITLE WEAK TOXIC VIRUS OF CUCUMBER MOSAIC VIRUS USING CLONED SATELLITE RNA

JOURNAL Patent: JP 1993003789-A 1 14-JAN-1993;
 NIPPON DERMONTE KK

COMMENT OS Cucurbit mosaic virus
 PN JP 1993003789-A/1
 PD 14-JAN-1993
 PF 30-SEP-1991 JP 1991252204
 PR 11-OCT-1990 JP 90P 274465
 PI KOMINATO MASAYUKI, SATO SADAICHI, SAYAMA HARUKI PC
 C12N15/33,A01N63/00,C12N1/21,C12N7/04,C12N15/10,C12N1/21, PC
 C12R1:19);
 CC strandedness: Single;
 CC topology: Linear;
 PH Key Location/Qualifiers
 FT misc_RNA 1..12
 FT /note= '5'-region of satellite RNA'.

FEATURES
 source
 1..12
 Location/Qualifiers
 /organism="Cucurbit mosaic virus"
 /mol_type="genomic RNA"
 /db_xref="taxon:12305"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAC 744
 |||||
 11 ACAACAAGAC 1

Db

RESULT 360
 E32720
 LOCUS Small triple strand-forming PNA oligo. 12 bp DNA linear PAT 18-JUN-2001
 DEFINITION
 ACCESSION E32720
 VERSION E32720.1 GI:13026825
 KEYWORDS JP 1999127876-A/1.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1 (bases 1 to 12)
 AUTHORS Naesubi,M.
 TITLE Small triple strand-forming PNA oligo
 JOURNAL Patent: JP 1999127876-A 1 18-MAY-1999;
 BOEHRINGER MANNHEIM GMBH

COMMENT OS Artificial Sequence
 PN JP 1999127876-A/1
 PD 18-MAY-1999
 PF 21-AUG-1998 JP 1998235065
 PR 22-AUG-1997 DE 97 114 512:3

PI NAESUBI MICHAEL
 PC C12N15/09,C07K9/00,C12Q1/68,C12N15/00
 CC
 FH Key Location/Qualifiers
 FT source 1..12
 FT /organism="Artificial Sequence".

FEATURES
 source
 1..12
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGAGAAAC 739
 |||||
 2 CCAGAGATAC 12

Db

RESULT 361
 I04321
 LOCUS Sequence 6 from Patent EP 0147819. 12 bp DNA linear PAT 02-DEC-1994
 DEFINITION
 ACCESSION I04321
 VERSION I04321.1 GI:591773
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Kung H.-F. and Yamazaki, S.
 TITLE Purification of recombinant interleukin-2
 JOURNAL Patent: EP 0147819-A2 6 10-JUL-1985;
 FEATURES
 source
 1..12
 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACAC 747
 |||||
 1 AACAGTGACC 11

Db

RESULT 362
 I07920/c
 LOCUS Sequence 32 from Patent EP 0159123. 12 bp DNA linear PAT 02-DEC-1994
 DEFINITION
 ACCESSION I07920
 VERSION I07920.1 GI:589373
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Hsiung,H.M., Schoner,R.G. and Schoner,B.E.
 TITLE Vectors for expressing bovine growth hormone derivatives
 JOURNAL Patent: EP 0159123-A2 32 23-OCT-1985;
 FEATURES
 source
 1..12
 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 2.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAG 741

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Db      11 AGGAGAGAG 1
|||||
RESULT 363
AR199085/c
LOCUS      AR199085          12 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 33 from patent US 6355418.
ACCESSION  AR199085
VERSION    AR199085.1  GI:20249159
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Schmidt, G.
TITLE     Chimeric oligonucleotides and uses thereof in the identification of
JOURNAL   antisense binding sites
FEATURES   Patent: US 6355418-A 33 12-MAR-2002;
SOURCE     Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      734 AGAAGAGAGAC 744
|||||
Db      12 AGGAGAGAGAC 2

RESULT 364
AR217452
LOCUS      AR217452          12 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 65 from patent US 6416959.
ACCESSION  AR217452
VERSION    AR217452.1  GI:23317145
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Giuliano, K. and Kapur, R.
TITLE     System for cell-based screening
JOURNAL   Patent: US 6416959-A 65 09-JUL-2002;
FEATURES   Location/Qualifiers
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 GGAGAGACAGA 742
|||||
Db      1 GTAGAGAGATAGA 11

RESULT 365
AR241771
LOCUS      AR241771          12 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 59 from patent US 6472154.
ACCESSION  AR241771
VERSION    AR241771.1  GI:27287583
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.

```

```

TITLE     Polymorphic repeats in human genes
JOURNAL   Patent: US 6472154-A 59 29-OCT-2002;
FEATURES   Location/Qualifiers
1..12
source     /organism="unknown"
/mol_type="genomic DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      730 CAGAGAGAAC 740
|||||
Db      1 CAGCAGCAGAC 11

RESULT 366
AR242041/c
LOCUS      AR242041          12 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 329 from patent US 6472154.
ACCESSION  AR242041
VERSION    AR242041.1  GI:27287853
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
TITLE     Polymorphic repeats in human genes
JOURNAL   Patent: US 6472154-A 329 29-OCT-2002;
FEATURES   Location/Qualifiers
1..12
source     /organism="unknown"
/mol_type="genomic DNA"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      732 CGAGAGACAGA 742
|||||
Db      12 CGAGAGAGAGA 2

RESULT 367
AX000276
LOCUS      AX000276          12 bp      DNA      linear      PAT 10-MAR-2000
DEFINITION Sequence 1 from Patent EP0897991.
ACCESSION  AX000276
VERSION    AX000276.1  GI:7240702
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Naesby, M.D.
TITLE     Small Triplex Forming PNA Oligos
JOURNAL   Patent: EP 0897991-A 1 24-FEB-1999;
FEATURES   BOEHRINGER MANNHEIM GMBH (DE)
SOURCE     Location/Qualifiers
1..12
source     /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      729 CCAGAGAGAAC 739
|||||
Db      2 CCAGAGAGATAC 12

```

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RESULT 368
AX035437/c
LOCUS AX035437 12 bp RNA linear PAT 15-NOV-2000
DEFINITION Sequence 12 from Patent EP1035209.
ACCESSION AX035437
VERSION AX035437.1 GI:11191079
KEYWORDS
SOURCE
ORGANISM
Influenza C virus
Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
REFERENCE
1
AUTHORS Azzey,M., Hobom,G., Menke,A. and Flick,R.
TITLE Stable recombinant influenza viruses free of helper viruses
JOURNAL Patent: EP 1035209-A 12 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
FEATURES
Location/Qualifiers
1..12
/organism="Influenza C virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11552"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2
RESULT 369
AX035439/c
LOCUS AX035439 12 bp RNA linear PAT 15-NOV-2000
DEFINITION Sequence 14 from Patent EP1035209.
ACCESSION AX035439
VERSION AX035439.1 GI:11191081
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Azzey,M., Hobom,G., Menke,A. and Flick,R.
TITLE Stable recombinant influenza viruses free of helper viruses
JOURNAL Patent: EP 1035209-A 14 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
FEATURES
Location/Qualifiers
1..12
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/Note="Modified influenza A 3' sequence (pH1948)"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGGAGAGCAG 2
RESULT 370
AX100746/c
LOCUS AX100746 12 bp RNA linear PAT 10-APR-2001
DEFINITION Sequence 3 from Patent WO0122083.
ACCESSION AX100746
VERSION AX100746.1 GI:13619692
KEYWORDS
SOURCE
ORGANISM
Influenza C virus
Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

```

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Influenzavirus C.
REFERENCE
1
AUTHORS Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
TITLE Method for identifying mhc-restricted antigens
JOURNAL Patent: WO 0122083-A 3 29-MAR-2001;
GSP-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
Pharmaceuticals GmbH (DE)
FEATURES
Location/Qualifiers
1..12
/organism="Influenza C virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11552"
misc_feature 1..12
/Note="3'-konservierte Region des Wildtyp-Influenzavirus"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2
RESULT 371
AX352659/c
LOCUS AX352659 12 bp RNA linear PAT 06-FEB-2002
DEFINITION Sequence 3 from Patent EP1174514.
ACCESSION AX352659
VERSION AX352659.1 GI:18617789
KEYWORDS
SOURCE
ORGANISM
Influenza C virus
Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
REFERENCE
1
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
genes in tandem arrangement
JOURNAL Patent: EP 1174514-A 3 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
Location/Qualifiers
1..12
/organism="Influenza C virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11552"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2
RESULT 372
AX362217/c
LOCUS AX362217 12 bp RNA linear PAT 15-FEB-2002
DEFINITION Sequence 3 from Patent WO0208434.
ACCESSION AX362217
VERSION AX362217.1 GI:18694555
KEYWORDS
SOURCE
ORGANISM
Influenza C virus
Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
REFERENCE
1
AUTHORS Hobom,G., Menke,A. and Meyer-Rogge,S.
TITLE Recombinant influenza viruses with bicistronic vrnas coding for two
genes in tandem arrangement
JOURNAL Patent: WO 0208434-A 3 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)

```

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FEATURES
  source
    Location/Qualifiers
      1..12
      /organism="Influenza C virus"
      /mol_type="unassigned RNA"
      /db_xref="taxon:11552"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 373
AX428930/c
LOCUS AX428930 12 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 3 from Patent EP1201760.
ACCESSION AX428930
VERSION AX428930.1 GI:21540314
KEYWORDS
SOURCE Influenza C virus
ORGANISM Influenza C virus
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus C.
REFERENCE
  1
  AUTHORS Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and
           Grassmann,R.
  TITLE Influenza virus vector for human dendritic cells
  JOURNAL Patent: EP 1201760-A 3 02-MAY-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..12
      /organism="Influenza C virus"
      /mol_type="unassigned RNA"
      /db_xref="taxon:11552"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 374
AX428953/c
LOCUS AX428953 12 bp RNA linear PAT 21-JUN-2002
DEFINITION Sequence 26 from Patent EP1201760.
ACCESSION AX428953
VERSION AX428953.1 GI:21540337
KEYWORDS
SOURCE Influenza C virus
ORGANISM Influenza C virus
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus C.
REFERENCE
  1
  AUTHORS Schuler,G.D., Hobom,G., Steinkasserer,A.D., Strobel,I.D. and
           Grassmann,R.
  TITLE Influenza virus vector for human dendritic cells
  JOURNAL Patent: EP 1201760-A 26 02-MAY-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..12
      /organism="synthetic construct"
      /mol_type="unassigned RNA"
      /db_xref="taxon:32630"
      /note="Modified influenza A 3'-sequence"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 375
AX512612/c
LOCUS AX512612 12 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 3 from Patent EP1233059.
ACCESSION AX512612
VERSION AX512612.1 GI:23503835
KEYWORDS
SOURCE Influenza C virus
ORGANISM Influenza C virus
          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
          Influenzavirus C.
REFERENCE
  1
  AUTHORS Hobom,G. and Menke,A.
  TITLE Influenza viruses with enhanced transcriptional and replicational
          capacities
  JOURNAL Patent: EP 1233059-A 3 21-AUG-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..12
      /organism="Influenza C virus"
      /mol_type="unassigned RNA"
      /db_xref="taxon:11552"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2

RESULT 376
AX512613/c
LOCUS AX512613 12 bp RNA linear PAT 03-OCT-2002
DEFINITION Sequence 4 from Patent EP1233059.
ACCESSION AX512613
VERSION AX512613.1 GI:23503836
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1
  AUTHORS Hobom,G. and Menke,A.
  TITLE Influenza viruses with enhanced transcriptional and replicational
          capacities
  JOURNAL Patent: EP 1233059-A 4 21-AUG-2002;
          ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..12
      /organism="synthetic construct"
      /mol_type="unassigned RNA"
      /db_xref="taxon:32630"
      /note="Modified influenza A 3'-sequence"

Query Match
  Best Local Similarity 35.5%; Score 7.8; DB 1; Length 12;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGTAAACAG 2

RESULT 377
AX522263/c
LOCUS AX522263 12 bp RNA linear PAT 24-OCT-2002

```

DEFINITION Sequence 3 from Patent WO02064757.
ACCESSION AX522263
VERSION AX522263.1 GI:24411217
KEYWORDS Influenza C virus
SOURCE Influenza C virus
ORGANISM Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
REFERENCE 1
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational capacities
JOURNAL Patent: WO 02064757-A 3 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES source
1. .12
/organism="Influenza C virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11552"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db 12 AGCAGAGCAG 2
RESULT 378
AX522264/C
LOCUS AX522264 12 bp RNA linear PAT 24-OCT-2002
DEFINITION Sequence 4 from Patent WO02064757.
ACCESSION AX522264
VERSION AX522264.1 GI:24411218
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hobom, G. and Menke, A.
TITLE Influenza viruses with enhanced transcriptional and replicational capacities
JOURNAL Patent: WO 02064757-A 4 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES source
1. .12
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza A 3'-sequence"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db 12 AGTAAACAG 2
RESULT 379
AX711980
LOCUS AX711980 12 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from Patent WO0208381.
ACCESSION AX711980
VERSION AX711980.1 GI:29787762
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Tcherkassov, D.

TITLE Method for determining gene expression
JOURNAL Patent: WO 0208381-A 1 07-NOV-2002;
Genovoxx GmbH (DE)
FEATURES source
1. .12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ermittelte Sequenz (Beispiel 4)"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 737 AACAGAACACC 747
Db 1 ACCAAACACC 11
RESULT 380
AX742026
LOCUS AX742026 12 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 6 from Patent WO03020968.
ACCESSION AX742026
VERSION AX742026.1 GI:30524538
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Tcherkassov, D.
TITLE Method for analyzing nucleic acid sequences and gene expression
JOURNAL Patent: WO 03020968-A 6 13-MAR-2003;
Genovoxx GmbH (DE)
FEATURES source
1. .12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequenz aus Beispiel 2"
Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 737 AACAGAACACC 747
Db 1 ACCAAACACC 11
RESULT 381
AX766776
LOCUS AX766776 12 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 65 from Patent EPI314980.
ACCESSION AX766776
VERSION AX766776.1 GI:32260532
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Giuliano, K.A. and Kapur, R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 65 28-MAY-2003;
Cellomics, Inc. (US)
FEATURES source
1. .12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Caspase-6 substrate recognition sequence"
Query Match 35.5%; Score 7.8; DB 1; Length 12;

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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAACAGCA 742
Db 1 GTAGAAATAGA 11

RESULT 382
BD139745/c
LOCUS
DEFINITION
Gene family with transformation modulating activity.
ACCESSION
BD139745
VERSION
BD139745.1 GI:23234690
KEYWORDS
JP 2002508154-A/26.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Pasternack,G.R., Kocheavar,G.J., Brody,J.R. and Kadkol,S.S.
TITLE
Gene family with transformation modulating activity
JOURNAL
Patent: JP 2002508154-A 26 19-MAR-2002;
THE JOHNS HOPKINS UNIVERSITY
COMMENT
OS Artificial Sequence
PN JP 2002508154-A/26
PD 19-MAR-2002
PF 11-DEC-1998 JP 2000524477
PR 12-DEC-1997 US 60/069677
PI GARY R PASTERNAK,GERALD J KOCHAVAR,JONATHAN R BRODY,SHRIHARI

PC S KADKOL
PC C12N15/09,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
,C12Q/68,G01N33/15,
PC G01N33/50,G01N33/53//C12P21/09,C12N15/00,C12N5/00 CC
recognition sequence
FH Key
FT source
1. .12
Location/Qualifiers
/organism="Artificial Sequence".
FEATURES
source
1. .12
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCA 745
Db 12 GAAAAAGAAAA 2

RESULT 383
ATH528392
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
162G09.
ACCESSION
AJ528392
VERSION
AJ528392.1 GI:26796652
KEYWORDS
left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
AUTHORS
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)

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MEDLINE
PUBMED
12363535
2 (bases 1 to 12)
REFERENCE
Balzergue,S.
TITLE
Direct Submission
JOURNAL
Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
source
1. .12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiliewskaja"
/db_xref="taxon:3702"
/clone="162G09"
/misc_feature 1. .12
/note="T-DNA flanking sequence
left border"

Query Match 35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACCA 745
Db 1 GAAAAAGATCA 11

RESULT 384
AR013804/c
LOCUS
DEFINITION
Sequence 5 from patent US 5773213.
ACCESSION
AR013804
VERSION
AR013804.1 GI:3971258
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Gullans,S.R., Kojima,R. and Randall,J.
TITLE
Method for conducting sequential nucleic acid hybridization steps
JOURNAL
Patent: US 5773213-A 5 30-JUN-1998;
FEATURES
Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAGCA 742
Db 10 AGAACAGCA 2

RESULT 385
AR026540
LOCUS
DEFINITION
Sequence 3 from patent US 5856103.
ACCESSION
AR026540
VERSION
AR026540.1 GI:5937380

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KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 10)				
AUTHORS	Gray, D.M. and Clark, C.L.				
TITLE	Method for selectively ranking sequences for antisense targeting				
JOURNAL	Patent: US 5856103-A 3 05-JAN-1999;				
FEATURES	Location/Qualifiers				
source	1..10				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	33.6%; Score 7.4; DB 1; Length 10;				
Best Local Similarity	88.9%; Pred. No. 2.5e+02;				
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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QY	728 GCCCGAGA 736				
Ddb	1 GCCCGAGA 9				
RESULT 386					
LOCUS	ARI07757	10 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 3 from patent US 6110667.				
ACCESSION	ARI07757				
VERSION	ARI07757.1 GI:12823244				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.				
TITLE	Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis				
JOURNAL	Patent: US 6110667-A 3 29-AUG-2000;				
FEATURES	Location/Qualifiers				
source	1..10				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	33.6%; Score 7.4; DB 1; Length 10;				
Best Local Similarity	88.9%; Pred. No. 2.5e+02;				
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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QY	728 GCCCAGGAGA 736				
Ddb	10 GCCCAGGAGA 2				
RESULT 387					
LOCUS	ARI07789/c	10 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 35 from patent US 6110667.				
ACCESSION	ARI07789				
VERSION	ARI07789.1 GI:12823276				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 10)				
AUTHORS	Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.				
TITLE	Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis				
JOURNAL	Patent: US 6110667-A 35 29-AUG-2000;				
FEATURES	Location/Qualifiers				
source	1..10				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	33.6%; Score 7.4; DB 1; Length 10;				
Best Local Similarity	88.9%; Pred. No. 2.5e+02;				
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
<hr/>					
QY	728 GCCCAGGAGA 736				
Ddb	10 GCCCAGGAGA 2				
RESULT 387					
LOCUS	ARI07789/c	10 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 35 from patent US 6110667.				
ACCESSION	ARI07789				
VERSION	ARI07789.1 GI:12823276				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 10)				
AUTHORS	Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.				
TITLE	Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis				
JOURNAL	Patent: US 6110667-A 35 29-AUG-2000;				
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DEFINITION	Sequence 35 from patent US 6110667.				
ACCESSION	ARI07789				
VERSION	ARI07789.1 GI:12823276				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
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AUTHORS	Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.				
TITLE	Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis				
JOURNAL	Patent: US 6110667-A 35 29-AUG-2000;				
FEATURES	Location/Qualifiers				
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ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 10)
TITLE	Joyce,G.F. and Breaker,R.R.
JOURNAL	Enzymatic DNA molecules
FEATURES	Patent: US 6326174-A 41 04-DEC-2001;
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LOCUS	BD238657 10 bp DNA linear PAT 17-JUL-2003
DEFINITION	Preparation and use of superior vaccines.
ACCESSION	BD238657
VERSION	BD238657.1 GI:33048427
KEYWORDS	JP 2002534056-A/75.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 10)
JOURNAL	Roberts,B.L. and Shankara,S.
COMMENT	Preparation and use of superior vaccines
	Patent: JP 2002534056-A 75 15-OCT-2002;
	GENZYME CORP
OS	Homo sapiens (human)
PN	JP 2002534056-A/75
PD	15-OCT-2002
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08-DEC-1998 US 60/111715
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BD238955 10 bp DNA linear PAT 17-JUL-2003
Preparation and use of superior vaccines.
BD238955
BD238955.1 GI:33048725
JP 2002534056-A/373.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 373 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/373
PD 15-OCT-2002
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LOCUS BD239177 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239177
VERSION BD239177.1 GI:33048947
KEYWORDS JP 2002534056-A/595.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 595 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/595
PD 15-OCT-2002
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LOCUS BD239362 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239362
VERSION BD239362.1 GI:33049132
KEYWORDS JP 2002534056-A/780.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 780 15-OCT-2002;
GENZYME CORP
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OS Homo sapiens (human)
PN JP 2002534056-A/780
PD 15-OCT-2002
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Db 9 TTCACGAG 1

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 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
 C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC

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CC Preparation and use of superior vaccines

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RESULT 401
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LOCUS BD239924 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239924

VERSION BD239924.1 GI:33049694

KEYWORDS JP 2002534056-A/1342.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)

Robert, B.L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 1342 15-OCT-2002;

GENZYME CORP

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PN JP 2002534056-A/1342

PD 15-OCT-2002

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PI BRUCE L ROBERTS,SRINIVAS SHANKARA

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LOCUS BD239978 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239978

VERSION BD239978.1 GI:33049748

KEYWORDS JP 2002534056-A/1396.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)

Robert, B.L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 1396 15-OCT-2002;

GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/1396

PD 15-OCT-2002

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08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

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ACCESSION BD240001
VERSION JP 2002534056-A/1419
KEYWORDS Homo sapiens (human)
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1419 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1419
PD 15-OCT-2002
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19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/090003,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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FH Key Location/Qualifiers
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/Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACAA 745
Db 1 AACAGAACAA 9

RESULT 405
LOCUS BD240355
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240355
VERSION JP 2002534056-A/1773
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1773 15-OCT-2002;
GENZYME CORP
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COMMENT OS Homo sapiens (human)
 PN JP 2002534056-A/1773
 PD 15-OCT-2002
 PF 18-JUN-1998 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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 19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
 08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
 PI BRUCE L ROBERTS, SRINIVAS SHANKARA
 PC C12N15/09, C12N15/05, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
 C12N1/19,
 G01N37/00,
 C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
 CC Preparation and use of superior vaccines
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 QY 733 GAGAAACAG 741
 Db 2 GAGAAACAG 10
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 RESULT 406
 BD240581/c
 LOCUS 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240581
 VERSION BD240581.1 GI:33050351
 KEYWORDS JP 2002534056-A/1999.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 10)
 AUTHORS Roberts,B.L. and Shankar,S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1999 15-OCT-2002;
 GENZYME CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002534056-A/1999
 PD 15-OCT-2002
 PF 18-JUN-1998 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/089853 PR
 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
 19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
 19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS, SRINIVAS SHANKARA
 PC C12N15/09, C12N15/05, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
 C12N1/19,
 G01N37/00,
 C12N15/00, C12N5/00, C12N15/00
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 QY 733 GAGAAACAG 741
 Db 9 GAGAAACAG 1
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 RESULT 407
 E16893
 LOCUS 10 bp DNA linear PAT 28-JUL-1999
 DEFINITION DNA sequence required for efficient protein transcription in
 Brevisbacterium flavum.
 ACCESSION E16893
 VERSION E16893.1 GI:5711576
 KEYWORDS JP 1998229881-A/34.
 SOURCE Corynebacterium glutamicum
 ORGANISM Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 1 (bases 1 to 10)
 AUTHORS Kobayashi M., Man T. and Yugawa H.
 TITLE DNA HAVING SEQUENCE CAPABLE OF EFFICIENTLY TRANSLATING PROTEIN IN
 CORYNEFORM BACTERIA
 JOURNAL Patent: JP 1998229881-A 34 02-SEP-1998;
 MITSUBISHI CHEM CORP
 COMMENT OS Brevisbacterium flavum
 PN JP 1998229881-A/34
 PD 02-SEP-1998
 PF 19-FEB-1997 JP 1997035338
 PI KOBAYASHI MIKI, MAN TOMOKO, YUGAWA HIDEAKI
 PC C12N15/09, C07H21/04, C12N1/21, C12N9/38, C12Q1/68, (C12N15/09, PC
 C12R1:19),
 PC (C12N1/21, C12R1:13), (C12N9/38, C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key Location/Qualifiers
 FT source 1..10
 /organism='Brevisbacterium flavum' FT
 /strains='MJ-233',
 Location/Qualifiers
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 /organism='Corynebacterium glutamicum'
 /mol_type='genomic DNA'
 /db_xref='taxon:1718'
 Query Match 33.6%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.5e+02; Mismatches 0; Indels 1; Gaps 0;

Matches 8; Conservative 0;

Qy 729 CCAGGAGAA 737
| | | | |
Db 1 CGAGGAGAA 9

RESULT 408
E17077/c
LOCUS
DEFINITION Fusarium sp. - specific sequence in 18S rRNA gene.
ACCESSION E17077
VERSION E17077.1 GI:57111760
KEYWORDS JP 1998234380-A/6.
SOURCE unidentified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 10)
AUTHORS Shibata,Y., Takashina,T., Shindo,Y. and Takahashi,I.
TITLE NUCLEIC ACID SEQUENCE FOR DETECTING FUNGUS OF GENUS FUSARIUM
JOURNAL Patent: JP 1998234380-A 6 08-SEP-1998;
SHINKINRUI KINOU KAIHATSU KENKYUSHO:KK

OS None
COMMENT OC Artificial sequences.
PN JP 1998234380-A/6
PD 08-SEP-1998
PF 28-FEB-1997 JP 1997062104
PI SHIBATA YOSHIKAZU, TAKASHINA TOMONORI, SHINDO YOSHIO, PI
TAKAHASHI ISAMU
PC C12N15/09,C07H21/04,C12Q1/68/C12N1/14,(C12N15/09,C12R1/77),
PC (C12Q1/68,
PC C12R1/77), (C12N1/14,C12R1/77);
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
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FH source 1..10
FT /organism='Artificial sequences'.
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/db_xref='taxon:32644'

Query Match 33.6%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 740 AGAACACCG 748
| | | | |
Db 10 ATAACACCG 2

RESULT 409
E39629
LOCUS
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39629
VERSION E39629.1 GI:18621720
KEYWORDS JP 2000279181-A/162.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 162 10-OCT-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/162
PD 10-OCT-2000

Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
| | | | |
Db 1 CGAGGAGAA 9

RESULT 410
E39712
LOCUS
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39712
VERSION E39712.1 GI:18621803
KEYWORDS JP 2000279181-A/245.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 245 10-OCT-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/245
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
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Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
| | | | |
Db 1 GGGAAACAG 9

RESULT 411
AR241847
LOCUS
DEFINITION Sequence 135 from patent US 6472154.
ACCESSION AR241847
VERSION AR241847.1 GI:27287659
KEYWORDS Unknown.
SOURCE

PF 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
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Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAG 735
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Db 2 TGGCAGGAG 10

RESULT 410
E39712
LOCUS
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39712
VERSION E39712.1 GI:18621803
KEYWORDS JP 2000279181-A/245.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 245 10-OCT-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/245
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
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Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
| | | | |
Db 1 GGGAAACAG 9

RESULT 411
AR241847
LOCUS
DEFINITION Sequence 135 from patent US 6472154.
ACCESSION AR241847
VERSION AR241847.1 GI:27287659
KEYWORDS Unknown.
SOURCE

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AX152484/c
LOCUS      AX152484      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 399 from Patent WO0138577.
ACCESSION  AX152484
VERSION     AX152484.1  GI:14534135
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 399 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAA 738
Db 10 CAGCAGAAA 2

RESULT 417
AX301498
LOCUS      AX301498      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 212 from Patent WO0185941.
ACCESSION  AX301498
VERSION     AX301498.1  GI:17382581
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       MYC targets
JOURNAL     Patent: WO 0185941-A 212 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
Db 2 AGGGAAAC 10

RESULT 418
AX687134/c
LOCUS      AX687134      10 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 55 from Patent WO03008638.
ACCESSION  AX687134
VERSION     AX687134.1  GI:29409629
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibelser,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
TITLE       Sorting and immobilization system for nucleic acids using synthetic
            binding systems
JOURNAL     Patent: WO 03008638-A 56 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES    Location/Qualifiers
            source
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Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 2 GATACAGAA 10

RESULT 420
BD007909
LOCUS      BD007909      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007909
VERSION     BD007909.1  GI:18636282
KEYWORDS    JP 2001069993-A/185.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.

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Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
Pignot,M. and Kienle,S.
TITLE       Sorting and immobilization system for nucleic acids using synthetic
            binding systems
JOURNAL     Patent: WO 03008638-A 55 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES    Location/Qualifiers
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Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GATACAGAA 1

RESULT 419
AX687135
LOCUS      AX687135      10 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 56 from Patent WO03008638.
ACCESSION  AX687135
VERSION     AX687135.1  GI:29409630
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibelser,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
TITLE       Sorting and immobilization system for nucleic acids using synthetic
            binding systems
JOURNAL     Patent: WO 03008638-A 56 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES    Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 2 GATACAGAA 10

RESULT 420
BD007909
LOCUS      BD007909      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007909
VERSION     BD007909.1  GI:18636282
KEYWORDS    JP 2001069993-A/185.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.

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TITLE
JOURNAL
COMMENT
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 185, 21-MAR-2001;
OS Japan Science and Technology Corp
PN JP 2001069993-A/185
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P23/00,
PC A61P31/00, C12P21/08, C12N15/00
CC
FH Key Location/Qualifiers
FT source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
| | | | |
Db 1 GGGAAACAG 9

RESULT 421
BD065085
LOCUS
DEFINITION
Characterization of the yeast transcriptome.
ACCESSION
BD065085
VERSION
BD065085.1 GI:22610688
KEYWORDS
JP 2001509017-A/21.
SOURCE
Saccharomyces cerevisiae (baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
1 (bases 1 to 10);
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 21 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/21
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source
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/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
| | | | |
Db 2 AGGAGACAC 10

RESULT 423
BD073423/c
LOCUS
DEFINITION
Utilization of transcription factor Brn-3a.
ACCESSION
BD073423
VERSION
BD073423.1 GI:22619026
KEYWORDS
JP 2001511344-A/5.
SOURCE
synthetic construct
artificial sequences.
1 (bases 1 to 10)
Damien, S.M. and Seymar, L.D.
Utilization of transcription factor Brn-3a
Patent: JP 2001511344-A 5 14-AUG-2001;
NEUROVEX LTD
OS Artificial Sequence
PN JP 2001511344-A/5
PD 14-AUG-2001
PF 27-JUL-1998 JP 2000504246
PR 25-JUL-1997 GB 9715823.2, 10-DEC-1997 US 08/988476 PI
SMITH MARTIN DAMIEN, LATCHMAN DAVID SEYMAR
PC C12N15/09, A61K38/17, A61K39/245, A61K48/00, A61P25/00, C07K14/47,
C12N7/00,
PC C12N15/00, A61K37/12
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source
1. .10
/organism="Artificial Sequence"
Location/Qualifiers
1. .10
/organism="synthetic construct"

TITLE
JOURNAL
COMMENT
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 185, 21-MAR-2001;
OS Japan Science and Technology Corp
PN JP 2001069993-A/185
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P23/00,
PC A61P31/00, C12P21/08, C12N15/00
CC
FH Key Location/Qualifiers
FT source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 745
| | | | |
Db 1 AACAGACCA 9

RESULT 421
BD065085
LOCUS
DEFINITION
Characterization of the yeast transcriptome.
ACCESSION
BD065085
VERSION
BD065085.1 GI:22610688
KEYWORDS
JP 2001509017-A/21.
SOURCE
Saccharomyces cerevisiae (baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
1 (bases 1 to 10);
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 21 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/21
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source
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Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 745
| | | | |
Db 1 AACAGACCA 9

RESULT 422
BD065354
LOCUS
DEFINITION
Characterization of the yeast transcriptome.
ACCESSION
BD065354
VERSION
BD065354.1 GI:22610957
KEYWORDS
JP 2001509017-A/290.
SOURCE
Saccharomyces cerevisiae (baker's yeast)
Saccharomycetes cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 10);
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 290 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/290
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source
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/organism="Saccharomyces cerevisiae (yeast)"
Location/Qualifiers
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/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

Query Match 33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
| | | | |
Db 2 AGGAGACAC 10

RESULT 423
BD073423/c
LOCUS
DEFINITION
Utilization of transcription factor Brn-3a.
ACCESSION
BD073423
VERSION
BD073423.1 GI:22619026
KEYWORDS
JP 2001511344-A/5.
SOURCE
synthetic construct
artificial sequences.
1 (bases 1 to 10)
Damien, S.M. and Seymar, L.D.
Utilization of transcription factor Brn-3a
Patent: JP 2001511344-A 5 14-AUG-2001;
NEUROVEX LTD
OS Artificial Sequence
PN JP 2001511344-A/5
PD 14-AUG-2001
PF 27-JUL-1998 JP 2000504246
PR 25-JUL-1997 GB 9715823.2, 10-DEC-1997 US 08/988476 PI
SMITH MARTIN DAMIEN, LATCHMAN DAVID SEYMAR
PC C12N15/09, A61K38/17, A61K39/245, A61K48/00, A61P25/00, C07K14/47,
C12N7/00,
PC C12N15/00, A61K37/12
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source
1. .10
/organism="Artificial Sequence"
Location/Qualifiers
1. .10
/organism="synthetic construct"

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
DB 10 GAACAGAA 2

RESULT 424
BD161340
LOCUS BD161340 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083320
VERSION BD083320.1 GI:22628930
KEYWORDS JP 2001327293-A/241.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 241 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/241
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC NAGAI

FH Key Location/Qualifiers
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/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGACACCG 748
DB 1 AGACACCG 9

RESULT 425
BD161340
LOCUS BD161340 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161340
VERSION BD161340.1 GI:27867098
KEYWORDS JP 2002186482-A/162.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 162 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/162
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
DB 9 GAATAGAA 1

RESULT 427
BD161433/c
LOCUS BD161433 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161433
VERSION BD161433.1 GI:27867191
KEYWORDS JP 2002186482-A/255.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)

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C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".
FEATURES
source 1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TCCAGGAG 735
DB 1 TGCTAGGAG 9

RESULT 426
BD161418/c
LOCUS BD161418 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161418
VERSION BD161418.1 GI:27867176
KEYWORDS JP 2002186482-A/240.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 240 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/240
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)".
FEATURES
source 1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAA 743
DB 9 GAATAGAA 1

RESULT 427
BD161433/c
LOCUS BD161433 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161433
VERSION BD161433.1 GI:27867191
KEYWORDS JP 2002186482-A/255.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)

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AUTHORS Nagai, S., Matsushima, K. and Hashimoto, S.
 TITLE Human activated Th1 and Th2 cell expression genes
 JOURNAL Patent: JP 2002186482-A 255 02-JUL-2002;
 COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
 OS Homo sapiens (human)
 PN JP 2002186482-A/255
 PD 02-JUL-2002
 PF 19-DEC-2000 JP 2000385816
 PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO
 C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human
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 Location/Qualifiers
 FT source 1..10
 /organism='Homo sapiens (human)'.
 FT

FEATURES
 source

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 739 CAGAACACC 747
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 Db 10 CAGAACACG 2

RESULT 428

BD166608
 LOCUS Human liver disease-expressing genes. 10 bp DNA linear PAT 17-JAN-2003
 DEFINITION
 ACCESSION BD166608
 VERSION BD166608.1 GI:27872420
 KEYWORDS JP 2002209591-A/153.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 153 30-JUL-2002;
 COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
 OS Homo sapiens (human)
 PN JP 2002209591-A/153
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
 YAMASHITA
 PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key
 FT source 1..10
 /organism='Homo sapiens (human)'.
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FEATURES
 source

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAAACAGAA 743
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 Db 1 GAAACAAA 9

RESULT 429

BD166767
 LOCUS Human liver disease-expressing genes. 10 bp DNA linear PAT 17-JAN-2003
 DEFINITION
 ACCESSION BD166767
 VERSION BD166767.1 GI:27872579
 KEYWORDS JP 2002209591-A/312.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 312 30-JUL-2002;
 COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
 OS Homo sapiens (human)
 PN JP 2002209591-A/312
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
 YAMASHITA
 PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key
 FT source 1..10
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 FT

FEATURES
 source

Query Match 33.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAACG 741
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 Db 1 GAGAACG 9

RESULT 430

BD166844/c
 LOCUS Human liver disease-expressing genes. 10 bp DNA linear PAT 17-JAN-2003
 DEFINITION
 ACCESSION BD166844
 VERSION BD166844.1 GI:27872656
 KEYWORDS JP 2002209591-A/389.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 389 30-JUL-2002;
 COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
 OS Homo sapiens (human)
 PN JP 2002209591-A/389
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
 YAMASHITA
 PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key
 FT source 1..10
 /organism='Homo sapiens (human)'.
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FEATURES
 source


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Qy      734 AGAACAACA 742
Db      11 AGAACAACA 3

RESULT 435
LOCUS      AR106012              11 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6103491.
ACCESSION  AR106012
VERSION     AR106012.1 GI:12820077
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Sampath,K.T.
TITLE     Methods and compositions for identifying morphogen analogs
JOURNAL   Patent: US 6103491-A 8 15-AUG-2000;
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="unknown"
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      736 AACACAGAAC 744
Db      3 AACACATAC 11

RESULT 436
LOCUS      I11798/c              11 bp      DNA      linear      PAT 26-JUL-1995
DEFINITION Sequence 3 from Patent US 5414077.
ACCESSION  I11798
VERSION     I11798.1 GI:909742
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Lin,K.-Y. and Matteucci,M.
TITLE     Non-nucleoside linkers for convenient attachment of labels to
            oligonucleotides using standard synthetic methods
JOURNAL   Patent: US 5414077-A 3 09-MAY-1995;
FEATURES   Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      732 GGAGAAACA 740
Db      9 GGAGAAAAA 1

RESULT 437
LOCUS      I35006              11 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 92 from patent US 5599704.
ACCESSION  I35006
VERSION     I35006.1 GI:2087974
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)

AUTHORS   Thompson,J.D. and Draper,K.G.
TITLE     ErbB2/neu targeted ribozymes
JOURNAL   Patent: US 5599704-A 92 04-FEB-1997;
FEATURES   Location/Qualifiers
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727 TGCCAGGAG 735
Db      1 TACCAGGAG 9

RESULT 438
LOCUS      AR207570              11 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 4 from patent US 6379881.
ACCESSION  AR207570
VERSION     AR207570.1 GI:21507358
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Fouchier,R.Adrianus. and Schuitemaker,J.
TITLE     Nucleic acids and methods for the discrimination between syncytium
            inducing and non syncytium inducing variants of the human
            immunodeficiency virus
JOURNAL   Patent: US 6379881-A 4 30-APR-2002;
FEATURES   Location/Qualifiers
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      734 AGAACAACA 742
Db      3 AGAACAACA 11

RESULT 439
LOCUS      AR301505              11 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 86 from patent US 6538173.
ACCESSION  AR301505
VERSION     AR301505.1 GI:31689307
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Heber-Katz,E.
TITLE     Compositions and methods for wound healing
JOURNAL   Patent: US 6538173-A 86 25-MAR-2003;
FEATURES   Location/Qualifiers
            source
            1..11
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      738 ACAGAACAAC 746
Db      1 ACAGAATCTC 9
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RESULT 440
AR301543
LOCUS AR301543 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 124 from patent US 6538173.
ACCESSION AR301543
VERSION AR301543.1 GI:31689345
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 124 25-MAR-2003;
JOURNAL Location/Qualifiers
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source
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 738 ACAGAACAC 746
| | | | |
Db 3 ACCGAACAC 11
| | | | |
RESULT 441
AR363438/c
LOCUS AR363438 11 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 10 from patent US 5214136.
ACCESSION AR363438
VERSION AR363438.1 GI:34425015
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Lin,K.-Y. and Matteucci,M.
TITLE Anthraquinone-derivatives oligonucleotides
JOURNAL Patent: US 5214136-A 10 25-MAY-1993;
JOURNAL Location/Qualifiers
FEATURES
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1. .11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 732 CGAGAACAC 740
| | | | |
Db 9 GGAGAAAA 1
| | | | |
RESULT 442
AX098763
LOCUS AX098763 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 70 from Patent WO0120025.
ACCESSION AX098763
VERSION AX098763.1 GI:13538004
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wojnowski,L. and Eiselt,R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
JOURNAL Patent: WO 0120025-A 70 22-MAR-2001;
JOURNAL Location/Qualifiers
FEATURES
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1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"

Epidauros Biotechnologie AG (DE)
Location/Qualifiers
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 735 GAAACAGAA 743
| | | | |
Db 2 GAAACAGTA 10
| | | | |
RESULT 443
AX098764/c
LOCUS AX098764 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 71 from Patent WO0120025.
ACCESSION AX098764
VERSION AX098764.1 GI:13538005
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wojnowski,L. and Eiselt,R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
JOURNAL Patent: WO 0120025-A 71 22-MAR-2001;
JOURNAL Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 735 GAAACAGAA 743
| | | | |
Db 10 GAAACAGTA 2
| | | | |
RESULT 444
AX098769/c
LOCUS AX098769 11 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 76 from Patent WO0120025.
ACCESSION AX098769
VERSION AX098769.1 GI:13538010
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Wojnowski,L. and Eiselt,R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
JOURNAL Patent: WO 0120025-A 76 22-MAR-2001;
JOURNAL Location/Qualifiers
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"
Query Match 33.6%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 2.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 11 CAGACCCC 3

RESULT 445
AX098770
LOCUS
DEFINITION Sequence 77 from Patent WO0120025.
ACCESSION AX098770
VERSION AX098770.1 GI:13538011
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Wojnowski, L. and Eiselt, R.
TITLE Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in
JOURNAL diagnostic and therapeutic applications
Patent: WO 0120025-A 77 22-MAR-2001;
Epidaurus Biotechnologie AG (DE)
FEATURES
Location/Qualifiers
source
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 1 CAGACCCC 9

RESULT 446
AX175318/c
LOCUS
DEFINITION Sequence 82 from Patent WO0144465.
ACCESSION AX175318
VERSION AX175318.1 GI:14598686
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 82 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Location/Qualifiers
source
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAAC 744
Db 10 AAACAAAC 2

RESULT 447
AX393136/c
LOCUS
DEFINITION Sequence 110 from Patent WO02053773.
ACCESSION AX470533
VERSION AX470533.1 GI:22205658
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro

DEFINITION Sequence 66 from Patent WO0210217.
ACCESSION AX393136
VERSION AX393136.1 GI:19701186
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS St Croix, B., Kinzler, K.W. and Vogelstein, B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 66 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACACAGA 742
Db 9 AGAAGCAGA 1

RESULT 448
AX470474/c
LOCUS
DEFINITION Sequence 51 from Patent WO02053773.
ACCESSION AX470474
VERSION AX470474.1 GI:22205599
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 51 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 11 CAGACACC 3

RESULT 449
AX470533/c
LOCUS
DEFINITION Sequence 110 from Patent WO02053773.
ACCESSION AX470533
VERSION AX470533.1 GI:22205658
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann, K., Conradt, M. and Petersohn, D.
TITLE Method for determining skin stress or skin ageing in vitro


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JOURNAL Patent: WO 02053773-A 110 11-JUL-2002;
FEATURES HENKEL KGAA (DE)
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAACAA 740
Db 9 GGAGAACAA 1

RESULT 450
AX470707/c
LOCUS AX470707 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 284 from Patent WO02053773.
ACCESSION AX470707
VERSION AX470707.1 GI:22205832
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 284 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 738 ACAGAGCAC 746
Db 9 ACAGAGCAC 1

RESULT 451
AX470708
LOCUS AX470708 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 285 from Patent WO02053773.
ACCESSION AX470708
VERSION AX470708.1 GI:22205833
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 285 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 1 CAGGAGAAA 9

RESULT 452
AX470758/c
LOCUS AX470758 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 335 from Patent WO02053773.
ACCESSION AX470758
VERSION AX470758.1 GI:22205883
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 335 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGAACAA 745
Db 10 AACAGAACAA 2

RESULT 453
AX470961
LOCUS AX470961 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 538 from Patent WO02053773.
ACCESSION AX470961
VERSION AX470961.1 GI:22206086
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 538 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 735 GAACAGAAA 743
Db 1 GAACAGAAA 9

RESULT 454
AX471049
LOCUS AX471049 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 626 from Patent WO02053773.
ACCESSION AX471049

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VERSION      AX471049.1  GI:22206174
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Hofmann,K., Conradt,M. and Petersohn,D.
TITLE        Method for determining skin stress or skin ageing in vitro
JOURNAL      Patent: WO 02053773-A 626 11-JUL-2002;
              HENKEL KGAA (DE)
FEATURES     Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match  33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          733 GAGAAACAG 741
Db          1 GGGAAACAG 9

RESULT 455
AX471085/c
LOCUS       AX471085      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 662 from Patent WO02053773.
ACCESSION  AX471085
VERSION    AX471085.1  GI:22206210
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 662 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match  33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          734 AGAAACAGA 742
Db          11 AGAAAAAGA 3

RESULT 456
AX471104/c
LOCUS       AX471104      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 681 from Patent WO02053773.
ACCESSION  AX471104
VERSION    AX471104.1  GI:22206229
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 681 11-JUL-2002;
            HENKEL KGAA (DE)

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FEATURES     Location/Qualifiers
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              /db_xref="taxon:9606"
Query Match  33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          736 AACACAGAC 744
Db          9 AACACAGAC 1

RESULT 457
AX471541/c
LOCUS       AX471541      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1118 from Patent WO02053773.
ACCESSION  AX471541
VERSION    AX471541.1  GI:22206666
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1118 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match  33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          738 ACAGAACAC 746
Db          10 ACAGAACAC 2

RESULT 458
AX471703
LOCUS       AX471703      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1280 from Patent WO02053773.
ACCESSION  AX471703
VERSION    AX471703.1  GI:22206828
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1280 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match  33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          739 CAGAACACC 747
Db          739 CAGAACACC 747

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Db      3  CAGGACACC 11
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RESULT 459
AX471709/c
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1286 from Patent WO02053773.
ACCESSION  AX471709
VERSION     AX471709.1  GI:22206834
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1286 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      735  GAAACAGAA 743
|||||
Db      10  GAGACAGAA 2

RESULT 460
AX471743
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 1320 from Patent WO02053773.
ACCESSION  AX471743
VERSION     AX471743.1  GI:22206868
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL    Patent: WO 02053773-A 1320 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1..11
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727  TGCCAGGAG 735
|||||
Db      2  TGGCAGGAG 10

RESULT 461
AX472086
LOCUS      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 77 from Patent WO02053775.
ACCESSION  AX472086
VERSION     AX472086.1  GI:22207127
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Hustert,E., Haberl,M. and Wojnowski,L.
TITLE      Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
JOURNAL    Patent: WO 02053775-A 77 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES   Location/Qualifiers
            source
            1..11
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Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      729  CCAGGAGAA 737
|||||
Db      2  CAAGGAGAA 10

RESULT 462
AX555201
LOCUS      11 bp      DNA      linear      PAT 27-NOV-2002
DEFINITION Sequence 37 from Patent WO02070720.
ACCESSION  AX555201
VERSION     AX555201.1  GI:25898729
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
SOURCE
ORGANISM
REFERENCE   1
AUTHORS    Hayashizaki,Y. and Carninci,P.
TITLE      Cloning vectors and method for molecular cloning
JOURNAL    Patent: WO 02070720-A 37 12-SEP-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
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            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="plasmid junction linker upper oligonucleotide"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      728  GCCAGGAGA 736
|||||
Db      2  GCCATGAGA 10

RESULT 463
AX623049/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 90 from Patent WO02053774.
ACCESSION  AX623049
VERSION     AX623049.1  GI:28450990
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 90 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers

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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 10 CAGAAACACC 2

RESULT 464
AX623106/c
LOCUS
DEFINITION Sequence 147 from Patent WO02053774.
ACCESSION AX623106
VERSION AX623106.1 GI:28451047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 147 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAC 739
Db 10 AGGAGACAC 2

RESULT 465
AX623331
LOCUS
DEFINITION Sequence 372 from Patent WO02053774.
ACCESSION AX623331
VERSION AX623331.1 GI:28451272
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 372 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 10 CAGAAACACC 2

RESULT 466
AX623380/c
LOCUS
DEFINITION Sequence 421 from Patent WO02053774.
ACCESSION AX623380
VERSION AX623380.1 GI:28451321
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 421 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAAC 745
Db 10 AACAGAAC 2

RESULT 467
AX623518/c
LOCUS
DEFINITION Sequence 559 from Patent WO02053774.
ACCESSION AX623518
VERSION AX623518.1 GI:28451459
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 559 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAG 742
Db 9 AGAAACAG 1

RESULT 468
AX623551/c
LOCUS
DEFINITION Sequence 592 from Patent WO02053774.
ACCESSION AX623551
VERSION AX623551.1 GI:28451492
KEYWORDS
SOURCE Homo sapiens (human)

```

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 592 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGCAACA 740
Db 9 GGAGCAACA 1

RESULT 469
AX623639/c
LOCUS AX623639 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 680 from Patent WO02053774.
ACCESSION AX623639
VERSION AX623639.1 GI:28451580
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 680 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 11 CAGAACACC 3

RESULT 470
AX623774/c
LOCUS AX623774 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 815 from Patent WO02053774.
ACCESSION AX623774
VERSION AX623774.1 GI:28451715
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 815 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 11 CAGAACACC 3

RESULT 471
AX623846
LOCUS AX623846 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 887 from Patent WO02053774.
ACCESSION AX623846
VERSION AX623846.1 GI:28451787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 887 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGATAAAC 739
Db 1 AGGATAAAC 9

RESULT 472
AX623862/c
LOCUS AX623862 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 903 from Patent WO02053774.
ACCESSION AX623862
VERSION AX623862.1 GI:28451803
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 903 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAG 735
Db 9 TTCCAGGAG 1
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RESULT 473
AX624809
LOCUS
DEFINITION
Sequence 1850 from Patent WO02053774.
ACCESSION
AX624809
VERSION
AX624809.1 GI:28452750
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 1850 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACACAGAA 743
Db 2 GAACACAGAA 10

RESULT 474
AX624839
LOCUS
DEFINITION
Sequence 1880 from Patent WO02053774.
ACCESSION
AX624839
VERSION
AX624839.1 GI:28452780
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 1880 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAG 741
Db 1 GGAACACAG 9

RESULT 475
AX625167
LOCUS
DEFINITION
Sequence 2208 from Patent WO02053774.
ACCESSION
AX625167
VERSION
AX625167.1 GI:28453108
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2208 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACACAGAA 743
Db 2 GATACAGAA 10

RESULT 476
AX625224
LOCUS
DEFINITION
Sequence 2265 from Patent WO02053774.
ACCESSION
AX625224
VERSION
AX625224.1 GI:28453165
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2265 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 33.6%; Score 7.4; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 AGAACACCG 748
Db 1 AGGACACCG 9

RESULT 477
AX625356/c
LOCUS
DEFINITION
Sequence 2397 from Patent WO02053774.
ACCESSION
AX625356
VERSION
AX625356.1 GI:28453297
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 2397 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 33.6%; Score 7.4; DB 1; Length 11; PAT 21-FEB-2003
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGA 736
Db 10 GCAAGGAGA 2
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RESULT 478
AX625496
LOCUS
DEFINITION Sequence 2537 from Patent WO02053774.
ACCESSION AX625496
VERSION AX625496.1 GI:28453437
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2537 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGA 736
Db 3 GTCAGGAGA 11
|||||

RESULT 479
AX625505
LOCUS
DEFINITION Sequence 2546 from Patent WO02053774.
ACCESSION AX625505
VERSION AX625505.1 GI:28453446
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2546 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 1 CAGGAGGAA 9
|||||

RESULT 480

AX625671/c
LOCUS
DEFINITION Sequence 2712 from Patent WO02053774.
ACCESSION AX625671
VERSION AX625671.1 GI:28453612
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2712 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 GGAGAAACA 740
Db 9 GGAGAAAAA 1
|||||

RESULT 481
AX625851/c
LOCUS
DEFINITION Sequence 2892 from Patent WO02053774.
ACCESSION AX625851
VERSION AX625851.1 GI:28453889
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2892 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAA 738
Db 10 CAGGGGAAA 2
|||||

RESULT 482
AX625896/c
LOCUS
DEFINITION Sequence 2937 from Patent WO02053774.
ACCESSION AX625896
VERSION AX625896.1 GI:28453934
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1

[illegible]

JOURNAL Patent: WO 02053774-A 3784 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
Db 9 ACAGAGCAC 1

RESULT 490
AX626781/c
LOCUS AX626781 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3822 from Patent WO02053774.
ACCESSION AX626781
VERSION AX626781.1 GI:28454819
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3822 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACA 740
Db 10 GAAGAAACA 2

RESULT 488
AX626529
LOCUS AX626529 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3570 from Patent WO02053774.
ACCESSION AX626529
VERSION AX626529.1 GI:28454567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3570 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
Db 2 ACAGATCAC 10

RESULT 489
AX626743/c
LOCUS AX626743 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3784 from Patent WO02053774.
ACCESSION AX626743
VERSION AX626743.1 GI:28454781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3784 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
AX626802
LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
ACCESSION AX626802
VERSION AX626802.1 GI:28454840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3843 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
AX626802
LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
ACCESSION AX626802
VERSION AX626802.1 GI:28454840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3843 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
AX626802
LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
ACCESSION AX626802
VERSION AX626802.1 GI:28454840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3843 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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/db_xref="taxon:9606"

Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
AX626802
LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
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VERSION AX626802.1 GI:28454840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3843 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
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LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
ACCESSION AX626802
VERSION AX626802.1 GI:28454840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3843 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
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QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
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LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
ACCESSION AX626802
VERSION AX626802.1 GI:28454840
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3843 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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/mol_type="unassigned DNA"
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 9 GAAACAGAA 1

RESULT 491
AX626802
LOCUS AX626802 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3843 from Patent WO02053774.
ACCESSION AX626802
VERSION AX626802.1 GI:28454840
KEYWORDS

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QY 729 CCAGGAGAA 737
Db 1 CCAGTAGAA 9

RESULT 492
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LOCUS AX626812 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 3853 from Patent WO02053774.
ACCESSION AX626812
VERSION AX626812.1 GI:28454850
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3853 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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QY 737 AACAGAACCA 745
Db 3 AACAGAACCA 11

RESULT 495
AX627101/c
LOCUS AX627101 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 4142 from Patent WO02053774.
ACCESSION AX627101
VERSION AX627101.1 GI:28455139
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4142 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
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QY 739 CAGAACACC 747
Db 9 CTGACACCC 1

RESULT 496
AX627201/c
LOCUS AX627201 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 4242 from Patent WO02053774.
ACCESSION AX627201
VERSION AX627201.1 GI:28455239
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4242 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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Qy 734 AGAAACAGCA 742
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RESULT 497
AX627513
LOCUS AX627513 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4554 from Patent WO02053774.
ACCESSION AX627513
VERSION AX627513.1 GI:28455551
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4554 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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Qy 728 GCCAGGAGA 736
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RESULT 498
AX627584/c
LOCUS AX627584 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4625 from Patent WO02053774.
ACCESSION AX627584
VERSION AX627584.1 GI:28455622
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4625 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match
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Qy 737 AACAGACA 745
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Db 11 AAAGAACA 3
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RESULT 499
AX627881/c
LOCUS AX627881 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4922 from Patent WO02053774.
ACCESSION AX627881
VERSION AX627881.1 GI:28455919
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4922 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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Qy 738 ACAGAACAC 746
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RESULT 500
AX628002/c
LOCUS AX628002 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5043 from Patent WO02053774.
ACCESSION AX628002
VERSION AX628002.1 GI:28456040
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5043 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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Qy 736 AAACAGAAC 744
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RESULT 501
AX628045
LOCUS AX628045 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5086 from Patent WO02053774.
ACCESSION AX628045
VERSION AX628045.1 GI:28456083
KEYWORDS
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5086 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAA 737
Db 2 CCAGGAGCA 10

RESULT 502
AX628233/c
LOCUS      AX628233
DEFINITION Sequence 5274 from Patent WO02053774.
ACCESSION  AX628233
VERSION     AX628233.1 GI:28456271
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5274 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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QY 738 ACAGAACAC 746
Db 10 ACAGAACAC 2

RESULT 503
AX628272
LOCUS      AX628272
DEFINITION Sequence 5313 from Patent WO02053774.
ACCESSION  AX628272
VERSION     AX628272.1 GI:28456310
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5313 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAA 743
Db 2 GAAACGAA 10

RESULT 504
AX628283/c
LOCUS      AX628283
DEFINITION Sequence 5324 from Patent WO02053774.
ACCESSION  AX628283
VERSION     AX628283.1 GI:28456321
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5324 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAG 735
Db 11 TGACAGGAG 3

RESULT 505
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LOCUS      AX628286
DEFINITION Sequence 5327 from Patent WO02053774.
ACCESSION  AX628286
VERSION     AX628286.1 GI:28456324
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5327 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
Db 3 CAGAACACC 11

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RESULT 506
AX628357/c
LOCUS AX628357 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5398 from Patent WO02053774.
ACCESSION AX628357
VERSION AX628357.1 GI:28456395
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5398 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Db 10 CAGAACACC 2
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RESULT 507
AX628361/c
LOCUS AX628361 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5402 from Patent WO02053774.
ACCESSION AX628361
VERSION AX628361.1 GI:28456399
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5402 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Db 10 CAGAACACC 2
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RESULT 508
AX628382/c
LOCUS AX628382 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5423 from Patent WO02053774.
ACCESSION AX628382
VERSION AX628382.1 GI:28456420
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5423 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Db 10 CCAGAGAA 2
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RESULT 509
AX628417
LOCUS AX628417 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5458 from Patent WO02053774.
ACCESSION AX628417
VERSION AX628417.1 GI:28456455
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5458 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
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Db 10 GGAGAAACA 2
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RESULT 509
AX628396
LOCUS AX628396 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5437 from Patent WO02053774.
ACCESSION AX628396
VERSION AX628396.1 GI:28456434
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5437 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 738 ACAGAACAC 746
Db 3 ACAGAACCC 11
|||||
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RESULT 510
AX628417
LOCUS AX628417 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5458 from Patent WO02053774.
ACCESSION AX628417
VERSION AX628417.1 GI:28456455
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5458 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 3 GCCAGGAGA 11

RESULT 511
AX628539
LOCUS      AX628539          11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5580 from Patent WO02053774.
ACCESSION  AX628539
VERSION     AX628539.1 GI:28456577
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5580 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACA 740
Db 3 GGAGAAACA 11

RESULT 512
AX628543/C
LOCUS      AX628543          11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5584 from Patent WO02053774.
ACCESSION  AX628543
VERSION     AX628543.1 GI:28456581
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5584 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
            Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAGACAGAA 743
Db 10 GAGACAGAA 2

/db_xref="taxon:9606"

Query Match      33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
Db 3 GCCAGGAGA 11

RESULT 515
AX628860
LOCUS      AX628860          11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5901 from Patent WO02053774.
ACCESSION  AX628860
VERSION     AX628860.1 GI:28456898
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5901 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 CCAGGAGAA 737
|||||
Db 1 CCAGTAGAA 9

RESULT 516
AX628903
LOCUS
AX628903
DEFINITION
Sequence 5944 from Patent WO02053774.
ACCESSION
AX628903
VERSION
AX628903.1 GI:28456941
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5944 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 737 AACAGACA 745
|||||
Db 1 AACAGATA 9

RESULT 517
AX629070
LOCUS
AX629070
DEFINITION
Sequence 6111 from Patent WO02053774.
ACCESSION
AX629070
VERSION
AX629070.1 GI:28457108
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6111 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAG 741
|||||
Db 1 GAGAAAGAG 9

RESULT 518
AX629180
LOCUS
AX629180
DEFINITION
Sequence 6221 from Patent WO02053774.
ACCESSION
AX629180
VERSION
AX629180.1 GI:28457218
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6221 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TCCAGGAG 735
|||||
Db 3 TTCCAGGAG 11

RESULT 519
AX629375
LOCUS
AX629375
DEFINITION
Sequence 6416 from Patent WO02053774.
ACCESSION
AX629375
VERSION
AX629375.1 GI:28457413
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6416 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAC 739
|||||
Db 2 AGGGGAAC 10

RESULT 520
AX629412
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Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	735	GAAACAGAA 743							
Db	3	GAAACAGCA 11							
RESULT 525	AX630801/c								
LOCUS	AX630801 11 bp DNA linear PAT 21-FEB-2003								
DEFINITION	Sequence 7842 from Patent WO02053774.								
ACCESSION	AX630801								
VERSION	AX630801.1 GI:28458841								
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 Petersohn,D., Conradt,M. and Hofmann,K.								
AUTHORS	Method for determining homeostasis of the skin								
TITLE	Patent: WO 02053774-A 7842 11-JUL-2002;								
JOURNAL	Henkel Kommanditgesellschaft auf Aktien (DE)								
FEATURES	Location/Qualifiers								
source	1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"								
Query Match	33.6%; Score 7.4; DB 1; Length 11;								
Best Local Similarity	88.9%; Pred. No. 2.7e+02;								
Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	737	AACAGACA 745							
Db	10	AAGAGACA 2							
RESULT 526	AX630939/c								
LOCUS	AX630939 11 bp DNA linear PAT 21-FEB-2003								
DEFINITION	Sequence 7980 from Patent WO02053774.								
ACCESSION	AX630939								
VERSION	AX630939.1 GI:28458981								
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 Petersohn,D., Conradt,M. and Hofmann,K.								
AUTHORS	Method for determining homeostasis of the skin								
TITLE	Patent: WO 02053774-A 7980 11-JUL-2002;								
JOURNAL	Henkel Kommanditgesellschaft auf Aktien (DE)								
FEATURES	Location/Qualifiers								
source	1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"								
Query Match	33.6%; Score 7.4; DB 1; Length 11;								
Best Local Similarity	88.9%; Pred. No. 2.7e+02;								
Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	734	AGAAACAGA 742							
Db	9	AGAAACAGA 1							
RESULT 527	AX630972/c								
LOCUS	AX630972 11 bp DNA linear PAT 21-FEB-2003								
DEFINITION	Sequence 8013 from Patent WO02053774.								

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9630 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACAGAA 743
||| |||||
Db 2 GATACAGAA 10
RESULT 535
AX632645
LOCUS AX632645 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9687 from Patent WO02053774.
ACCESSION AX632645
VERSION AX632645.1 GI:28468260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9687 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 740 AGAACACCG 748
||| |||||
Db 1 AGGACACCG 9
RESULT 536
AX632777/c
LOCUS AX632777 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9819 from Patent WO02053774.
ACCESSION AX632777
VERSION AX632777.1 GI:28468392
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9819 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers

source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCACGAGAA 736
||| |||||
Db 10 GCACGAGAA 2
RESULT 537
BD095115
LOCUS BD095115 11 bp DNA linear PAT 27-AUG-2002
DEFINITION A polynucleotide encoding mouse histidine decarboxylase.
ACCESSION BD095115
VERSION BD095115.1 GI:22640703
KEYWORDS WO 0132892-A/8.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Otsu,H.
AUTHORS A polynucleotide encoding mouse histidine decarboxylase
TITLE Patent: WO 0132892-A 8 10-MAY-2001;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP,HIROSHI OTSU
COMMENT OS Mus sp. (mouse)
PN WO 0132892-A/8
PD 10-MAY-2001
PF 01-NOV-2000 WO 2000JP007689
PR 02-NOV-1999 JP 99P 312559,23-MAR-2000 JP 00P 082953 PI
HIROSHI OTSU
PC C12N15/60,C12N9/88
CC A polynucleotide encoding mouse histidine decarboxylase FH
Key Location/Qualifiers
FT source 1..11
/organism="Mus sp. (mouse)".
FEATURES Location/Qualifiers
source 1..11
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
Query Match 33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGACAC 746
||| |||||
Db 3 ACAGACAC 11
RESULT 538
BD124255
LOCUS BD124255 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124255
VERSION BD124255.1 GI:23219200
KEYWORDS JP 2002503460-A/86.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Katz,E.H.
AUTHORS 1 (bases 1 to 11)
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 86 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)


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FEATURES
  source
    Location/Qualifiers
      1..8
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Hba specific oligonucleotides"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 7 AGGAGAA 1

RESULT 542
AX017049/c
LOCUS AX017049 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 12 from Patent WO9947706.
ACCESSION AX017049
VERSION AX017049.1 GI:10042015
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 8)
    AUTHORS Schwarz,T. and Reeve,M.A.
    TITLE Sequencing by hybridisation
    JOURNAL Patent: WO 9947706-A 12 23-SEP-1999;
    SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
    (GB)
FEATURES
  source
    Location/Qualifiers
      1..8
        /organism="synthetic construct"
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        /note="Hbs specific oligonucleotides"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 8 AGGAGAA 2

RESULT 543
AX017086
LOCUS AX017086 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 49 from Patent WO9947706.
ACCESSION AX017086
VERSION AX017086.1 GI:10042052
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 8)
    AUTHORS Schwarz,T. and Reeve,M.A.
    TITLE Sequencing by hybridisation
    JOURNAL Patent: WO 9947706-A 49 23-SEP-1999;
    SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
    (GB)
FEATURES
  source
    Location/Qualifiers
      1..8
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Fluorescently labelled capture oligonucleotide"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 8 AGGAGAA 2

RESULT 544
AX017087
LOCUS AX017087 8 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 50 from Patent WO9947706.
ACCESSION AX017087
VERSION AX017087.1 GI:10042053
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1 (bases 1 to 8)
    AUTHORS Schwarz,T. and Reeve,M.A.
    TITLE Sequencing by hybridisation
    JOURNAL Patent: WO 9947706-A 50 23-SEP-1999;
    SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
    (GB)
FEATURES
  source
    Location/Qualifiers
      1..8
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        /db_xref="taxon:32630"
        /note="Fluorescently labelled capture oligonucleotide"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAA 737
Db 2 AGGAGAA 8

RESULT 545
AX573622/c
LOCUS AX573622 8 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 32 from Patent WO02079467.
ACCESSION AX573622
VERSION AX573622.1 GI:27551292
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
    AUTHORS Nielsen,P.E. and Good,L.
    TITLE Antibiotic-free bacterial strain selection with antisense molecules
    JOURNAL Patent: WO 02079467-A 32 10-OCT-2002;
    Koebenhavns Universitet (DK)
FEATURES
  source
    Location/Qualifiers
      1..8
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="Peptide nucleic acid no. 1832"

misc_feature
  /note="A lysine residue is linked to COOH-terminal of the
  PNA"

Query Match
  Best Local Similarity 31.8%; Score 7; DB 1; Length 8;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAG 741
Db 8 GAAACAG 2

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RESULT 546
BD217832/c
LOCUS      BD217832      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217832
VERSION    BD217832.1 GI:33027602
KEYWORDS  JP 2002509701-A/11.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 11 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
OS         Artificial Sequence
PN         JP 2002509701-A/11
PD         02-APR-2002
PF         19-MAR-1999 JP 2000536888
PI         MICHAEL ALAN REEVE,TEREK SCHWARZ
PC         C12Q1/69,C12N15/09,C12N15/00
CC         Description of Artificial Sequence:HBA SPECIFIC CC
OLIGONUCLEOTIDE
FH         Key Location/Qualifiers
FT         source 1..8
           /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..8
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      731 AGGAGAA 737
Db      7 AGGAGAA 1

RESULT 547
BD217833/c
LOCUS      BD217833      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217833
VERSION    BD217833.1 GI:33027603
KEYWORDS  JP 2002509701-A/12.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 12 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
OS         Artificial Sequence
PN         JP 2002509701-A/12
PD         02-APR-2002
PF         19-MAR-1999 JP 2000536888
PI         MICHAEL ALAN REEVE,TEREK SCHWARZ
PC         C12Q1/69,C12N15/09,C12N15/00
CC         Description of Artificial Sequence:HBS SPECIFIC CC
OLIGONUCLEOTIDE
FH         Key Location/Qualifiers
FT         source 1..8
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Query Match      31.8%; Score 7; DB 1; Length 8;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      731 AGGAGAA 737
Db      7 AGGAGAA 1

RESULT 548
BD217870
LOCUS      BD217870      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217870
VERSION    BD217870.1 GI:33027640
KEYWORDS  JP 2002509701-A/49.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 49 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
OS         Artificial Sequence
PN         JP 2002509701-A/49
PD         02-APR-2002
PF         19-MAR-1999 JP 2000536888
PI         MICHAEL ALAN REEVE,TEREK SCHWARZ
PC         C12Q1/69,C12N15/09,C12N15/00
CC         Description of Artificial Sequence:FLUORESCENTLY LABELLED CC
CAPTURE
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Query Match      31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      731 AGGAGAA 737
Db      2 AGGAGAA 8

RESULT 549
BD217871
LOCUS      BD217871      8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence determination by hybridization.
ACCESSION  BD217871
VERSION    BD217871.1 GI:33027641
KEYWORDS  JP 2002509701-A/50.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 8)
AUTHORS    Reeve,M.A. and Schwarz,T.
TITLE      Sequence determination by hybridization
JOURNAL    Patent: JP 2002509701-A 50 02-APR-2002;
COMMENT    NYCOMED AMERSHAM PLC
OS         Artificial Sequence
PN         JP 2002509701-A/50
PD         02-APR-2002
PF         19-MAR-1999 JP 2000536888

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PR 19-MAR-1998 GB 9805918.1
PI MICHAEL ALAN REEVE,TEREK SCHWARZ
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence:FLUORESCENTLY LABELLED CC
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Query Match 31.8%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 1 AGGAGAA 7

RESULT 550
LOCUS AX350493/c 9 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0179561.
ACCESSION AX350493
VERSION AX350493.1 GI:18616095
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 5 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
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Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 8 AGGAGAA 2

RESULT 551
AX573621/c
LOCUS AX573621 9 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 31 from Patent WO02079467.
ACCESSION AX573621
VERSION AX573621.1 GI:27551291
KEYWORDS synthetic construct
SOURCE synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Nielsen,P.E. and Good,L.
TITLE Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL Patent: WO 02079467-A 31 10-OCT-2002;
Koebenhavns Universitet (DK)
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/mol_type='genomic DNA'
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misc_feature 9
/note='A lysine residue is linked to COOH-terminal of the
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Query Match 31.8%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 735 GAAACAG 741
Db 9 GAAACAG 3

RESULT 552
LOCUS A06372 10 bp DNA linear PAT 26-AUG-1993
DEFINITION Nucleotide sequence 15 from patent number EP0139076.
ACCESSION A06372
VERSION A06372.1 GI:411246
KEYWORDS synthetic construct
SOURCE synthetic construct
    artificial sequences.
ORGANISM Mayer,H.
REFERENCE 1 (bases 1 to 10)
AUTHORS Human-Parathyroid hormone (human-PTH) producing hybrid vectors,
TITLE human-Parathyroid hormone gene, eucaryotic cells containing the
JOURNAL hybrid vector and their use
    Patent: EP 0139076-A 15 02-MAY-1985;
    Gesellschaft fuer Biotechnologische Forschung mbH (GBF)
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 731 AGGAGAA 737
Db 2 AGGAGAA 8

RESULT 553
AR018737
LOCUS AR018737 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 19 from patent US 5783182.
ACCESSION AR018737
VERSION AR018737.1 GI:3973851
KEYWORDS Unknown.
SOURCE Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Thompson,T.C.
TITLE Method for identifying metastatic sequences
JOURNAL Patent: US 5783182-A 19 21-JUL-1998;
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TGCCAGG 733
Db 727 TGCCAGG 733

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Db 4 TGCCAGG 10

RESULT 554
ARI07767/c
LOCUS ARI07767 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6110667.
ACCESSION ARI07767
VERSION ARI07767.1 GI:12823254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 13 25-AUG-2000;
FEATURES
source
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Query Match 31.8%; Score 7; DB 1; Length 10;
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QY 728 GCCAGGA 734
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Db 9 GCCAGGA 3

RESULT 555
ARI076672
LOCUS ARI076672 10 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6312894.
ACCESSION ARI076672
VERSION ARI076672.1 GI:17919027
KEYWORDS
SOURCE Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hedgpeth,J., Afonina,I.A., Kutayavin,I.V., Lukhtanov,E.A., Belousov,E.S. and Meyer,R.B. Jr.
TITLE Hybridization and mismatch discrimination using oligonucleotides conjugated to minor groove binders
JOURNAL Patent: US 6312894-A 3 06-NOV-2001;
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 AACAGGA 742
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Db 4 AACAGGA 10

RESULT 556
BD238798/c
LOCUS BD238798 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238798
VERSION BD238798.1 GI:33048569
KEYWORDS JP 2002534056-A/216.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 216 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/216
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/15, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
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QY 729 CCAGGAG 735
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Db 9 CCAGGAG 3

RESULT 557
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LOCUS BD238923 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238923
VERSION BD238923.1 GI:33048693
KEYWORDS JP 2002534056-A/341.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 341 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/341
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
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Qy 729 CCAGGAG 735
Db 4 CCAGGAG 10
RESULT 558
BD238950/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238950
VERSION BD238950.1 GI:33048720
KEYWORDS JP 2002534056-A/368.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
ROBERTS, B.L. and Shankara, S.
Preparation and use of superior vaccines
TITLE
JOURNAL
PATENT: JP 2002534056-A 368 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/368
PD 15-OCT-2002
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 729 CCAGGAG 735
Db 4 CCAGGAG 10
RESULT 558
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LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238950
VERSION BD238950.1 GI:33048720
KEYWORDS JP 2002534056-A/368.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
ROBERTS, B.L. and Shankara, S.
Preparation and use of superior vaccines
TITLE
JOURNAL
PATENT: JP 2002534056-A 368 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/368
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 731 AGGAGAA 737
Db 10 AGGAGAA 4
RESULT 559
BD239270
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239270
VERSION BD239270.1 GI:33049040
KEYWORDS JP 2002534056-A/688.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
ROBERTS, B.L. and Shankara, S.
Preparation and use of superior vaccines
TITLE
JOURNAL
PATENT: JP 2002534056-A 688 15-OCT-2002;
GENZYME CORP
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PN JP 2002534056-A/688
PD 15-OCT-2002
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
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PAT 17-JUL-2003

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OS Homo sapiens (human)
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PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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Qy 733 GAGAAAC 739
Db 7 GAGAAAC 1

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LOCUS BD240042 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240042
VERSION BD240042.1 GI:33049812
KEYWORDS JP 2002534056-A/1460.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1460 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1460
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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08-DEC-1998 US 60/111715
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Qy 728 GCCAGGA 734
Db 2 GCCAGGA 8

RESULT 563
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LOCUS BD239958 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239958
VERSION BD239958.1 GI:33049728
KEYWORDS JP 2002534056-A/1376.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1376 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1376
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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08-DEC-1998 US 60/111715
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Qy 728 GCCAGGA 734
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QY 727 TGCCAGG 733

Db 7 TGCCAGG 1

RESULT 565

BD240058/c

LOCUS BD240058 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240058
 VERSION BD240058.1 GI:33049828
 KEYWORDS JP 2002534056-A/1476.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

AUTHORS Roberts, B.L. and Shankara, S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1476 15-OCT-2002;
 GENZYME CORP

COMMENT

OS Homo sapiens (human)
 PN JP 2002534056-A/1476
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QY 742 AACACCG 748

Db 7 AACACCG 1

RESULT 566

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LOCUS BD240326 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240326
 VERSION BD240326.1 GI:33050096
 KEYWORDS JP 2002534056-A/1744.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

AUTHORS Roberts, B.L. and Shankara, S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 1744 15-OCT-2002;
 GENZYME CORP

COMMENT

OS Homo sapiens (human)
 PN JP 2002534056-A/1744
 PD 15-OCT-2002
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RESULT 567

BD240451/c

LOCUS BD240451 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240451
 VERSION BD240451.1 GI:33050221
 KEYWORDS JP 2002534056-A/1869.
 SOURCE Homo sapiens (human)

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens	1 (bases 1 to 10)	Roberts,B.L. and Shankara,S.	Preparation and use of superior vaccines	Patent: JP 2002534056-A 1869 15-OCT-2002;	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
OS	Homo sapiens (human)				
PN	JP 2002534056-A/1869				
PD	15-OCT-2002				
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
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QY 728 GCCAGGA 734
Db 10 GCCAGGA 4
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BD260023
LOCUS
DEFINITION
Hybridization and mismatch discrimination using oligonucleotides
conjugated to minor groove binders.
ACCESSION
BD260023
VERSION
BD260023.1 GI:33069793
KEYWORDS
JP 2002527040-A/3.
SOURCE
Escherichia coli
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hedgpeth, J., Afonina, I.A., Kutyavina, I.V., Lukhtanov, E.A.,
Belousov, E.S. and Jr, R.B.M.
TITLE
Hybridization and mismatch discrimination using oligonucleotides
conjugated to minor groove binders
JOURNAL
Patent: JP 2002527040-A 3 27-AUG-2002;
EPOCH BIOSCIENCES INC
COMMENT
CS Escherichia coli
PN JP 2002527040-A/3
PD 27-AUG-2002
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PI JOEL HEDGPETH, IRINA A AFONINA, IGOR V KUTYAVIN, EUGENY A PI
LUKHTANOV,
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RESULT 571
E39508
LOCUS
DEFINITION
Genes with human dendritic cell expression.
ACCESSION
E39508
VERSION
E39508.1 GI:18621599
KEYWORDS
JP 2000279181-A/41.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hashimoto, S., Matsushima, K. and Suzuki, T.
TITLE
Genes with human dendritic cell expression
JOURNAL
Patent: JP 2000279181-A 41 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT
OS Homo sapiens (human)
PN JP 2000279181-A/41
PD 10-OCT-2000
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PI SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI
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QY 739 CAGACGA 745
Db 2 CAGACGA 8
RESULT 572
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LOCUS
DEFINITION
Genes with human dendritic cell expression.
ACCESSION
E39646
VERSION
E39646.1 GI:18621737
KEYWORDS
JP 2000279181-A/179.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hashimoto, S., Matsushima, K. and Suzuki, T.
TITLE
Genes with human dendritic cell expression
JOURNAL
Patent: JP 2000279181-A 179 10-OCT-2000;
SCIENCE & TECH AGENCY
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QY 738 ACAGAAC 744
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Db 3 ACAGAAC 9

RESULT 573
E39648/c
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DEFINITION Genes with human dendritic cell expression.
ACCESSION E39648
VERSION E39648.1 GI:18621739
KEYWORDS JP 2000279181-A/181.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Hashimoto,S., Matsushima,K. and Suzuki,T.
  Genes with human dendritic cell expression
  Patent: JP 2000279181-A 181 10-OCT-2000;
  JOURNAL SCIENCE & TECH AGENCY
COMMENT
  OS Homo sapiens (human)
  PN JP 2000279181-A/181
  PD 10-OCT-2000
  PF 01-APR-1999 JP 1999095481
  PR
  PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
  C12N15/09,C07K14/475,C07K16/18,C12N15/00
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QY 728 GCCAGCA 734
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Db 2 GCCAGCA 8

RESULT 575
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LOCUS E39743 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39743
VERSION E39743.1 GI:18621834
KEYWORDS JP 2000279181-A/276.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 10)
  Hashimoto,S., Matsushima,K. and Suzuki,T.
  Genes with human dendritic cell expression
  Patent: JP 2000279181-A 276 10-OCT-2000;
  JOURNAL SCIENCE & TECH AGENCY
COMMENT
  OS Homo sapiens (human)
  PN JP 2000279181-A/276
  PD 10-OCT-2000
  PF 01-APR-1999 JP 1999095481
  PR
  PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
  C12N15/09,C07K14/475,C07K16/18,C12N15/00
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QY 727 TGCCAGG 733
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Db 9 TGCCAGG 3

RESULT 576
E54698/c
LOCUS E54698 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54698
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VERSION E54698.1 GI:22556181
KEYWORDS JP 2001211883-A/50.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 50 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/50
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
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QY 740 AGAACAC 746
DB 10 AGAACAC 4

RESULT 577
E54746
LOCUS Human normal liver cell expression genes.
DEFINITION E54746
ACCESSION E54746
VERSION E54746.1 GI:22556229
KEYWORDS JP 2001211883-A/98.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 98 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/98
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
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QY 740 AGAACAC 746
DB 10 AGAACAC 4

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DEFINITION E54746
ACCESSION E54746
VERSION E54746.1 GI:22556229
KEYWORDS JP 2001211883-A/98.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 98 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
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PD 07-AUG-2001
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QY 740 AGAACAC 746
DB 10 AGAACAC 4

RESULT 577
E54750
LOCUS Human normal liver cell expression genes.
DEFINITION E54750
ACCESSION E54750
VERSION E54750.1 GI:22556233
KEYWORDS JP 2001211883-A/102.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 102 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/102
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
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FH Key Location/Qualifiers.
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QY 729 CCAGGAG 735
DB 10 CCAGGAG 4

RESULT 579
E58380
LOCUS Sequence 14 from patent US 5652106.
DEFINITION E58380
ACCESSION E58380
VERSION E58380.1 GI:2477618
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Plikaytis,B.B., Shinnick,T.M. and Crawford,J.T.
TITLE Rapid amplification-based subtyping of mycobacterium tuberculosis
JOURNAL Patent: US 5652106-A 14 29-JUL-1997;
FEATURES
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Query Match 31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
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QY 742 AACACCG 748
DB 9 AACACCG 3

RESULT 580
AR282625
LOCUS

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DEFINITION Sequence 21 from patent US 6521747.
ACCESSION AR282625
VERSION AR282625.1 GI:29719223
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Anastasio,A.E., Finkel,K., Koshy,B. and Lee,H.
TITLE Haplotypes of the AGTR1 gene
JOURNAL Patent: US 6521747-A 21 18-FEB-2003;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 735 GAAACAG 741
Db 3 GAAACAG 9
RESULT 581
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LOCUS AR303410 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 135 from patent US 6544736.
ACCESSION AR303410
VERSION AR303410.1 GI:31692186
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 135 08-APR-2003;
FEATURES Location/Qualifiers
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Qy 732 GGAGAAA 738
Db 9 GGAGAAA 3
RESULT 582
AR303594/c
LOCUS AR303594 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 319 from patent US 6544736.
ACCESSION AR303594
VERSION AR303594.1 GI:31692370
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 319 08-APR-2003;
FEATURES Location/Qualifiers
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 735 GAAACAG 741
Db 8 GAAACAG 2
RESULT 583
AR336847/c
LOCUS AR336847 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6566130.
ACCESSION AR336847
VERSION AR336847.1 GI:33722697
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 22 20-MAY-2003;
FEATURES Location/Qualifiers
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Qy 731 AGGAGAA 737
Db 9 AGGAGAA 3
RESULT 584
AR336854
LOCUS AR336854 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 29 from patent US 6566130.
ACCESSION AR336854
VERSION AR336854.1 GI:33722704
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 29 20-MAY-2003;
FEATURES Location/Qualifiers
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Qy 739 CAGAACCA 745
Db 2 CAGAACCA 8
RESULT 585
AR409234/c
LOCUS AR409234 10 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 52 from patent US 6632919.
ACCESSION AR409234
VERSION AR409234.1 GI:40159877
KEYWORDS

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LOCUS	AX152442	10 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 357 from Patent WO0138577.				
ACCESSION	AX152442				
VERSION	AX152442.1	GI:14534093			
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ORGANISM	Homo sapiens				
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REFERENCE	1				
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.				
TITLE	Human transcriptomes				
JOURNAL	Patent: WO 0138577-A 357 31-MAY-2001;				
	The Johns Hopkins University (US)				
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RESULT 591					
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LOCUS	AX152463	10 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 378 from Patent WO0138577.				
ACCESSION	AX152463				
VERSION	AX152463.1	GI:14534114			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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REFERENCE	1				
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.				
TITLE	Human transcriptomes				
JOURNAL	Patent: WO 0138577-A 378 31-MAY-2001;				
	The Johns Hopkins University (US)				
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DEFINITION	Sequence 379 from Patent WO0138577.				
ACCESSION	AX152464				
VERSION	AX152464.1	GI:14534115			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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REFERENCE	1				
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.				

TITLE	Human transcriptomes				
JOURNAL	Patent: WO 0138577-A 379 31-MAY-2001;				
	The Johns Hopkins University (US)				
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RESULT 593					
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LOCUS	AX152485	10 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 400 from Patent WO0138577.				
ACCESSION	AX152485				
VERSION	AX152485.1	GI:14534136			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.				
TITLE	Human transcriptomes				
JOURNAL	Patent: WO 0138577-A 400 31-MAY-2001;				
	The Johns Hopkins University (US)				
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Db	8 TGCCAGG 2				
RESULT 594					
AX152786/c					
LOCUS	AX152786	10 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 701 from Patent WO0138577.				
ACCESSION	AX152786				
VERSION	AX152786.1	GI:14534437			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.				
TITLE	Human transcriptomes				
JOURNAL	Patent: WO 0138577-A 701 31-MAY-2001;				
	The Johns Hopkins University (US)				
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The Johns Hopkins University (US)									
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Db	1	GAGAAAC	7						
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AX153258									
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DEFINITION									
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ACCESSION									
AX153258									
VERSION									
AX153258.1 GI:14534909									
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.									
TITLE									
Human transcriptomes									
JOURNAL									
Patent: WO 0138577-A 1173 31-MAY-2001;									
The Johns Hopkins University (US)									
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DEFINITION									
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ACCESSION									
AX153267									
VERSION									
AX153267.1 GI:14534918									
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
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AUTHORS									
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.									
TITLE									
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JOURNAL									
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The Johns Hopkins University (US)									
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RESULT 604									
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DEFINITION									
Sequence 1420 from Patent WO0138577.									
ACCESSION									
AX153505									
VERSION									
AX153505.1 GI:14535156									

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KEYWORDS      Homo sapiens (human)
SOURCE
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1420 31-MAY-2001;
             The Johns Hopkins University (US)
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Query Match      31.8%; Score 7; DB 1; Length 10;
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QY      728 GCCAGGA 734
Db      4 GCCAGGA 10
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RESULT 605
LOCUS      AX153594
DEFINITION Sequence 1509 from Patent WO0138577.
ACCESSION  AX153594
VERSION     AX153594.1 GI:14535245
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1509 31-MAY-2001;
             The Johns Hopkins University (US)
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Query Match      31.8%; Score 7; DB 1; Length 10;
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QY      728 GCCAGGA 734
Db      4 GCCAGGA 10
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RESULT 606
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DEFINITION Sequence 1509 from Patent WO0138577.
ACCESSION  AX153594
VERSION     AX153594.1 GI:14535245
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1509 31-MAY-2001;
             The Johns Hopkins University (US)
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DEFINITION Sequence 433 from Patent WO0185941.
ACCESSION  AX301719
VERSION     AX301719.1 GI:17382802
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SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Versteeg,R. and Caron,H.N.
TITLE        Myc targets
JOURNAL      Patent: WO 0185941-A 433 15-NOV-2001;
             Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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ACCESSION  AX301719
VERSION     AX301719.1 GI:17382802
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS      Versteeg,R. and Caron,H.N.
TITLE        Myc targets
JOURNAL      Patent: WO 0185941-A 433 15-NOV-2001;
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QY      739 CAGAACA 745
Db      2 CAGAACA 8
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RESULT 607
LOCUS      AX391458
DEFINITION Sequence 21 from Patent EP1184456.
ACCESSION  AX391458
VERSION     AX391458.1 GI:19700068
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Anastasio,A.E., Koshy,B., Finkel,K. and Lee,H.H.
TITLE        Haplotypes of the agr1 gene
JOURNAL      Patent: EP 1184456-A 21 06-MAR-2002;
             Geneseece Pharmaceuticals, Inc. (US)
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DEFINITION Sequence 30 from Patent WO02079467.
ACCESSION  AX573620
VERSION     AX573620.1 GI:27551290
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
             artificial sequences.
REFERENCE
AUTHORS      Nielsen,P.B. and Good,L.
TITLE        Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL      Patent: WO 02079467-A 30 10-OCT-2002;
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Query Match      31.8%; Score 7; DB 1; Length 10;
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LOCUS	BD007849/c									PAT 31-JAN-2002
DEFINITION	LPS activated human monocyte expressing genes.									
ACCESSION	BD007849									
VERSION	BD007849.1 GI:18636222									
KEYWORDS	JP 2001069993-A/125									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	1 (bases 1 to 10)									
TITLE	Matsushima,K., Hashimoto,S. and Suzuki,T.									
JOURNAL	LPS activated human monocyte expressing genes									
COMMENT	Patent: JP 2001069993-A 125 21-MAR-2001; JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2001069993-A/125 PD 21-MAR-2001 PF 28-APR-2000 JP 2000131079 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC A61P29/00, PC A61P31/00,C12P21/08,C12N15/00 CC FH Key Location/Qualifiers FT source 1..10 /organism='Homo sapiens (human)'. FEATURES source 1..10 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'									
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LOCUS	BD007949									PAT 31-JAN-2002
DEFINITION	LPS activated human monocyte expressing genes.									
ACCESSION	BD007949									
VERSION	BD007949.1 GI:18636322									
KEYWORDS	JP 2001069993-A/225									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	1 (bases 1 to 10)									
TITLE	Matsushima,K., Hashimoto,S. and Suzuki,T.									
JOURNAL	LPS activated human monocyte expressing genes									
COMMENT	Patent: JP 2001069993-A 225 21-MAR-2001; JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2001069993-A/225 PD 21-MAR-2001 PF 28-APR-2000 JP 2000131079 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC A61P29/00, PC A61P31/00,C12P21/08,C12N15/00 CC FH Key Location/Qualifiers FT source 1..10 /organism='Homo sapiens (human)'. FEATURES source 1..10 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'									
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QY	729	CCAGGAG	735							
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RESULT 610										
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DEFINITION	LPS activated human monocyte expressing genes.									
ACCESSION	BD007771									
VERSION	BD007771.1 GI:18636144									
KEYWORDS	JP 2001069993-A/47									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	1 (bases 1 to 10)									
TITLE	Matsushima,K., Hashimoto,S. and Suzuki,T.									
JOURNAL	LPS activated human monocyte expressing genes									
COMMENT	Patent: JP 2001069993-A 47 21-MAR-2001; JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2001069993-A/47 PD 21-MAR-2001 PF 28-APR-2000 JP 2000131079 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC A61P29/00, PC A61P31/00,C12P21/08,C12N15/00 CC FH Key Location/Qualifiers FT source 1..10 /organism='Homo sapiens (human)'. FEATURES source 1..10 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'									
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QY 728 GCCAGG 734
DB 2 GCCAGG 8

RESULT 613
LOCUS BD007979/c 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007979
VERSION BD007979.1 GI:18636352
KEYWORDS JP 2001069993-A/255.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 255 21-MAR-2001,
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT
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PN JP 2001069993-A/255
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
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QY 727 TGCCAGG 733
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RESULT 614
LOCUS BD008032 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD008032
VERSION BD008032.1 GI:18636405
KEYWORDS JP 2001069993-A/308.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 308 21-MAR-2001,
JAPAN SCIENCE AND TECHNOLOGY CORP
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OS Homo sapiens (human)
PN JP 2001069993-A/308
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
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QY 739 CAGACA 745
DB 2 CAGACA 8

RESULT 615
LOCUS BD065275/c 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065275
VERSION BD065275.1 GI:23610878
KEYWORDS JP 2001509017-A/211.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes.
REFERENCE
1 (bases 1 to 10)
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 211 10-JUL-2001,
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/211
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
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Qy 729 CCAGGAG 735
Db 10 CCAGGAG 4
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RESULT 616
BD083173 10 bp DNA linear PAT 27-AUG-2002
LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083173
VERSION BD083173.1 GI:22628783
KEYWORDS JP 2001327293-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 94 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/94
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
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Qy 739 CAGAACA 745
Db 2 CAGAACA 8
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RESULT 617
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LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083179
VERSION BD083179.1 GI:22628789
KEYWORDS JP 2001327293-A/100.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 100 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/100
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
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Qy 727 TGCCAGG 733
Db 8 TGCCAGG 2
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RESULT 619
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LOCUS Human matured/activated dendritic cell expression genes.
DEFINITION
ACCESSION BD083361
VERSION BD083361.1 GI:22628971
KEYWORDS JP 2001327293-A/282.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 282 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/282
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
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PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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QY 738 CAGAACA 744
DB 3 CAGAACA 9

RESULT 620
LOCUS BD161207 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161207
VERSION BD161207.1 GI:278666965
KEYWORDS JP 2002186482-A/29.
SOURCE Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
    1 (bases 1 to 10)
    Nagai, S., Matsushima, K. and Hashimoto, S.
    Human activated Th1 and Th2 cell expression genes
    Patent: JP 2002186482-A 29 02-JUL-2002;
    JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
    COMMENT
        OS Homo sapiens (human)
        PN JP 2002186482-A/29
        PD 02-JUL-2002
        PF 19-DEC-2000 JP 2000385816
        PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
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QY 739 CAGAACA 745
DB 2 CAGAACA 8

RESULT 621
LOCUS BD161244 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161244
VERSION BD161244.1 GI:27867002
KEYWORDS JP 2002186482-A/66.
SOURCE Homo sapiens (human)
ORGANISM
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REFERENCE
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Nagai, S., Matsushima, K. and Hashimoto, S.
Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 66 02-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
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    PN JP 2002186482-A/66
    PD 02-JUL-2002
    PF 19-DEC-2000 JP 2000385816
    PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
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QY 739 CAGAACA 745
DB 2 CAGAACA 8

RESULT 622
LOCUS BD161338 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161338
VERSION BD161338.1 GI:27867096
KEYWORDS JP 2002186482-A/160.
SOURCE Homo sapiens (human)
ORGANISM
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    1 (bases 1 to 10)
    Nagai, S., Matsushima, K. and Hashimoto, S.
    Human activated Th1 and Th2 cell expression genes
    Patent: JP 2002186482-A 160 02-JUL-2002;
    JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
    COMMENT
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        PN JP 2002186482-A/160
        PD 02-JUL-2002
        PF 19-DEC-2000 JP 2000385816
        PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
        C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12N15/00 CC Human
        activated Th1 and Th2 cell expression genes FH Key
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QY 728 GCCAGGA 734
DB 7 GCCAGGA 1

RESULT 623
LOCUS BD161404 10 bp DNA linear PAT 17-JAN-2003

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DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161404
VERSION BD161404.1 GI:27867162
KEYWORDS JP 2002186482-A/226
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 226 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/226
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
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DEFINITION Human activated Th1 and Th2 cell expression genes
ACCESSION BD161472
VERSION BD161472.1 GI:27867230
KEYWORDS JP 2002186482-A/294
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 294 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/294
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
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DEFINITION Human liver disease-expressing genes
ACCESSION BD166678
VERSION BD166678.1 GI:27872490
KEYWORDS JP 2002209591-A/223
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 223 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/223
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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DEFINITION Human liver disease-expressing genes
ACCESSION BD166539
VERSION BD166539.1 GI:27872351
KEYWORDS JP 2002209591-A/84
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 84 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/84
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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DB 9 CCAGGAG 3
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DEFINITION Human liver disease-expressing genes
ACCESSION BD166678
VERSION BD166678.1 GI:27872490
KEYWORDS JP 2002209591-A/223
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 223 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/223
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167093.1 GI:27872905
VERSION     JP 2002209591-A/638.
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     Patent: JP 2002209591-A 638 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002209591-A/638
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
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DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167149.1 GI:27872961
VERSION     JP 2002209591-A/694.
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     Patent: JP 2002209591-A 694 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
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Db 10 CCAGGAG 4
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RESULT 632
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LOCUS      BD167220          10 bp      DNA          linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167220.1 GI:27873032
VERSION     JP 2002209591-A/765.
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE       Human liver disease-expressing genes
JOURNAL     Patent: JP 2002209591-A 765 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002209591-A/765
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
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Db 10 AGAACAC 4
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RESULT 633
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DEFINITION Methods for the diagnosis and treatment of lung cancer.
ACCESSION  BD225309.1 GI:33035079
VERSION     JP 2002509706-A/8.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Jen,J., Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE       Methods for the diagnosis and treatment of lung cancer
JOURNAL     Patent: JP 2002509706-A 8 02-APR-2002;
            GENZYME CORP,JOHN HOPKINS UNIVERSITY

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COMMENT OS Artificial Sequence
PN JP 2002509706-A/8
PD 02-APR-2002
PF 30-MAR-1999 JP 2000540746
PR 31-MAR-1998 US 60/080044
PI JIN JEN GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
C12N15/09,A61K45/00,A61K48/00,A61P35/00,C12Q1/68,G01N33/50, PC
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Matches 7; Conservative 0; Mismatches 0;

QY 729 CCAGGAG 735
Db 7 CCAGGAG 1

RESULT 634
BD225320/c
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DEFINITION BD225320 10 bp DNA linear PAT 17-JUL-2003
Compositions and methods for the identification of lung tumor
cells.
ACCESSION BD225320
VERSION BD225320.1 GI:33035090
KEYWORDS JP 2002509707-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Compositions and methods for the identification of lung tumor cells
JOURNAL Patent: JP 2002509707-A 2 02-APR-2002;
GENZYME CORP
COMMENT OS Artificial Sequence
PN JP 2002509707-A/2
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1998 US 60/080037
PI GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
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Search completed: October 18, 2004, 14:05:40
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 14:07:13 ; Search time 1 Seconds
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Title: US-09-695-451-1

Perfect score: 22

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Scoring table: IDENTITY_NUC

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Searched: 1491 segs, 18660 residues

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Minimum DB seq length: 8

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1491 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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C 6	17	77.3	18	1	ABT05017
C 7	15.4	70.0	18	1	AA116398
C 8	15.4	70.0	18	1	AAAC62593
C 9	15.4	70.0	18	1	AA113315
C 10	15.4	70.0	18	1	AAAC62673
C 11	15.4	70.0	18	1	ABX89547
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C 19	14.6	66.4	22	1	AAAD2815
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C 21	14.4	65.5	19	1	AAH60839
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C 23	14.2	64.5	19	1	AAH61103
C 24	14.2	64.5	21	1	AAAD30255
C 25	14	63.6	18	1	AAV14110
C 26	13.8	62.7	18	1	AAV02721
C 27	13.8	62.7	20	1	AAAL1105
C 28	13.8	62.7	20	1	AAZ57075
C 29	13.6	61.8	20	1	ABT05166
C 30	13.4	60.9	20	1	AAV14107
C 31	13.4	60.9	18	1	AAV14104
C 32	13.4	60.9	18	1	AAV14106
C 33	13.4	60.9	20	1	AAV77255

C 34	13.2	60.0	19	1	AAA85942
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C 108	10.4	47.3	15	1	AAT54806	Mouse reIA hammerh	C 181	9.8	44.5	15	1	AAF50109	IGF-I oligonucleot
C 109	10.4	47.3	15	1	AAT50236	Rabbit CPTP HH rib	C 182	9.8	44.5	15	1	AAF54011	IGF-I oligonucleot
C 110	10.4	47.3	15	1	AA331078	Tag sequence of a	C 183	9.8	44.5	15	1	AAF50112	IGF-I oligonucleot
C 111	10.4	47.3	15	1	AA331812	Transcript tag seq	C 184	9.8	44.5	15	1	AAF53454	Nucleotide sequenc
C 112	10.4	47.3	15	1	AA318254	ASO primer #1 to d	C 185	9.8	44.5	15	1	AAF79911	Human P450(cytochr
C 113	10.4	47.3	15	1	ABQ88673	Human CFU1 ASO PCR	C 186	9.8	44.5	15	1	ABN80567	Human ALDH5 allele
C 114	10.4	47.3	15	1	ABV99770	Human PFKFB2 allele	C 187	9.8	44.5	15	1	ABN80567	Duplex forming PNA
C 115	10.4	47.3	15	1	AA319913	ASO probe #7 to de	C 188	9.8	44.5	15	1	ABD24257	Human colon cancer
C 116	10.4	47.3	15	1	ABK09887	P23Y1 gene allele-	C 189	9.8	44.5	15	1	ABK23259	Hepatitis C virus
C 117	10.4	47.3	15	1	ABK37666	Human colorectal a	C 190	9.8	44.5	15	1	ABX00872	CCBP2 detecting AS
C 118	10.4	47.3	15	1	ABK32031	Human colon cancer	C 191	9.8	44.5	15	1	ABX39513	Human CYP7A1 allel
C 119	10.4	47.3	15	1	ACD56204	HBV enzymatic nucl	C 192	9.8	44.5	15	1	ABV99157	Triple helix formi
C 120	10.4	47.3	16	1	AA303274	PCR primer 1 used	C 193	9.8	44.5	15	1	ABK98147	M. avium 23S rRNA
C 121	10.4	47.3	16	1	AA356811	Target validation	C 194	9.8	44.5	15	1	ABX76569	Human skin stress/
C 122	10.4	47.3	16	1	AA356768	B22 protein ribozy	C 195	9.8	44.5	15	1	ABQ87464	Human skin EST 468
C 123	10.4	47.3	16	1	AA356037	HBV DNA polymerase	C 196	9.8	44.5	15	1	ABV66898	Herpesvirus inhibi
C 124	10.4	47.3	16	1	ABN83342	Human rhinovirus P	C 197	9.8	44.5	15	1	AAQ24029	NF-AT complex bind
C 125	10.2	46.4	15	1	AAQ74220	Influenza virus st	C 198	9.8	44.5	15	1	AAQ37032	Organic material d
C 126	10.2	46.4	15	1	AAZ63881	Substrate for ham	C 199	9.8	44.5	15	1	AAZ41801	Released tag used
C 127	10.2	46.4	15	1	AAZ63880	Substrate for ham	C 200	9.8	44.5	15	1	AAZ41801	Microbe detection
C 128	10.2	46.4	15	1	AAZ43128	IGF-I oligonucleot	C 201	9.8	44.5	15	1	AAZ41585	DNA encoding caspa
C 129	10.2	46.4	15	1	ABX00933	Hepatitis C virus	C 202	9.8	44.5	15	1	AAZ41585	Primer used to ill
C 130	10.2	46.4	15	1	ABX00934	Hepatitis C virus	C 203	9.8	44.5	15	1	AAZ41585	Human hypocrerin r
C 131	10.2	46.4	15	1	AA356173	Human TSLP furin c	C 204	9.8	44.5	15	1	AAZ41585	Oligonucleotide pr
C 132	10.4	47.3	15	1	ABL91866	Human LIPG gene pr	C 205	9.8	44.5	15	1	AAH21574	Oligonucleotide pr
C 133	10.4	47.3	15	1	AAZ28124	Vesicular stomatit	C 206	9.8	44.5	15	1	ABH75383	Oligonucleotide pr
C 134	10.4	47.3	15	1	ABV65653	Human skin EST 343	C 207	9.8	44.5	15	1	ABH88475	Oligonucleotide pr
C 135	10.4	47.3	15	1	ABF80071	Oligonucleotide SE	C 208	9.8	44.5	15	1	ABH97824	Oligonucleotide pr
C 136	10.4	47.3	15	1	ABH64252	Oligonucleotide SE	C 209	9.8	44.5	15	1	ABH97824	Oligonucleotide pr
C 137	10.4	47.3	15	1	ABH64253	Oligonucleotide SE	C 210	9.8	44.5	15	1	ABH94121	Oligonucleotide pr
C 138	10.4	47.3	15	1	ABF80070	Oligonucleotide SE	C 211	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 139	10.4	47.3	15	1	AA393779	Human B-raf target	C 212	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 140	10.4	47.3	15	1	AA331401	Tag sequence of a	C 213	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 141	10.4	47.3	15	1	AA331401	ASO primer #11 to	C 214	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 142	10.4	47.3	15	1	AA331448	Human FOS gene all	C 215	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 143	10.4	47.3	15	1	ABK81356	Human LIPG gene al	C 216	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 144	10.4	47.3	15	1	ABK81356	Human colon cancer	C 217	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 145	10.4	47.3	15	1	ABK81356	Hepatitis C virus	C 218	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 146	10.4	47.3	15	1	ABK81356	Oligonucleotide SE	C 219	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 147	10.4	47.3	15	1	ABK81356	Oligonucleotide SE	C 220	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 148	10.4	47.3	15	1	ABF97937	Oligonucleotide SE	C 221	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 149	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 222	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 150	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 223	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 151	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 224	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 152	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 225	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 153	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 226	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 154	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 227	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 155	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 228	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 156	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 229	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 157	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 230	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 158	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 231	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 159	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 232	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 160	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 233	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 161	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 234	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 162	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 235	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 163	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 236	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 164	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 237	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 165	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 238	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 166	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 239	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 167	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 240	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 168	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 241	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 169	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 242	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 170	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 243	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 171	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 244	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 172	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 245	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 173	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 246	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 174	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 247	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 175	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 248	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 176	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 249	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 177	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 250	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 178	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 251	9.8	44.5	15	1	ABH70673	Oligonucleotide pr
C 179	10.4	47.3	15	1	ABH32900	Oligonucleotide SE	C 252	9.8	44.5	15	1	ABH70673	Oligonucleotide pr

253	9.4	42.7	13	1	ABF56511	Oligonucleotide SE
254	9.4	42.7	13	1	ABH13113	Oligonucleotide SE
C 255	9.4	42.7	13	1	ABH48836	Oligonucleotide SE
256	9.4	42.7	13	1	ABC73159	Oligonucleotide SE
257	9.4	42.7	13	1	ABC77827	Oligonucleotide SE
258	9.4	42.7	13	1	ABC57780	Oligonucleotide SE
259	9.4	42.7	13	1	ABC30258	Oligonucleotide SE
260	9.4	42.7	13	1	ABF96837	Oligonucleotide SE
261	9.4	42.7	13	1	ABF96837	Oligonucleotide SE
262	9.4	42.7	13	1	ABF96837	Oligonucleotide SE
C 263	9.4	42.7	13	1	ABC37749	Oligonucleotide SE
264	9.4	42.7	13	1	ABF75624	Oligonucleotide SE
C 265	9.4	42.7	13	1	ABC82727	Oligonucleotide SE
C 266	9.4	42.7	13	1	ABC58200	Oligonucleotide SE
C 267	9.4	42.7	13	1	ABC37748	Oligonucleotide SE
C 268	9.4	42.7	13	1	ABF24394	Oligonucleotide SE
C 269	9.4	42.7	13	1	ABF30260	Oligonucleotide SE
C 270	9.4	42.7	13	1	ABC72270	Oligonucleotide SE
C 271	9.4	42.7	13	1	ABC51768	Oligonucleotide SE
C 272	9.4	42.7	13	1	ABC57782	Oligonucleotide SE
273	9.4	42.7	13	1	ABC58201	Oligonucleotide SE
274	9.4	42.7	13	1	ABH11964	Oligonucleotide SE
275	9.4	42.7	13	1	ABC24377	Oligonucleotide SE
C 276	9.4	42.7	13	1	ABF74449	Oligonucleotide SE
C 277	9.4	42.7	13	1	ABF75625	Oligonucleotide SE
C 278	9.4	42.7	13	1	ABF56387	Oligonucleotide SE
279	9.4	42.7	13	1	ABH15112	Oligonucleotide SE
280	9.4	42.7	13	1	ABF66157	Oligonucleotide SE
C 281	9.4	42.7	13	1	ABF66269	Oligonucleotide SE
C 282	9.4	42.7	13	1	ABC67296	Oligonucleotide SE
C 283	9.4	42.7	13	1	ABC50423	Oligonucleotide SE
C 284	9.4	42.7	13	1	ABC77826	Oligonucleotide SE
C 285	9.4	42.7	13	1	ABF24376	Oligonucleotide SE
C 286	9.4	42.7	13	1	ABF24395	Oligonucleotide SE
C 287	9.4	42.7	13	1	ABF80900	Oligonucleotide SE
C 288	9.4	42.7	13	1	ABC57783	Oligonucleotide SE
C 289	9.4	42.7	13	1	ABC10581	Oligonucleotide SE
C 290	9.4	42.7	13	1	ABH23091	Oligonucleotide SE
C 291	9.4	42.7	13	1	ABF75626	Oligonucleotide SE
C 292	9.4	42.7	13	1	ABC71282	Oligonucleotide SE
C 293	9.4	42.7	13	1	ABC51769	Oligonucleotide SE
294	9.4	42.7	13	1	ABC83627	Oligonucleotide SE
C 295	9.4	42.7	13	1	ABC66042	Oligonucleotide SE
C 296	9.4	42.7	13	1	ABF25407	Oligonucleotide SE
C 297	9.4	42.7	13	1	ABF74292	Oligonucleotide SE
C 298	9.4	42.7	13	1	ABF74448	Oligonucleotide SE
C 299	9.4	42.7	13	1	ABF66159	Oligonucleotide SE
C 300	9.4	42.7	13	1	ABF66268	Oligonucleotide SE
C 301	9.4	42.7	13	1	ABH50906	Oligonucleotide SE
C 302	9.4	42.7	13	1	ABC57781	Oligonucleotide SE
C 303	9.4	42.7	13	1	ABF66156	Oligonucleotide SE
C 304	9.4	42.7	13	1	ABC73158	Oligonucleotide SE
C 305	9.4	42.7	13	1	ABC66043	Oligonucleotide SE
C 306	9.4	42.7	13	1	ABF30261	Oligonucleotide SE
C 307	9.4	42.7	13	1	ABF80901	Oligonucleotide SE
C 308	9.4	42.7	13	1	ABF66158	Oligonucleotide SE
C 309	9.4	42.7	13	1	ABC67297	Oligonucleotide SE
C 310	9.4	42.7	13	1	ABC56821	Oligonucleotide SE
C 311	9.4	42.7	13	1	ABH19618	Oligonucleotide SE
C 312	9.4	42.7	13	1	ABF87397	Oligonucleotide SE
C 313	9.4	42.7	13	1	ABH54888	Oligonucleotide SE
C 314	9.4	42.7	13	1	ABC27521	Oligonucleotide SE
C 315	9.4	42.7	13	1	ABC11965	Oligonucleotide SE
C 316	9.4	42.7	13	1	ABH14817	Oligonucleotide SE
C 317	9.4	42.7	13	1	ABH14817	Oligonucleotide SE
C 318	9.4	42.7	13	1	ABC72271	Oligonucleotide SE
C 319	9.4	42.7	13	1	ABC72902	Oligonucleotide SE
C 320	9.4	42.7	13	1	ABC83626	Oligonucleotide SE
C 321	9.4	42.7	13	1	ABC83626	Oligonucleotide SE
C 322	9.4	42.7	13	1	ABF56386	Oligonucleotide SE
C 323	9.4	42.7	13	1	ABF87396	Oligonucleotide SE
C 324	9.4	42.7	13	1	ABH50907	Oligonucleotide SE
C 325	9.4	42.7	13	1	ABC71283	Oligonucleotide SE

1	ABC72903	Oligonucleotide SE
1	ABC50422	Oligonucleotide SE
1	ABC68228	Oligonucleotide SE
1	ABC82728	Oligonucleotide SE
1	ABF30259	Oligonucleotide SE
1	ABH19619	Oligonucleotide SE
1	ABF50801	Oligonucleotide SE
1	ABH48837	Oligonucleotide SE
1	ABF75627	Oligonucleotide SE
1	ABF56510	Oligonucleotide SE
1	ABF72819	Rod opsin hammer
1	AAT76263	Human IL6 receptor
1	AAT76249	Human IL6 receptor
1	AAH54053	Human IL-6 recepto
1	AAH54039	Human IL-6 recepto
1	AAH54623	Endothelial moocy
1	AAH54623	Low adenosine anti
1	AAA33483	Human adenosine re
1	AAA34070	Low adenosine anti
1	AAA33497	Human endothelial
1	AAH20192	Human IL6 receptor
1	AAH19619	Human IL6 receptor
1	AAH19605	Human IL6 recepto
1	AAH55226	Modified end-block
1	AAH57799	Anisense oligonuc
1	AAH37793	RNA region of modi
1	AAH37793	Influenza C virus
1	ABQ75477	Influenza C, 3', co
1	ABK15512	Human IL-6 recepto
1	ABZ95399	Human monocyte act
1	ABZ95886	Human IL-6 recepto
1	ABZ95313	Human phosphodiect
1	ACF63279	Anisense oligonuc
1	AQ78386	Human nucleic acid
1	ABZ97154	Human nucleic acid
1	AAH19155	Human dendritic ce
1	AAH55188	Human dendritic ce
1	AAH79359	Metastatic breast
1	AAH28656	Human VTR1 intron9
1	AAH20544	Human DRD2 polymor
1	AAH70411	Yeast NORF gene SA
1	AAH42486	Primer-extension o
1	AAH19577	Colony stimulating
1	AAH98810	Mouse neuronal reg
1	ABL99040	Human LIPE gene po
1	ABK96032	Human FOS gene all
1	ABK81376	Human Th1 cell pre
1	ABV78423	Human FCDH2 ASO PC
1	ABH199152	CCBP2 detecting AS
1	AAH39543	Prostaglandin D sy
1	AAH54592	Human adenosine re
1	AAH34039	Human prostaglandi
1	AAH20161	Human skin stress/
1	ABQ86412	Human skin EST 959
1	ABV71807	Human skin EST 179
1	ABV62393	Human skin EST 760
1	ABV69814	Human skin EST 344
1	ABV65662	Human skin EST 344
1	ABV64386	Human skin EST 217
1	ABV64098	Human skin EST 188
1	ABV71519	Human skin EST 930
1	ABV7302	Human skin EST 508
1	ABA89897	ESR-alpha gene Liv
1	ABA89949	ESR-alpha gene Cor
1	ABZ95855	Human prostaglandi
1	AAA93388	DNA encoding proca
1	AAA93381	DNA encoding proca
1	AAH27581	DNA encoding proca
1	AAH27581	DNA encoding prote
1	ABS71506	DNA encoding prote

399	9	40.9	12	1	ABS71499	DNA encoding prote	C 472	8.8	40.0	12	1	ABI233606	Oligonucleotide pr
C 400	9	40.9	12	1	ALA46301	Human M33 protein	C 473	8.8	40.0	12	1	ABI30553	Oligonucleotide pr
C 401	9	40.9	12	1	ADC19373	Protease recogniti	C 474	8.8	40.0	12	1	ABI46968	Oligonucleotide pr
C 402	9	40.9	12	1	ADC19387	Protease recogniti	C 475	8.8	40.0	12	1	ABI67539	Oligonucleotide pr
C 403	9	40.9	13	1	ABF34134	Oligonucleotide SE	C 476	8.8	40.0	12	1	ABI65215	Oligonucleotide pr
C 404	9	40.9	13	1	ABF34135	Oligonucleotide SE	C 477	8.8	40.0	12	1	ABI23702	Oligonucleotide pr
C 405	9	40.9	13	1	ABF24040	Oligonucleotide SE	C 478	8.8	40.0	12	1	ABI47510	Oligonucleotide pr
C 406	9	40.9	13	1	ABC80017	Oligonucleotide SE	C 479	8.8	40.0	12	1	ABI26708	Oligonucleotide pr
C 407	9	40.9	13	1	ABF24041	Oligonucleotide SE	C 480	8.8	40.0	12	1	ABH81408	Oligonucleotide pr
C 408	9	40.9	13	1	ABC80016	Oligonucleotide SE	C 481	8.8	40.0	12	1	ABH81826	Oligonucleotide pr
C 409	9	40.9	13	1	ABF81152	Oligonucleotide SE	C 482	8.8	40.0	12	1	ABI08687	Oligonucleotide pr
C 410	9	40.9	13	1	ABF81154	Oligonucleotide SE	C 483	8.8	40.0	12	1	ABI15833	Oligonucleotide pr
C 411	9	40.9	13	1	ABF81155	Oligonucleotide SE	C 484	8.8	40.0	12	1	AA520481	Oligonucleotide us
C 412	9	40.9	13	1	ABH65494	Oligonucleotide SE	C 485	8.8	40.0	12	1	ADD71434	Stimulus-responsiv
C 413	9	40.9	13	1	ABC68266	Oligonucleotide SE	C 486	8.8	40.0	12	1	ABE14282	Optineurin promote
C 414	9	40.9	13	1	ABF34137	Oligonucleotide SE	C 487	8.8	40.0	13	1	AA79398	HLA-DR typing prob
C 415	9	40.9	13	1	ABF81153	Oligonucleotide SE	C 488	8.8	40.0	13	1	AAV06763	Target oligonucleo
C 416	9	40.9	13	1	ABC68267	Oligonucleotide SE	C 489	8.8	40.0	13	1	AAV42361	Transition point O
C 417	9	40.9	13	1	ABH65495	Oligonucleotide SE	C 490	8.8	40.0	13	1	AAV16594	Probe H30 used to
C 418	9	40.9	13	1	ABF34136	Oligonucleotide SE	C 491	8.8	40.0	13	1	AAV81348	Mouse agouti wild
C 419	8.8	40.0	12	1	AAA05941	Human XIAP IRES po	C 492	8.8	40.0	13	1	AA556464	Locked nucleoside
C 420	8.8	40.0	12	1	AAA05942	Human XIAP IRES w1	C 493	8.8	40.0	13	1	AA556496	Locked nucleoside
C 421	8.8	40.0	12	1	AAO65946	Oligonucleotide pr	C 494	8.8	40.0	13	1	AAA62335	Mouse wild-type ag
C 422	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 495	8.8	40.0	13	1	ABC76054	Oligonucleotide SE
C 423	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 496	8.8	40.0	13	1	ABC09298	Oligonucleotide SE
C 424	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 497	8.8	40.0	13	1	ABC09299	Oligonucleotide SE
C 425	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 498	8.8	40.0	13	1	ABC64866	Oligonucleotide SE
C 426	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 499	8.8	40.0	13	1	ABF24769	Oligonucleotide SE
C 427	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 500	8.8	40.0	13	1	ABF43128	Oligonucleotide SE
C 428	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 501	8.8	40.0	13	1	ABF43129	Oligonucleotide SE
C 429	8.8	40.0	12	1	ABH75798	Oligonucleotide pr	C 502	8.8	40.0	13	1	ABH02517	Oligonucleotide SE
C 430	8.8	40.0	12	1	ABH68614	Oligonucleotide pr	C 503	8.8	40.0	13	1	ABC48561	Oligonucleotide SE
C 431	8.8	40.0	12	1	ABH89478	Oligonucleotide pr	C 504	8.8	40.0	13	1	ABC24672	Oligonucleotide SE
C 432	8.8	40.0	12	1	ABH66990	Oligonucleotide pr	C 505	8.8	40.0	13	1	ABC76052	Oligonucleotide SE
C 433	8.8	40.0	12	1	ABH67357	Oligonucleotide pr	C 506	8.8	40.0	13	1	ABF07388	Oligonucleotide SE
C 434	8.8	40.0	12	1	ABH74521	Oligonucleotide pr	C 507	8.8	40.0	13	1	ABF07389	Oligonucleotide SE
C 435	8.8	40.0	12	1	ABH75098	Oligonucleotide pr	C 508	8.8	40.0	13	1	ABC82381	Oligonucleotide SE
C 436	8.8	40.0	12	1	ABH88943	Oligonucleotide pr	C 509	8.8	40.0	13	1	ABC37925	Oligonucleotide SE
C 437	8.8	40.0	12	1	ABH67468	Oligonucleotide pr	C 510	8.8	40.0	13	1	ABC64865	Oligonucleotide SE
C 438	8.8	40.0	12	1	ABH75557	Oligonucleotide pr	C 511	8.8	40.0	13	1	ABF23389	Oligonucleotide SE
C 439	8.8	40.0	12	1	ABH80821	Oligonucleotide pr	C 512	8.8	40.0	13	1	ABH19990	Oligonucleotide SE
C 440	8.8	40.0	12	1	ABH22903	Oligonucleotide pr	C 513	8.8	40.0	13	1	ABF48664	Oligonucleotide SE
C 441	8.8	40.0	12	1	ABH76378	Oligonucleotide pr	C 514	8.8	40.0	13	1	ABF73772	Oligonucleotide SE
C 442	8.8	40.0	12	1	ABH01710	Oligonucleotide pr	C 515	8.8	40.0	13	1	ABF82673	Oligonucleotide SE
C 443	8.8	40.0	12	1	ABH73881	Oligonucleotide pr	C 516	8.8	40.0	13	1	ABH40261	Oligonucleotide SE
C 444	8.8	40.0	12	1	ABH04383	Oligonucleotide pr	C 517	8.8	40.0	13	1	ABH41118	Oligonucleotide SE
C 445	8.8	40.0	12	1	ABH79549	Oligonucleotide pr	C 518	8.8	40.0	13	1	ABC24673	Oligonucleotide SE
C 446	8.8	40.0	12	1	ABH07767	Oligonucleotide pr	C 519	8.8	40.0	13	1	ABC29854	Oligonucleotide SE
C 447	8.8	40.0	12	1	ABH33484	Oligonucleotide pr	C 520	8.8	40.0	13	1	ABF23388	Oligonucleotide SE
C 448	8.8	40.0	12	1	ABH53341	Oligonucleotide pr	C 521	8.8	40.0	13	1	ABH29482	Oligonucleotide SE
C 449	8.8	40.0	12	1	ABH17388	Oligonucleotide pr	C 522	8.8	40.0	13	1	ABH29485	Oligonucleotide SE
C 450	8.8	40.0	12	1	ABH05566	Oligonucleotide pr	C 523	8.8	40.0	13	1	ABF59006	Oligonucleotide SE
C 451	8.8	40.0	12	1	ABH84329	Oligonucleotide pr	C 524	8.8	40.0	13	1	ABH40262	Oligonucleotide SE
C 452	8.8	40.0	12	1	ABH16214	Oligonucleotide pr	C 525	8.8	40.0	13	1	ABC48960	Oligonucleotide SE
C 453	8.8	40.0	12	1	ABH17624	Oligonucleotide pr	C 526	8.8	40.0	13	1	ABC37924	Oligonucleotide SE
C 454	8.8	40.0	12	1	ABH70326	Oligonucleotide pr	C 527	8.8	40.0	13	1	ABC79247	Oligonucleotide SE
C 455	8.8	40.0	12	1	ABH11213	Oligonucleotide pr	C 528	8.8	40.0	13	1	ABF27769	Oligonucleotide SE
C 456	8.8	40.0	12	1	ABH12547	Oligonucleotide pr	C 529	8.8	40.0	13	1	ABF39592	Oligonucleotide SE
C 457	8.8	40.0	12	1	ABH25965	Oligonucleotide pr	C 530	8.8	40.0	13	1	ABH25372	Oligonucleotide SE
C 458	8.8	40.0	12	1	ABH48399	Oligonucleotide pr	C 531	8.8	40.0	13	1	ABH02516	Oligonucleotide SE
C 459	8.8	40.0	12	1	ABH30861	Oligonucleotide pr	C 532	8.8	40.0	13	1	ABH2516	Oligonucleotide SE
C 460	8.8	40.0	12	1	ABH86305	Oligonucleotide pr	C 533	8.8	40.0	13	1	ABH82574	Oligonucleotide SE
C 461	8.8	40.0	12	1	ABH72010	Oligonucleotide pr	C 534	8.8	40.0	13	1	ABH42798	Oligonucleotide SE
C 462	8.8	40.0	12	1	ABH659747	Oligonucleotide pr	C 535	8.8	40.0	13	1	ABH43252	Oligonucleotide SE
C 463	8.8	40.0	12	1	ABH97184	Oligonucleotide pr	C 536	8.8	40.0	13	1	ABH53941	Oligonucleotide SE
C 464	8.8	40.0	12	1	ABH98666	Oligonucleotide pr	C 537	8.8	40.0	13	1	ABH54081	Oligonucleotide SE
C 465	8.8	40.0	12	1	ABH08983	Oligonucleotide pr	C 538	8.8	40.0	13	1	ABC94297	Oligonucleotide SE
C 466	8.8	40.0	12	1	ABH47139	Oligonucleotide pr	C 539	8.8	40.0	13	1	ABC23145	Oligonucleotide SE
C 467	8.8	40.0	12	1	ABH58619	Oligonucleotide pr	C 540	8.8	40.0	13	1	ABC06154	Oligonucleotide SE
C 468	8.8	40.0	12	1	ABH70467	Oligonucleotide pr	C 541	8.8	40.0	13	1	ABC82380	Oligonucleotide SE
C 469	8.8	40.0	12	1	ABH71132	Oligonucleotide pr	C 542	8.8	40.0	13	1	ABF30658	Oligonucleotide SE
C 470	8.8	40.0	12	1	ABH44609	Oligonucleotide pr	C 543	8.8	40.0	13	1	ABH19407	Oligonucleotide SE
C 471	8.8	40.0	12	1	ABH7498	Oligonucleotide pr	C 544	8.8	40.0	13	1	ABH02515	Oligonucleotide SE

545	8.8	40.0	13	1	ABH42937	Oligonucleotide SE
546	8.8	40.0	13	1	ABH42938	Oligonucleotide SE
547	8.8	40.0	13	1	ABH49474	Oligonucleotide SE
548	8.8	40.0	13	1	ABC32956	Oligonucleotide SE
549	8.8	40.0	13	1	ABC87410	Oligonucleotide SE
550	8.8	40.0	13	1	ABH42939	Oligonucleotide SE
551	8.8	40.0	13	1	ABH48475	Oligonucleotide SE
552	8.8	40.0	13	1	ABH50480	Oligonucleotide SE
553	8.8	40.0	13	1	ABC01518	Oligonucleotide SE
554	8.8	40.0	13	1	ABC01519	Oligonucleotide SE
555	8.8	40.0	13	1	ABC29855	Oligonucleotide SE
556	8.8	40.0	13	1	ABC07303	Oligonucleotide SE
557	8.8	40.0	13	1	ABC09300	Oligonucleotide SE
558	8.8	40.0	13	1	ABC87411	Oligonucleotide SE
559	8.8	40.0	13	1	ABH24319	Oligonucleotide SE
560	8.8	40.0	13	1	ABF49924	Oligonucleotide SE
561	8.8	40.0	13	1	ABF56045	Oligonucleotide SE
562	8.8	40.0	13	1	ABH33790	Oligonucleotide SE
563	8.8	40.0	13	1	ABH34756	Oligonucleotide SE
564	8.8	40.0	13	1	ABC94294	Oligonucleotide SE
565	8.8	40.0	13	1	ABC06155	Oligonucleotide SE
566	8.8	40.0	13	1	ABC37605	Oligonucleotide SE
567	8.8	40.0	13	1	ABF24592	Oligonucleotide SE
568	8.8	40.0	13	1	ABF41880	Oligonucleotide SE
569	8.8	40.0	13	1	ABF41881	Oligonucleotide SE
570	8.8	40.0	13	1	ABC27868	Oligonucleotide SE
571	8.8	40.0	13	1	ABC32873	Oligonucleotide SE
572	8.8	40.0	13	1	ABC09301	Oligonucleotide SE
573	8.8	40.0	13	1	ABC59860	Oligonucleotide SE
574	8.8	40.0	13	1	ABF27768	Oligonucleotide SE
575	8.8	40.0	13	1	ABF48665	Oligonucleotide SE
576	8.8	40.0	13	1	ABH24318	Oligonucleotide SE
577	8.8	40.0	13	1	ABH40263	Oligonucleotide SE
578	8.8	40.0	13	1	ABH41119	Oligonucleotide SE
579	8.8	40.0	13	1	ABC67855	Oligonucleotide SE
580	8.8	40.0	13	1	ABC94296	Oligonucleotide SE
581	8.8	40.0	13	1	ABC69697	Oligonucleotide SE
582	8.8	40.0	13	1	ABC76055	Oligonucleotide SE
583	8.8	40.0	13	1	ABC55567	Oligonucleotide SE
584	8.8	40.0	13	1	ABC07302	Oligonucleotide SE
585	8.8	40.0	13	1	ABC88808	Oligonucleotide SE
586	8.8	40.0	13	1	ABF24593	Oligonucleotide SE
587	8.8	40.0	13	1	ABF73773	Oligonucleotide SE
588	8.8	40.0	13	1	ABH25373	Oligonucleotide SE
589	8.8	40.0	13	1	ABF56044	Oligonucleotide SE
590	8.8	40.0	13	1	ABH10380	Oligonucleotide SE
591	8.8	40.0	13	1	ABH36000	Oligonucleotide SE
592	8.8	40.0	13	1	ABH40260	Oligonucleotide SE
593	8.8	40.0	13	1	ABH42948	Oligonucleotide SE
594	8.8	40.0	13	1	ABC39716	Oligonucleotide SE
595	8.8	40.0	13	1	ABC64867	Oligonucleotide SE
596	8.8	40.0	13	1	ABH29484	Oligonucleotide SE
597	8.8	40.0	13	1	ABF82672	Oligonucleotide SE
598	8.8	40.0	13	1	ABH40318	Oligonucleotide SE
599	8.8	40.0	13	1	ABH40319	Oligonucleotide SE
600	8.8	40.0	13	1	ABH49233	Oligonucleotide SE
601	8.8	40.0	13	1	ABH53840	Oligonucleotide SE
602	8.8	40.0	13	1	ABC67854	Oligonucleotide SE
603	8.8	40.0	13	1	ABH19405	Oligonucleotide SE
604	8.8	40.0	13	1	ABH42799	Oligonucleotide SE
605	8.8	40.0	13	1	ABH42949	Oligonucleotide SE
606	8.8	40.0	13	1	ABC76053	Oligonucleotide SE
607	8.8	40.0	13	1	ABC59861	Oligonucleotide SE
608	8.8	40.0	13	1	ABC39717	Oligonucleotide SE
609	8.8	40.0	13	1	ABF24768	Oligonucleotide SE
610	8.8	40.0	13	1	ABH19991	Oligonucleotide SE
611	8.8	40.0	13	1	ABF49925	Oligonucleotide SE
612	8.8	40.0	13	1	ABH29483	Oligonucleotide SE
613	8.8	40.0	13	1	ABF59007	Oligonucleotide SE
614	8.8	40.0	13	1	ABH36001	Oligonucleotide SE
615	8.8	40.0	13	1	ABC69696	Oligonucleotide SE
616	8.8	40.0	13	1	ABC55566	Oligonucleotide SE
617	8.8	40.0	13	1	ABC31753	Oligonucleotide SE
1	ABH02514		13	1		Oligonucleotide SE
1	ABF82675		13	1		Oligonucleotide SE
1	ABH49232		13	1		Oligonucleotide SE
1	ABC23144		13	1		Oligonucleotide SE
1	ABC37604		13	1		Oligonucleotide SE
1	ABC64864		13	1		Oligonucleotide SE
1	ABH42936		13	1		Oligonucleotide SE
1	ABC94295		13	1		Oligonucleotide SE
1	ABC27869		13	1		Oligonucleotide SE
1	ABC31752		13	1		Oligonucleotide SE
1	ABC32872		13	1		Oligonucleotide SE
1	ABC88809		13	1		Oligonucleotide SE
1	ABF30859		13	1		Oligonucleotide SE
1	ABF39593		13	1		Oligonucleotide SE
1	ABH19404		13	1		Oligonucleotide SE
1	ABH19406		13	1		Oligonucleotide SE
1	ABH33791		13	1		Oligonucleotide SE
1	ABH10381		13	1		Oligonucleotide SE
1	ABH43253		13	1		Oligonucleotide SE
1	AA928554		13	1		HLA-DR typing prob
1	AA517271		13	1		Exon1-exon2 Juncti
1	ABX11332		13	1		Wild-type human ag
1	ADH14088		13	1		Optineurin promote
1	ABF45517		13	1		Oligonucleotide SE
1	ABF45516		13	1		Oligonucleotide SE
1	ABF48368		13	1		Oligonucleotide SE
1	ABF16962		13	1		Oligonucleotide SE
1	ABF48369		13	1		Oligonucleotide SE
1	ABF16963		13	1		Oligonucleotide SE
1	AA137783		13	1		Oligonucleotide SE
1	ABQ75466		13	1		Influenza virus B
1	ABX15502		13	1		Wild type influenz
1	AO96882		13	1		HIV-1 NL4-3 nef ge
1	AAZ78747		10	1		Human dendritic ce
1	AAZ78748		10	1		Human dendritic ce
1	AAZ77903		10	1		Metastatic breast
1	AAZ81993		10	1		Metastatic breast
1	AAZ80828		10	1		Metastatic breast
1	AAZ83448		10	1		Metastatic breast
1	AAZ81077		10	1		Metastatic breast
1	AAZ81577		10	1		Metastatic breast
1	AAZ81330		10	1		Metastatic breast
1	AAZ81855		10	1		Metastatic breast
1	AAZ82611		10	1		Metastatic breast
1	AAZ82802		10	1		Metastatic breast
1	AAZ86557		10	1		Metastatic breast
1	AAZ74106		10	1		Human dendritic ce
1	AAH63394		10	1		Human ubiquitously
1	AAH64523		10	1		Human ubiquitously
1	AAH64453		10	1		Human SLC6A4 allel
1	AAH74014		10	1		eIF-2-associated p
1	ABA83142		10	1		Yeast NORF gene SA
1	AAH35790		10	1		Yeast NORF gene SA
1	AAH43163		10	1		Yeast NORF gene SA
1	AAH43395		10	1		Yeast NORF gene SA
1	AAH43736		10	1		Yeast NORF gene SA
1	AAH40688		10	1		Yeast NORF gene SA
1	AAH38499		10	1		Yeast NORF gene SA
1	AAH37393		10	1		Yeast NORF gene SA
1	AAH38223		10	1		Yeast NORF gene SA
1	AAH42636		10	1		Yeast NORF gene SA
1	AAH42385		10	1		Yeast NORF gene SA
1	AAH35570		10	1		Yeast NORF gene SA
1	AAH41687		10	1		Human MMP3 gene po
1	ABL01295		10	1		Human MMP3 gene po
1	ABL01310		10	1		Human maturation/a
1	ABL42763		10	1		Primer-extension o
1	AAH44466		10	1		Human methionine a
1	ABV84410		10	1		Human methionine a
1	ABV84609		10	1		Human DKG2P5861102
1	ABV84344		10	1		Human ARG energy m
1	AAH60146		10	1		Human skin stress/
1	ABQ86777		11	1		

C 691	8.4	38.2	11	1	ABQ86292	Human skin stress/	764	8.4	38.2	12	1	ABI05037	Oligonucleotide pr
C 692	8.4	38.2	11	1	ABQ86858	Human skin stress/	765	8.4	38.2	12	1	ABI07062	Oligonucleotide pr
C 693	8.4	38.2	11	1	ABQ86986	Human skin stress/	C 766	8.4	38.2	12	1	ABH84195	Oligonucleotide pr
C 694	8.4	38.2	11	1	ABQ86782	Human skin stress/	767	8.4	38.2	12	1	ABH87477	Oligonucleotide pr
C 695	8.4	38.2	11	1	ABV68185	Human skin EST 597	C 768	8.4	38.2	12	1	ABH13642	Oligonucleotide pr
C 696	8.4	38.2	11	1	ABV65377	Human skin EST 316	C 769	8.4	38.2	12	1	ABH90374	Oligonucleotide pr
C 697	8.4	38.2	11	1	ABV71340	Human skin EST 912	770	8.4	38.2	12	1	ABJ57707	Oligonucleotide pr
C 698	8.4	38.2	11	1	ABV64226	Human skin EST 201	C 771	8.4	38.2	12	1	ABI30960	Oligonucleotide pr
C 699	8.4	38.2	11	1	ABV70263	Human skin EST 804	772	8.4	38.2	12	1	ABI34891	Oligonucleotide pr
C 700	8.4	38.2	11	1	ABV67021	Human skin EST 480	773	8.4	38.2	12	1	ABI11095	Oligonucleotide pr
C 701	8.4	38.2	11	1	ABV62887	Human skin EST 673	774	8.4	38.2	12	1	ABI36833	Oligonucleotide pr
C 702	8.4	38.2	11	1	ABV63919	Human skin EST 170	775	8.4	38.2	12	1	ABH87388	Oligonucleotide pr
C 703	8.4	38.2	11	1	ABV66596	Human skin EST 438	776	8.4	38.2	12	1	ABI14255	Oligonucleotide pr
C 704	8.4	38.2	11	1	ABV63295	Human skin EST 708	C 777	8.4	38.2	12	1	ABI17022	Oligonucleotide pr
C 705	8.4	38.2	11	1	ABV62842	Human skin EST 628	C 778	8.4	38.2	12	1	ABI67389	Oligonucleotide pr
C 706	8.4	38.2	11	1	ABV67553	Human skin EST 533	779	8.4	38.2	12	1	ABI77598	Oligonucleotide pr
C 707	8.4	38.2	11	1	ABV71647	Human skin EST 943	C 780	8.4	38.2	12	1	ABH95015	Oligonucleotide pr
C 708	8.4	38.2	11	1	ABV68446	Human skin EST 623	C 781	8.4	38.2	12	1	ABH80275	Oligonucleotide pr
C 709	8.4	38.2	11	1	ABV66482	Human skin EST 426	C 782	8.4	38.2	12	1	ABI13568	Oligonucleotide pr
C 710	8.4	38.2	11	1	ABV69554	Human skin EST 734	C 783	8.4	38.2	12	1	ABI13570	Oligonucleotide pr
C 711	8.4	38.2	11	1	ABV70308	Human skin EST 809	C 784	8.4	38.2	12	1	ABI69013	Oligonucleotide pr
C 712	8.4	38.2	12	1	AAV39563	Mass spectrometric	C 785	8.4	38.2	12	1	ABI78823	Oligonucleotide pr
C 713	8.4	38.2	12	1	AAV39558	Antisense 12-chain	C 786	8.4	38.2	12	1	ABH73493	Oligonucleotide pr
C 714	8.4	38.2	12	1	AAV19666	12-mer oligonucleo	787	8.4	38.2	12	1	ABH76898	Oligonucleotide pr
C 715	8.4	38.2	12	1	AAV19669	Promoter p13H2 tra	788	8.4	38.2	12	1	ABI29029	Oligonucleotide pr
C 716	8.4	38.2	12	1	AAH87791	Human XIAP IRES mu	C 789	8.4	38.2	12	1	ABI06481	Oligonucleotide pr
C 717	8.4	38.2	12	1	AAO69594	Oligonucleotide co	C 790	8.4	38.2	12	1	ABI16605	Oligonucleotide pr
C 718	8.4	38.2	12	1	AAV91860	Oligonucleotide A	C 791	8.4	38.2	12	1	ABI45554	Oligonucleotide pr
C 719	8.4	38.2	12	1	AAV91863	Oligonucleotide pr	792	8.4	38.2	12	1	ABI70289	Oligonucleotide pr
C 720	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 793	8.4	38.2	12	1	ABH70967	Oligonucleotide pr
C 721	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 794	8.4	38.2	12	1	ABH97274	Oligonucleotide pr
C 722	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	795	8.4	38.2	12	1	ABH72613	Oligonucleotide pr
C 723	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 796	8.4	38.2	12	1	ABI49158	Oligonucleotide pr
C 724	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 797	8.4	38.2	12	1	ABI52327	Oligonucleotide pr
C 725	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 798	8.4	38.2	12	1	ABI70863	Oligonucleotide pr
C 726	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	799	8.4	38.2	12	1	ABI57396	Oligonucleotide pr
C 727	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 800	8.4	38.2	12	1	ABH92353	Oligonucleotide pr
C 728	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 801	8.4	38.2	12	1	ABH70419	Oligonucleotide pr
C 729	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 802	8.4	38.2	12	1	ABH74364	Oligonucleotide pr
C 730	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 803	8.4	38.2	12	1	ABH79493	Oligonucleotide pr
C 731	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 804	8.4	38.2	12	1	ABI32451	Oligonucleotide pr
C 732	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 805	8.4	38.2	12	1	ABH89176	Oligonucleotide pr
C 733	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 806	8.4	38.2	12	1	ABI17825	Oligonucleotide pr
C 734	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 807	8.4	38.2	12	1	ABI18090	Oligonucleotide pr
C 735	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 808	8.4	38.2	12	1	ABI23297	Oligonucleotide pr
C 736	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 809	8.4	38.2	12	1	ABI25971	Oligonucleotide pr
C 737	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 810	8.4	38.2	12	1	ABI10323	Oligonucleotide pr
C 738	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 811	8.4	38.2	12	1	ABH88014	Oligonucleotide pr
C 739	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 812	8.4	38.2	12	1	ABI38684	Oligonucleotide pr
C 740	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 813	8.4	38.2	12	1	ABI14975	Oligonucleotide pr
C 741	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 814	8.4	38.2	12	1	ABH92293	Oligonucleotide pr
C 742	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 815	8.4	38.2	12	1	ABI45553	Oligonucleotide pr
C 743	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 816	8.4	38.2	12	1	ABI73813	Oligonucleotide pr
C 744	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 817	8.4	38.2	12	1	ABI181805	Oligonucleotide pr
C 745	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 818	8.4	38.2	12	1	ABI28482	Oligonucleotide pr
C 746	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 819	8.4	38.2	12	1	ABH85326	Oligonucleotide pr
C 747	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 820	8.4	38.2	12	1	ABI15309	Oligonucleotide pr
C 748	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 821	8.4	38.2	12	1	ABI40624	Oligonucleotide pr
C 749	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 822	8.4	38.2	12	1	ABI42417	Oligonucleotide pr
C 750	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 823	8.4	38.2	12	1	ABI51839	Oligonucleotide pr
C 751	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 824	8.4	38.2	12	1	ABI55800	Oligonucleotide pr
C 752	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 825	8.4	38.2	12	1	ABI73488	Oligonucleotide pr
C 753	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 826	8.4	38.2	12	1	ABI705036	Oligonucleotide pr
C 754	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 827	8.4	38.2	12	1	ABI08156	Oligonucleotide pr
C 755	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 828	8.4	38.2	12	1	ABI59320	Oligonucleotide pr
C 756	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 829	8.4	38.2	12	1	AAV07924	Human transcriptio
C 757	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 830	8.4	38.2	12	1	AAV07921	Human transcriptio
C 758	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 831	8.4	38.2	12	1	ABA05981	HSV-1 antisense ol
C 759	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 832	8.4	38.2	12	1	ABA05984	HSV-1 antisense ol
C 760	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 833	8.4	38.2	12	1	AAK99268	P15B4 promoter tra
C 761	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 834	8.4	38.2	12	1	AAK99265	P13H2 promoter tra
C 762	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 835	8.4	36.4	8	1	AAK29674	Primer for human D
C 763	8.4	38.2	12	1	ABH72592	Oligonucleotide pr	C 836	8.4	36.4	8	1	ADE14111	Optineurin promote

837	8	36.4	10	1	AAO96884	HIV-1 NL4-3 nef ge	C 910	1	ABV71634	Human skin EST 942
838	8	36.4	10	1	AAO96883	HIV-1 NL4-3 nef ge	C 911	11	ABV64213	Human skin EST 199
839	8	36.4	10	1	AAZ78109	Human dendritic ce	C 912	11	ABV64254	Human skin EST 204
840	8	36.4	10	1	AAZ80857	Metastatic breast	C 913	11	ABV65855	Human skin EST 344
841	8	36.4	10	1	AAZ82836	Metastatic breast	C 914	11	ABL91967	Human Pan-Endothel
842	8	36.4	10	1	AAZ82679	Metastatic breast	C 915	11	ABQ81877	Kaposi's Sarcoma S
843	8	36.4	10	1	AAZ81170	Metastatic breast	C 916	11	ABQ71892	DNA tag used to id
844	8	36.4	10	1	AAZ85201	Metastatic breast	C 917	12	ABX71892	Kaposi's Sarcoma S
845	8	36.4	10	1	AAZ81797	Metastatic breast	C 918	12	AAZ81797	Antisense oligonuc
846	8	36.4	10	1	AAZ83594	Metastatic breast	C 919	12	AAZ83594	Antisense oligonuc
847	8	36.4	10	1	AAZ82358	Metastatic breast	C 920	12	AAZ82358	Triple helix third
848	8	36.4	10	1	AAZ83845	Metastatic breast	C 921	12	ABH74751	Oligonucleotide pr
849	8	36.4	10	1	AAZ81230	Metastatic breast	C 922	12	ABH74751	Oligonucleotide pr
850	8	36.4	10	1	AAZ85663	Metastatic breast	C 923	12	ABH74751	Oligonucleotide pr
851	8	36.4	10	1	AAH63186	Human colon epithe	C 924	12	ABH74751	Oligonucleotide pr
852	8	36.4	10	1	AAH63245	Human colon epithe	C 925	12	ABH74751	Oligonucleotide pr
853	8	36.4	10	1	AAH63239	Human colon epithe	C 926	12	ABH74751	Oligonucleotide pr
854	8	36.4	10	1	AAH64481	Human colon epithe	C 927	12	ABH74751	Oligonucleotide pr
855	8	36.4	10	1	AAH63237	Human colon epithe	C 928	12	ABH74751	Oligonucleotide pr
856	8	36.4	10	1	AAF37890	Yeast NORF gene SA	C 929	12	ABH74751	Oligonucleotide pr
857	8	36.4	10	1	AAF35950	Yeast NORF gene SA	C 930	12	ABH74751	Oligonucleotide pr
858	8	36.4	10	1	AAF41069	Yeast NORF gene SA	C 931	12	ABH74751	Oligonucleotide pr
859	8	36.4	10	1	AAF38498	Yeast NORF gene SA	C 932	12	ABH74751	Oligonucleotide pr
860	8	36.4	10	1	AAF38885	Yeast NORF gene SA	C 933	12	ABH74751	Oligonucleotide pr
861	8	36.4	10	1	AAF33978	Yeast NORF gene SA	C 934	12	ABH74751	Oligonucleotide pr
862	8	36.4	10	1	AAF35089	Yeast NORF gene SA	C 935	12	ABH74751	Oligonucleotide pr
863	8	36.4	10	1	ABK24254	Retinaldehyde-bind	C 936	12	ABH74751	Oligonucleotide pr
864	8	36.4	10	1	ABK69700	Human SCVA2 gene a	C 937	12	ABH74751	Oligonucleotide pr
865	8	36.4	10	1	ABL42788	Human maturation/a	C 938	12	ABH74751	Oligonucleotide pr
866	8	36.4	10	1	AAZ48074	Human CSF3 gene al	C 939	12	ABH74751	Oligonucleotide pr
867	8	36.4	10	1	ABV93817	Human PRKBF2 PCR p	C 940	12	ABH74751	Oligonucleotide pr
868	8	36.4	10	1	ABV78493	Human COP9 SAGE ta	C 941	12	ABH74751	Oligonucleotide pr
869	8	36.4	10	1	ABK23469	Transcript tag DNA	C 942	12	ABH74751	Oligonucleotide pr
870	8	36.4	10	1	ABK96609	Human interleukin	C 943	12	ABH74751	Oligonucleotide pr
871	8	36.4	10	1	ABK96611	Human interleukin	C 944	12	ABH74751	Oligonucleotide pr
872	8	36.4	10	1	AAZ19962	Primer-extension o	C 945	12	ABH74751	Oligonucleotide pr
873	8	36.4	10	1	AAZ43004	Human cerberus 1 (C 946	12	ABH74751	Oligonucleotide pr
874	8	36.4	10	1	ABL45804	Human MMP13 gene a	C 947	12	ABH74751	Oligonucleotide pr
875	8	36.4	10	1	ABN81268	Oligonucleotide pr	C 948	12	ABH74751	Oligonucleotide pr
876	8	36.4	10	1	ACC78771	Normal estrogen re	C 949	12	ABH74751	Oligonucleotide pr
877	8	36.4	10	1	AAZ58112	Leader DNA #2 used	C 950	12	ABH74751	Oligonucleotide pr
878	8	36.4	10	1	ADD71433	Stimulus-responsiv	C 951	12	ABH74751	Oligonucleotide pr
879	8	36.4	10	1	AAZ82244	DNA sequence that	C 952	12	ABH74751	Oligonucleotide pr
880	8	36.4	10	1	ABA01034	Mutational DNA exo	C 953	12	ABH74751	Oligonucleotide pr
881	8	36.4	10	1	AAZ05724	Polypyrimidine-ric	C 954	12	ABH74751	Oligonucleotide pr
882	8	36.4	10	1	AAZ05726	Polypyrimidine-ric	C 955	12	ABH74751	Oligonucleotide pr
883	8	36.4	10	1	AAZ164929	Human Cream prote	C 956	12	ABH74751	Oligonucleotide pr
884	8	36.4	10	1	ABQ87632	Human skin stress/	C 957	12	ABH74751	Oligonucleotide pr
885	8	36.4	10	1	ABQ85959	Human skin stress/	C 958	12	ABH74751	Oligonucleotide pr
886	8	36.4	10	1	ABQ86697	Human skin stress/	C 959	12	ABH74751	Oligonucleotide pr
887	8	36.4	10	1	ABV68978	Human skin EST 476	C 960	12	ABH74751	Oligonucleotide pr
888	8	36.4	10	1	ABV70231	Human skin EST 801	C 961	12	ABH74751	Oligonucleotide pr
889	8	36.4	10	1	ABV71675	Human skin EST 946	C 962	12	ABH74751	Oligonucleotide pr
890	8	36.4	10	1	ABV67502	Human skin EST 528	C 963	12	ABH74751	Oligonucleotide pr
891	8	36.4	10	1	ABV67881	Human skin EST 566	C 964	12	ABH74751	Oligonucleotide pr
892	8	36.4	10	1	ABV71609	Human skin EST 939	C 965	12	ABH74751	Oligonucleotide pr
893	8	36.4	10	1	ABV64703	Human skin EST 248	C 966	12	ABH74751	Oligonucleotide pr
894	8	36.4	10	1	ABV65140	Human skin EST 292	C 967	12	ABH74751	Oligonucleotide pr
895	8	36.4	10	1	ABV62451	Human skin EST 237	C 968	12	ABH74751	Oligonucleotide pr
896	8	36.4	10	1	ABV64507	Human skin EST 229	C 969	12	ABH74751	Oligonucleotide pr
897	8	36.4	10	1	ABV62810	Human skin EST 596	C 970	12	ABH74751	Oligonucleotide pr
898	8	36.4	10	1	ABV65528	Human skin EST 331	C 971	12	ABH74751	Oligonucleotide pr
899	8	36.4	10	1	ABV68871	Human skin EST 665	C 972	12	ABH74751	Oligonucleotide pr
900	8	36.4	10	1	ABV69872	Human skin EST 765	C 973	12	ABH74751	Oligonucleotide pr
901	8	36.4	10	1	ABV66245	Human skin EST 403	C 974	12	ABH74751	Oligonucleotide pr
902	8	36.4	10	1	ABV64188	Human skin EST 197	C 975	12	ABH74751	Oligonucleotide pr
903	8	36.4	10	1	ABV69727	Human skin EST 751	C 976	12	ABH74751	Oligonucleotide pr
904	8	36.4	10	1	ABV66934	Human skin EST 472	C 977	12	ABH74751	Oligonucleotide pr
905	8	36.4	10	1	ABV71928	Human skin EST 971	C 978	12	ABH74751	Oligonucleotide pr
906	8	36.4	10	1	ABV62306	Human skin EST 92	C 979	12	ABH74751	Oligonucleotide pr
907	8	36.4	10	1	ABV67368	Human skin EST 515	C 980	12	ABH74751	Oligonucleotide pr
908	8	36.4	10	1	ABV68010	Human skin EST 579	C 981	12	ABH74751	Oligonucleotide pr
909	8	36.4	10	1	ABV68605	Human skin EST 639	C 982	12	ABH74751	Oligonucleotide pr

983	7.8	35.5	11	1	ABV70065	Human skin EST 785	1056	7.8	35.5	12	1	AB112030	Oligonucleotide pr
984	7.8	35.5	11	1	ABV71919	Human skin EST 970	c1057	7.8	35.5	12	1	AB145744	Oligonucleotide pr
985	7.8	35.5	11	1	ABV62644	Human skin EST 430	1058	7.8	35.5	12	1	AB156179	Oligonucleotide pr
c 986	7.8	35.5	11	1	ABV61108	Human skin EST 389	c1059	7.8	35.5	12	1	AB171623	Oligonucleotide pr
987	7.8	35.5	11	1	ABV65524	Human skin EST 431	1060	7.8	35.5	12	1	AB160839	Oligonucleotide pr
c 988	7.8	35.5	11	1	ABV69076	Human skin EST 686	c1061	7.8	35.5	12	1	AB118875	Oligonucleotide pr
989	7.8	35.5	11	1	ABV68102	Human skin EST 588	1062	7.8	35.5	12	1	ABH69811	Oligonucleotide pr
990	7.8	35.5	11	1	ABV68680	Human skin EST 646	c1063	7.8	35.5	12	1	ABH96375	Oligonucleotide pr
991	7.8	35.5	11	1	ABV69886	Human skin EST 767	1064	7.8	35.5	12	1	ABH71578	Oligonucleotide pr
992	7.8	35.5	11	1	ABV62465	Human skin EST 251	c1065	7.8	35.5	12	1	ABH98926	Oligonucleotide pr
c 993	7.8	35.5	11	1	ABV65390	Human skin EST 317	c1066	7.8	35.5	12	1	ABH75639	Oligonucleotide pr
994	7.8	35.5	11	1	ABV70491	Human skin EST 827	1067	7.8	35.5	12	1	ABH75709	Oligonucleotide pr
995	7.8	35.5	11	1	ABV71042	Human skin EST 882	c1068	7.8	35.5	12	1	ABH77101	Oligonucleotide pr
996	7.8	35.5	11	1	AB191951	Human Pan-Endothel	1069	7.8	35.5	12	1	ABH77342	Oligonucleotide pr
c 997	7.8	35.5	11	1	AB295864	Human eosinophil d	1070	7.8	35.5	12	1	ABH78437	Oligonucleotide pr
998	7.8	35.5	11	1	ABX71876	DNA tag used to id	c1071	7.8	35.5	12	1	AB129767	Oligonucleotide pr
999	7.8	35.5	11	1	ACA61506	Modified promoter	1072	7.8	35.5	12	1	AB131517	Oligonucleotide pr
1000	7.8	35.5	11	1	ACA61501	Modified promoter	c1073	7.8	35.5	12	1	ABH81430	Oligonucleotide pr
1001	7.8	35.5	12	1	AAQ80191	Sequence of probe/	c1074	7.8	35.5	12	1	ABH84641	Oligonucleotide pr
c1002	7.8	35.5	12	1	AAQ88668	Human mitochondria	c1075	7.8	35.5	12	1	ABH10189	Oligonucleotide pr
1003	7.8	35.5	12	1	AAT11908	Antisense DNA to i	1076	7.8	35.5	12	1	ABH11030	Oligonucleotide pr
1004	7.8	35.5	12	1	AAV05933	Translation rate c	c1077	7.8	35.5	12	1	ABH86856	Oligonucleotide pr
c1005	7.8	35.5	12	1	AAT63016	TNF-alpha mRNA ser	c1078	7.8	35.5	12	1	ABH86857	Oligonucleotide pr
1006	7.8	35.5	12	1	AAV53018	CCR-5 gene targeti	c1079	7.8	35.5	12	1	ABH39657	Oligonucleotide pr
1007	7.8	35.5	12	1	AAV16650	Probe H30 used to	1080	7.8	35.5	12	1	ABH91152	Oligonucleotide pr
1008	7.8	35.5	12	1	AAQ08771	Antioxidant respon	c1081	7.8	35.5	12	1	AB141426	Oligonucleotide pr
1009	7.8	35.5	12	1	AAQ14842	Triple helix formi	c1082	7.8	35.5	12	1	AB116969	Oligonucleotide pr
1010	7.8	35.5	12	1	AAQ14964	Triple helix formi	c1083	7.8	35.5	12	1	ABH67263	Oligonucleotide pr
1011	7.8	35.5	12	1	AAQ14828	Triple helix formi	1084	7.8	35.5	12	1	AB142846	Oligonucleotide pr
1012	7.8	35.5	12	1	AAQ22069	Probe analyte #1.	c1085	7.8	35.5	12	1	AB167458	Oligonucleotide pr
1013	7.8	35.5	12	1	AAQ93283	DNA encoding caspa	c1086	7.8	35.5	12	1	AB168462	Oligonucleotide pr
1014	7.8	35.5	12	1	AAQ0712	VSGF derived short	c1087	7.8	35.5	12	1	AB168928	Oligonucleotide pr
1015	7.8	35.5	12	1	AAQ27583	DNA encoding caspa	1088	7.8	35.5	12	1	AB157057	Oligonucleotide pr
c1016	7.8	35.5	12	1	AAQ82229	pp32 upstream cons	c1089	7.8	35.5	12	1	AB172322	Oligonucleotide pr
1017	7.8	35.5	12	1	AAQ20822	Complex PCR amplif	c1090	7.8	35.5	12	1	AB162385	Oligonucleotide pr
c1018	7.8	35.5	12	1	AAQ61471	Wildtype influenza	c1091	7.8	35.5	12	1	AB163323	Oligonucleotide pr
c1019	7.8	35.5	12	1	AB117626	Oligonucleotide pr	1092	7.8	35.5	12	1	AB177334	Oligonucleotide pr
c1020	7.8	35.5	12	1	ABH94714	Oligonucleotide pr	c1093	7.8	35.5	12	1	AB117457	Oligonucleotide pr
c1021	7.8	35.5	12	1	ABH69699	Oligonucleotide pr	c1094	7.8	35.5	12	1	ABH94174	Oligonucleotide pr
1022	7.8	35.5	12	1	ABH95393	Oligonucleotide pr	1095	7.8	35.5	12	1	ABH96946	Oligonucleotide pr
1023	7.8	35.5	12	1	AB122321	Oligonucleotide pr	c1096	7.8	35.5	12	1	ABH99367	Oligonucleotide pr
c1024	7.8	35.5	12	1	ABH97378	Oligonucleotide pr	c1097	7.8	35.5	12	1	AB125367	Oligonucleotide pr
c1025	7.8	35.5	12	1	ABH98878	Oligonucleotide pr	c1098	7.8	35.5	12	1	AB126855	Oligonucleotide pr
1026	7.8	35.5	12	1	AB100237	Oligonucleotide pr	c1099	7.8	35.5	12	1	AB101762	Oligonucleotide pr
1027	7.8	35.5	12	1	ABH75522	Oligonucleotide pr	1100	7.8	35.5	12	1	AB103834	Oligonucleotide pr
1028	7.8	35.5	12	1	AB103349	Oligonucleotide pr	c1101	7.8	35.5	12	1	AB105890	Oligonucleotide pr
c1029	7.8	35.5	12	1	AB129614	Oligonucleotide pr	c1102	7.8	35.5	12	1	AB105981	Oligonucleotide pr
c1030	7.8	35.5	12	1	AB129614	Oligonucleotide pr	c1103	7.8	35.5	12	1	ABH81103	Oligonucleotide pr
c1031	7.8	35.5	12	1	AB130078	Oligonucleotide pr	c1104	7.8	35.5	12	1	ABH81845	Oligonucleotide pr
1032	7.8	35.5	12	1	AB107757	Oligonucleotide pr	1105	7.8	35.5	12	1	AB132585	Oligonucleotide pr
c1033	7.8	35.5	12	1	ABH07919	Oligonucleotide pr	1106	7.8	35.5	12	1	ABH83841	Oligonucleotide pr
c1034	7.8	35.5	12	1	ABH84262	Oligonucleotide pr	c1107	7.8	35.5	12	1	ABH83992	Oligonucleotide pr
c1035	7.8	35.5	12	1	ABH92118	Oligonucleotide pr	1108	7.8	35.5	12	1	AB109859	Oligonucleotide pr
c1036	7.8	35.5	12	1	AB146539	Oligonucleotide pr	c1109	7.8	35.5	12	1	ABH85351	Oligonucleotide pr
c1037	7.8	35.5	12	1	AB168995	Oligonucleotide pr	c1110	7.8	35.5	12	1	AB135476	Oligonucleotide pr
1038	7.8	35.5	12	1	AB169973	Oligonucleotide pr	c1111	7.8	35.5	12	1	ABH89723	Oligonucleotide pr
c1039	7.8	35.5	12	1	AB156400	Oligonucleotide pr	1112	7.8	35.5	12	1	AB141302	Oligonucleotide pr
1040	7.8	35.5	12	1	AB157976	Oligonucleotide pr	c1113	7.8	35.5	12	1	AB146706	Oligonucleotide pr
c1041	7.8	35.5	12	1	AB161268	Oligonucleotide pr	c1114	7.8	35.5	12	1	AB149128	Oligonucleotide pr
1042	7.8	35.5	12	1	AB176796	Oligonucleotide pr	c1115	7.8	35.5	12	1	AB149581	Oligonucleotide pr
1043	7.8	35.5	12	1	AB166989	Oligonucleotide pr	c1116	7.8	35.5	12	1	AB152144	Oligonucleotide pr
c1044	7.8	35.5	12	1	AB117663	Oligonucleotide pr	1117	7.8	35.5	12	1	AB167896	Oligonucleotide pr
c1045	7.8	35.5	12	1	ABH93682	Oligonucleotide pr	1118	7.8	35.5	12	1	AB155064	Oligonucleotide pr
c1046	7.8	35.5	12	1	ABH94122	Oligonucleotide pr	c1119	7.8	35.5	12	1	AB160846	Oligonucleotide pr
1047	7.8	35.5	12	1	ABH70233	Oligonucleotide pr	1120	7.8	35.5	12	1	ABH67704	Oligonucleotide pr
1048	7.8	35.5	12	1	ABH70846	Oligonucleotide pr	1121	7.8	35.5	12	1	AB117899	Oligonucleotide pr
1049	7.8	35.5	12	1	ABH71165	Oligonucleotide pr	1122	7.8	35.5	12	1	ABH68620	Oligonucleotide pr
c1050	7.8	35.5	12	1	ABH96584	Oligonucleotide pr	c1123	7.8	35.5	12	1	AB119106	Oligonucleotide pr
c1051	7.8	35.5	12	1	AB123586	Oligonucleotide pr	1124	7.8	35.5	12	1	AB119218	Oligonucleotide pr
c1052	7.8	35.5	12	1	AB124526	Oligonucleotide pr	1125	7.8	35.5	12	1	ABH95505	Oligonucleotide pr
c1053	7.8	35.5	12	1	AB102156	Oligonucleotide pr	1126	7.8	35.5	12	1	ABH73050	Oligonucleotide pr
c1054	7.8	35.5	12	1	AB102367	Oligonucleotide pr	1127	7.8	35.5	12	1	ABH98296	Oligonucleotide pr
1055	7.8	35.5	12	1	AB135801	Oligonucleotide pr	c1128	7.8	35.5	12	1	ABH98427	Oligonucleotide pr

1129	1	ABH98584	12	35.5	7.8	c1202	Oligonucleotide pr	1	ABH98594	12	35.5	7.8	c1202	Oligonucleotide pr
1130	1	ABH75538	12	35.5	7.8	c1203	Oligonucleotide pr	1	ABH75214	12	35.5	7.8	c1203	Oligonucleotide pr
c1131	1	ABH77615	12	35.5	7.8	1204	Oligonucleotide pr	1	ABH81321	12	35.5	7.8	1204	Oligonucleotide pr
c1132	1	ABH73493	12	35.5	7.8	1205	Oligonucleotide pr	1	ABH06387	12	35.5	7.8	1205	Oligonucleotide pr
1133	1	ABH04382	12	35.5	7.8	1206	Oligonucleotide pr	1	ABH06563	12	35.5	7.8	1206	Oligonucleotide pr
1134	1	ABH79505	12	35.5	7.8	1207	Oligonucleotide pr	1	ABH08091	12	35.5	7.8	1207	Oligonucleotide pr
c1135	1	ABH05140	12	35.5	7.8	1208	Oligonucleotide pr	1	ABH33927	12	35.5	7.8	1208	Oligonucleotide pr
1136	1	ABH81597	12	35.5	7.8	1209	Oligonucleotide pr	1	ABH37823	12	35.5	7.8	1209	Oligonucleotide pr
c1137	1	ABH31926	12	35.5	7.8	c1210	Oligonucleotide pr	1	ABH37865	12	35.5	7.8	c1210	Oligonucleotide pr
c1138	1	ABH82802	12	35.5	7.8	c1211	Oligonucleotide pr	1	ABH13546	12	35.5	7.8	c1211	Oligonucleotide pr
c1139	1	ABH33250	12	35.5	7.8	1212	Oligonucleotide pr	1	ABH40033	12	35.5	7.8	1212	Oligonucleotide pr
c1140	1	ABH09315	12	35.5	7.8	1213	Oligonucleotide pr	1	ABH41019	12	35.5	7.8	1213	Oligonucleotide pr
c1141	1	ABH84745	12	35.5	7.8	c1214	Oligonucleotide pr	1	ABH42044	12	35.5	7.8	c1214	Oligonucleotide pr
c1142	1	ABH13398	12	35.5	7.8	1215	Oligonucleotide pr	1	ABH43358	12	35.5	7.8	1215	Oligonucleotide pr
c1143	1	ABH88743	12	35.5	7.8	1216	Oligonucleotide pr	1	ABH43358	12	35.5	7.8	1216	Oligonucleotide pr
1144	1	ABH89349	12	35.5	7.8	1217	Oligonucleotide pr	1	ABH48485	12	35.5	7.8	1217	Oligonucleotide pr
c1145	1	ABH15497	12	35.5	7.8	c1218	Oligonucleotide pr	1	ABH48743	12	35.5	7.8	c1218	Oligonucleotide pr
c1146	1	ABH48367	12	35.5	7.8	c1219	Oligonucleotide pr	1	ABH56761	12	35.5	7.8	c1219	Oligonucleotide pr
c1147	1	ABH50627	12	35.5	7.8	c1220	Oligonucleotide pr	1	ABH71030	12	35.5	7.8	c1220	Oligonucleotide pr
c1148	1	ABH68739	12	35.5	7.8	c1221	Oligonucleotide pr	1	ABH59260	12	35.5	7.8	c1221	Oligonucleotide pr
c1149	1	ABH58123	12	35.5	7.8	c1222	Oligonucleotide pr	1	ABH62103	12	35.5	7.8	c1222	Oligonucleotide pr
1150	1	ABH72256	12	35.5	7.8	c1223	Oligonucleotide pr	1	ABH65270	12	35.5	7.8	c1223	Oligonucleotide pr
c1151	1	ABH74036	12	35.5	7.8	c1224	Oligonucleotide pr	1	ABH75112	12	35.5	7.8	c1224	Oligonucleotide pr
1152	1	ABH68860	12	35.5	7.8	c1225	Oligonucleotide pr	1	ABH72846	12	35.5	7.8	c1225	Oligonucleotide pr
c1153	1	ABH94151	12	35.5	7.8	c1226	Oligonucleotide pr	1	ABH72846	12	35.5	7.8	c1226	Oligonucleotide pr
c1154	1	ABH94621	12	35.5	7.8	1227	Oligonucleotide pr	1	ABH73930	12	35.5	7.8	1227	Oligonucleotide pr
1155	1	ABH94759	12	35.5	7.8	c1228	Oligonucleotide pr	1	ABH73930	12	35.5	7.8	c1228	Oligonucleotide pr
c1156	1	ABH121173	12	35.5	7.8	c1229	Oligonucleotide pr	1	ABH75112	12	35.5	7.8	c1229	Oligonucleotide pr
c1157	1	ABH96687	12	35.5	7.8	c1230	Oligonucleotide pr	1	ABH75112	12	35.5	7.8	c1230	Oligonucleotide pr
c1158	1	ABH20882	12	35.5	7.8	c1231	Oligonucleotide pr	1	ABH76862	12	35.5	7.8	c1231	Oligonucleotide pr
c1159	1	ABH72736	12	35.5	7.8	1232	Oligonucleotide pr	1	ABH83179	12	35.5	7.8	1232	Oligonucleotide pr
c1160	1	ABH73248	12	35.5	7.8	1233	Oligonucleotide pr	1	ABH83179	12	35.5	7.8	1233	Oligonucleotide pr
c1161	1	ABH73280	12	35.5	7.8	1234	Oligonucleotide pr	1	ABH83179	12	35.5	7.8	1234	Oligonucleotide pr
1162	1	ABH73236	12	35.5	7.8	c1235	Oligonucleotide pr	1	ABH84624	12	35.5	7.8	c1235	Oligonucleotide pr
c1163	1	ABH73413	12	35.5	7.8	c1236	Oligonucleotide pr	1	ABH84624	12	35.5	7.8	c1236	Oligonucleotide pr
1164	1	ABH98987	12	35.5	7.8	c1237	Oligonucleotide pr	1	ABH85966	12	35.5	7.8	c1237	Oligonucleotide pr
c1165	1	ABH74242	12	35.5	7.8	c1238	Oligonucleotide pr	1	ABH87594	12	35.5	7.8	c1238	Oligonucleotide pr
c1166	1	ABH74441	12	35.5	7.8	1239	Oligonucleotide pr	1	ABH89324	12	35.5	7.8	1239	Oligonucleotide pr
c1167	1	ABH25571	12	35.5	7.8	1240	Oligonucleotide pr	1	ABH89324	12	35.5	7.8	1240	Oligonucleotide pr
1168	1	ABH75743	12	35.5	7.8	c1241	Oligonucleotide pr	1	ABH15677	12	35.5	7.8	c1241	Oligonucleotide pr
c1169	1	ABH101324	12	35.5	7.8	1242	Oligonucleotide pr	1	ABH16497	12	35.5	7.8	1242	Oligonucleotide pr
1170	1	ABH02443	12	35.5	7.8	1243	Oligonucleotide pr	1	ABH48081	12	35.5	7.8	1243	Oligonucleotide pr
c1171	1	ABH03120	12	35.5	7.8	1244	Oligonucleotide pr	1	ABH50311	12	35.5	7.8	1244	Oligonucleotide pr
c1172	1	ABH29661	12	35.5	7.8	1245	Oligonucleotide pr	1	ABH51092	12	35.5	7.8	1245	Oligonucleotide pr
1173	1	ABH06318	12	35.5	7.8	c1246	Oligonucleotide pr	1	ABH53202	12	35.5	7.8	c1246	Oligonucleotide pr
1174	1	ABH07219	12	35.5	7.8	c1247	Oligonucleotide pr	1	ABH57058	12	35.5	7.8	c1247	Oligonucleotide pr
1175	1	ABH82668	12	35.5	7.8	c1248	Oligonucleotide pr	1	ABH72935	12	35.5	7.8	c1248	Oligonucleotide pr
c1176	1	ABH09948	12	35.5	7.8	c1249	Oligonucleotide pr	1	ABH92402	12	35.5	7.8	c1249	Oligonucleotide pr
1177	1	ABH86977	12	35.5	7.8	c1250	Oligonucleotide pr	1	ABH17866	12	35.5	7.8	c1250	Oligonucleotide pr
c1178	1	ABH73777	12	35.5	7.8	1251	Oligonucleotide pr	1	ABH70369	12	35.5	7.8	1251	Oligonucleotide pr
c1179	1	ABH13567	12	35.5	7.8	1252	Oligonucleotide pr	1	ABH71401	12	35.5	7.8	1252	Oligonucleotide pr
c1180	1	ABH39120	12	35.5	7.8	1253	Oligonucleotide pr	1	ABH97515	12	35.5	7.8	1253	Oligonucleotide pr
c1181	1	ABH14455	12	35.5	7.8	c1254	Oligonucleotide pr	1	ABH97515	12	35.5	7.8	c1254	Oligonucleotide pr
1182	1	ABH15116	12	35.5	7.8	c1255	Oligonucleotide pr	1	ABH97598	12	35.5	7.8	c1255	Oligonucleotide pr
1183	1	ABH18138	12	35.5	7.8	c1256	Oligonucleotide pr	1	ABH97598	12	35.5	7.8	c1256	Oligonucleotide pr
c1184	1	ABH50150	12	35.5	7.8	c1257	Oligonucleotide pr	1	ABH74520	12	35.5	7.8	c1257	Oligonucleotide pr
c1185	1	ABH5368	12	35.5	7.8	c1258	Oligonucleotide pr	1	ABH75109	12	35.5	7.8	c1258	Oligonucleotide pr
1186	1	ABH54086	12	35.5	7.8	1259	Oligonucleotide pr	1	ABH75109	12	35.5	7.8	1259	Oligonucleotide pr
1187	1	ABH69359	12	35.5	7.8	c1260	Oligonucleotide pr	1	ABH101097	12	35.5	7.8	c1260	Oligonucleotide pr
c1188	1	ABH158539	12	35.5	7.8	c1261	Oligonucleotide pr	1	ABH101648	12	35.5	7.8	c1261	Oligonucleotide pr
c1189	1	ABH72502	12	35.5	7.8	c1262	Oligonucleotide pr	1	ABH102112	12	35.5	7.8	c1262	Oligonucleotide pr
1190	1	ABH59927	12	35.5	7.8	1263	Oligonucleotide pr	1	ABH28665	12	35.5	7.8	1263	Oligonucleotide pr
c1191	1	ABH75454	12	35.5	7.8	1264	Oligonucleotide pr	1	ABH30226	12	35.5	7.8	1264	Oligonucleotide pr
c1192	1	ABH75528	12	35.5	7.8	c1265	Oligonucleotide pr	1	ABH30226	12	35.5	7.8	c1265	Oligonucleotide pr
c1193	1	ABH62507	12	35.5	7.8	c1266	Oligonucleotide pr	1	ABH107748	12	35.5	7.8	c1266	Oligonucleotide pr
1194	1	ABH77328	12	35.5	7.8	c1267	Oligonucleotide pr	1	ABH108342	12	35.5	7.8	c1267	Oligonucleotide pr
c1195	1	ABH65867	12	35.5	7.8	c1268	Oligonucleotide pr	1	ABH109340	12	35.5	7.8	c1268	Oligonucleotide pr
1196	1	ABH6074	12	35.5	7.8	1269	Oligonucleotide pr	1	ABH135703	12	35.5	7.8	1269	Oligonucleotide pr
c1197	1	ABH93366	12	35.5	7.8	c1270	Oligonucleotide pr	1	ABH86393	12	35.5	7.8	c1270	Oligonucleotide pr
1198	1	ABH68684	12	35.5	7.8	c1271	Oligonucleotide pr	1	ABH11961	12	35.5	7.8	c1271	Oligonucleotide pr
1199	1	ABH21464	12	35.5	7.8	c1272	Oligonucleotide pr	1	ABH14631	12	35.5	7.8	c1272	Oligonucleotide pr
c1200	1	ABH22137	12	35.5	7.8	c1273	Oligonucleotide pr	1	ABH49237	12	35.5	7.8	c1273	Oligonucleotide pr
1201	1	ABH23106	12	35.5	7.8	1274	Oligonucleotide pr	1	ABH52148	12	35.5	7.8	1274	Oligonucleotide pr

1	ABH73267	12	35.5	7.8	1275	Oligonucleotide pr
2	ABH73949	12	35.5	7.8	c1276	Oligonucleotide pr
3	ABH77744	12	35.5	7.8	1277	Oligonucleotide pr
4	ABH77997	12	35.5	7.8	1278	Oligonucleotide pr
5	ABH95109	12	35.5	7.8	c1279	Oligonucleotide pr
6	ABH21172	12	35.5	7.8	c1280	Oligonucleotide pr
7	ABH21190	12	35.5	7.8	c1281	Oligonucleotide pr
8	ABH96220	12	35.5	7.8	c1282	Oligonucleotide pr
9	ABH79581	12	35.5	7.8	c1283	Oligonucleotide pr
10	ABH22752	12	35.5	7.8	1284	Oligonucleotide pr
11	ABH97940	12	35.5	7.8	c1285	Oligonucleotide pr
12	ABH98624	12	35.5	7.8	c1286	Oligonucleotide pr
13	ABH24220	12	35.5	7.8	1287	Oligonucleotide pr
14	ABH24290	12	35.5	7.8	c1288	Oligonucleotide pr
15	ABH25115	12	35.5	7.8	1289	Oligonucleotide pr
16	ABH101758	12	35.5	7.8	c1290	Oligonucleotide pr
17	ABH77031	12	35.5	7.8	c1291	Oligonucleotide pr
18	ABH77113	12	35.5	7.8	1292	Oligonucleotide pr
19	ABH77616	12	35.5	7.8	c1293	Oligonucleotide pr
20	ABH78361	12	35.5	7.8	c1294	Oligonucleotide pr
21	ABH78561	12	35.5	7.8	c1295	Oligonucleotide pr
22	ABH78561	12	35.5	7.8	1296	Oligonucleotide pr
23	ABH78561	12	35.5	7.8	c1302	Oligonucleotide pr
24	ABH78561	12	35.5	7.8	c1303	Oligonucleotide pr
25	ABH90392	12	35.5	7.8	c1304	Oligonucleotide pr
26	ABH16970	12	35.5	7.8	c1305	Oligonucleotide pr
27	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
28	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
29	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
30	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
31	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
32	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
33	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
34	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
35	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
36	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
37	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
38	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
39	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
40	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
41	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
42	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
43	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
44	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
45	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
46	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
47	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
48	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
49	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
50	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
51	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
52	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
53	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
54	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
55	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
56	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
57	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
58	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
59	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
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63	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
64	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
65	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
66	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
67	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
68	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
69	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
70	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
71	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
72	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
73	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
74	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
75	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
76	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
77	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
78	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
79	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
80	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
81	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
82	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
83	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
84	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
85	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
86	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
87	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
88	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
89	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
90	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
91	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
92	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
93	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
94	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
95	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
96	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
97	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
98	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
99	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
100	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
101	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
102	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
103	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
104	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
105	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
106	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
107	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
108	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
109	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
110	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
111	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
112	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
113	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
114	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
115	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
116	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
117	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
118	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
119	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
120	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
121	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
122	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
123	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
124	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
125	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
126	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
127	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
128	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
129	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
130	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
131	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
132	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
133	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
134	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
135	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
136	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
137	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
138	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
139	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
140	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
141	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
142	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
143	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
144	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
145	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
146	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
147	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
148	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
149	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
150	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
151	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
152	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
153	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
154	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
155	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
156	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
157	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
158	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
159	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
160	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
161	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
162	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
163	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
164	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
165	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
166	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
167	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
168	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
169	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
170	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
171	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
172	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
173	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
174	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
175	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
176	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
177	ABH84458	12	35.5	7.8	c1298	Oligonucleotide pr
178	ABH77031	12	35.5	7.8	1299	Oligonucleotide pr
179	ABH77113	12	35.5	7.8	c1306	Oligonucleotide pr
180	ABH77616	12	35.5	7.8	1300	Oligonucleotide pr
181	ABH86327	12	35.5	7.8	1301	Oligonucleotide pr
182	ABH86327	12	35.5	7.8	c1302	Oligonucleotide pr
183	ABH14362	12	35.5	7.8	c1303	Oligonucleotide pr
184	ABH14362	12	35.5	7.8	c1304	Oligonucleotide pr
185	ABH90392	12	35.5	7.8	c1305	Oligonucleotide pr
186	ABH16970	12	35.5	7.8	c1306	Oligonucleotide pr
187	ABH84458	12</				

1421	7.8	35.5	12	1	ABI55216	oligonucleotide pr
1422	7.8	35.5	12	1	ABI80460	oligonucleotide pr
1423	7.8	35.5	12	1	ABI67260	oligonucleotide pr
1424	7.8	35.5	12	1	ABH68427	oligonucleotide pr
1425	7.8	35.5	12	1	ABI20393	oligonucleotide pr
1426	7.8	35.5	12	1	ABH73762	oligonucleotide pr
1427	7.8	35.5	12	1	ABH75483	oligonucleotide pr
1428	7.8	35.5	12	1	ABI28569	oligonucleotide pr
1429	7.8	35.5	12	1	ABH79548	oligonucleotide pr
1430	7.8	35.5	12	1	ABH80335	oligonucleotide pr
1431	7.8	35.5	12	1	ABH80462	oligonucleotide pr
1432	7.8	35.5	12	1	ABI05650	oligonucleotide pr
1433	7.8	35.5	12	1	ABI06182	oligonucleotide pr
1434	7.8	35.5	12	1	ABI32093	oligonucleotide pr
1435	7.8	35.5	12	1	ABH84551	oligonucleotide pr
1436	7.8	35.5	12	1	ABI13475	oligonucleotide pr
1437	7.8	35.5	12	1	ABH90450	oligonucleotide pr
1438	7.8	35.5	12	1	ABI15662	oligonucleotide pr
1439	7.8	35.5	12	1	ABI49818	oligonucleotide pr
1440	7.8	35.5	12	1	ABI52057	oligonucleotide pr
1441	7.8	35.5	12	1	ABI52706	oligonucleotide pr
1442	7.8	35.5	12	1	ABI53175	oligonucleotide pr
1443	7.8	35.5	12	1	ABI76815	oligonucleotide pr
1444	7.8	35.5	12	1	ABI78370	oligonucleotide pr
1445	7.8	35.5	12	1	ABI78401	oligonucleotide pr
1446	7.8	35.5	12	1	ABI66145	oligonucleotide pr
1447	7.8	35.5	12	1	ABI82035	oligonucleotide pr
1448	7.8	35.5	12	1	ABI17694	oligonucleotide pr
1449	7.8	35.5	12	1	ABH92991	oligonucleotide pr
1450	7.8	35.5	12	1	ABH94505	oligonucleotide pr
1451	7.8	35.5	12	1	ABH95694	oligonucleotide pr
1452	7.8	35.5	12	1	ABH71751	oligonucleotide pr
1453	7.8	35.5	12	1	ABH72328	oligonucleotide pr
1454	7.8	35.5	12	1	ABI23966	oligonucleotide pr
1455	7.8	35.5	12	1	ABH74796	oligonucleotide pr
1456	7.8	35.5	12	1	ABH76081	oligonucleotide pr
1457	7.8	35.5	12	1	ABI26715	oligonucleotide pr
1458	7.8	35.5	12	1	ABI02659	oligonucleotide pr
1459	7.8	35.5	12	1	ABI03308	oligonucleotide pr
1460	7.8	35.5	12	1	ABI28965	oligonucleotide pr
1461	7.8	35.5	12	1	ABH75806	oligonucleotide pr
1462	7.8	35.5	12	1	ABH80068	oligonucleotide pr
1463	7.8	35.5	12	1	ABI05818	oligonucleotide pr
1464	7.8	35.5	12	1	ABI06252	oligonucleotide pr
1465	7.8	35.5	12	1	ABI09548	oligonucleotide pr
1466	7.8	35.5	12	1	ABH88308	oligonucleotide pr
1467	7.8	35.5	12	1	ABH89677	oligonucleotide pr
1468	7.8	35.5	12	1	ABI41860	oligonucleotide pr
1469	7.8	35.5	12	1	ABI45273	oligonucleotide pr
1470	7.8	35.5	12	1	ABI46462	oligonucleotide pr
1471	7.8	35.5	12	1	ABI47815	oligonucleotide pr
1472	7.8	35.5	12	1	ABI49456	oligonucleotide pr
1473	7.8	35.5	12	1	ABI54085	oligonucleotide pr
1474	7.8	35.5	12	1	ABI68631	oligonucleotide pr
1475	7.8	35.5	12	1	ABI57978	oligonucleotide pr
1476	7.8	35.5	12	1	AAF92714	Multiple allele de
1477	7.8	35.5	12	1	AAL37779	3' conserved RNA r
1478	7.8	35.5	12	1	AAL37802	Modified 3' RNA re
1479	7.8	35.5	12	1	ABH71501	DNA encoding prote
1480	7.8	35.5	12	1	ABQ75462	Modified influenza
1481	7.8	35.5	12	1	ABQ75461	Influenza virus C
1482	7.8	35.5	12	1	ABX9290	Hepatitis C virus
1483	7.8	35.5	12	1	ABX15139	Wild type Influenz
1484	7.8	35.5	12	1	AAD39657	Luc (luciferase)-1
1485	7.8	35.5	12	1	ABQ77279	Sequencing oligonu
1486	7.8	35.5	12	1	ABQ77340	Parallel sequencin
1487	7.8	35.5	12	1	ABX80004	EST polymorphic DN
1488	7.8	35.5	12	1	ABX79734	EST polymorphic DN
1489	7.8	35.5	12	1	ADA18488	NSKF target DNA se
1490	7.8	35.5	12	1	ADC22510	Protein binding do
1491	7.8	35.5	12	1	ADC18377	Protease recogniti

ALIGNMENTS

RESULT 1

AAL49614/c

ID AAL49614 standard; DNA; 21 BP.

XX AAL49614;

AC AAL49614;

XX 27-NOV-2002 (first entry)

DT Tumour differentiation effecting protein TL4 related PCR primer #18.

DE Mouse; tumour differentiation; rhabdosarcoma; leiomyosarcoma; rat; ss;

XX muscular dystrophy; uterine myoma; cytostatic; plasmic change; TL4;

XX human; PCR; primer.

XX Unidentified.

XX WO200266049-A1.

XX 29-AUG-2002.

XX 21-FEB-2002; 2002WO-JF001536.

XX 23-FEB-2001; 2001JP-00049450.

XX (TAKE) TAKEDA CHEM IND LTD.

XX PA Hikichi Y, Shintani Y, Matsui H;

XX WPI; 2002-674894/72.

XX Plasmic change agents and antibodies to them for diagnosis and treatment

XX of tumours of muscle tissue and of muscular dystrophy.

XX Example 1; Page 127; 136pp; Japanese.

XX The present invention relates to plasmic change agents with cell

XX differentiation activity containing protein TL4. These can be used in the

XX treatment, prevention and diagnosis of rhabdosarcoma, leiomyosarcoma,

XX muscular dystrophy and uterine myeloma. The present sequence is a PCR

XX primer used in the exemplification of the invention

XX SQ Sequence 21 BP; 1 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 727 TGCCAGGAGAAACAGACACC 747

DB 21 TGCCAGGAGAAACAGACACC 1

RESULT 2

ABT05081/c

ID ABT05081 standard; DNA; 18 BP.

XX ABT05081;

XX 11-OCT-2002 (first entry)

DT TNFRI expression modulation related antisense oligo SEQ ID No 111.

DE Antisense compound; tumour necrosis factor receptor 1; liver disease;

XX TNFRI; hepatitis; liver injury; hyperproliferative disorder; cancer;

XX human; ds.

XX Homo sapiens.

XX WO200248168-A1.

XX

PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NM;
PI WPI; 2002-583481/62.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
XX Example 18; Page 56; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 81.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACAGAAC 744
DB 18 TGCCAGGAGAAACAGAAC 1
RESULT 3
ID ABT05082/C
XX ABT05082 standard; DNA; 18 BP.
XX
AC ABT05082;
XX
XX 11-OCT-2002 (first entry)
DT
DE TNFR1 expression modulation related antisense oligo SEQ ID No 112.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
XX WO200248168-A1.
PN
XX
PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NM;
PI WPI; 2002-583481/62.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding tumor

PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
PS Example 18; Page 56; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 0 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 81.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAAACAGAAC 746
DB 18 CCAGGAGAAACAGAAC 1
RESULT 4
ID ABT05083/C
XX ABT05083 standard; DNA; 18 BP.
XX
AC ABT05083;
XX
XX 11-OCT-2002 (first entry)
DT
DE TNFR1 expression modulation related antisense oligo SEQ ID No 113.
XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
XX WO200248168-A1.
PN
XX
PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowser LM, Zhang H, Dean NM;
PI WPI; 2002-583481/62.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
XX Example 18; Page 56; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting

CC the expression of TNFR1. The antisense compound is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC This polynucleotide sequence represents a human oligonucleotide relating
 CC to the TNFR1 of the invention
 XX
 SQ Sequence 18 BP; 0 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 81.8%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 731 AGGAGAAACAGAACACCG 748
 |||||
 Db 18 AGGAGAAACAGAACACCG 1
 RESULT 5
 AAZ48521/C
 ID AAZ48521 standard; DNA; 18 BP.
 XX
 AC AAZ48521;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18914.
 XX
 KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
 XX inflammation; tumour formation; TNFR1; anticancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US6007995-A.
 XX
 PD 28-DEC-1999.
 XX
 PF 26-JUN-1998; 98US-00106038.
 XX
 PR 26-JUN-1998; 98US-00106038.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Baker BF, Cowser LM;
 XX
 DR WPI; 2000-105333/09.
 XX
 PT Antisense inhibition of tumor necrosis factor type 1 expression for
 PT diagnosis, treatment and prevention of disease, particularly tumors.
 XX
 PS Claim 1; Col 25; 34pp; English.
 XX
 CC The invention provides antisense compounds targeted to human tumour
 CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
 CC can be used in a method of inhibiting the expression of TNFR1 human cells
 CC or tissues. The antisense compounds specifically hybridize with one or
 CC more nucleic acids encoding TNFR1 modulating the function of nucleic acid
 CC molecules encoding TNFR1, ultimately modulating the amount of TNFR1
 CC produced. The antisense compounds and method are useful as research
 CC reagents and diagnostics, and in the treatment and prophylaxis of
 CC infection, inflammation or tumour formation. Sequences AAZ48482-565
 CC represent antisense oligos used for inhibition of the human TNFR1 mRNA
 XX
 SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 77.3%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GGAGAAACAGAACACCG 748
 |||||
 Db 18 GGAGAAACAGAACACCG 2

RESULT 6
 ABT05017/C
 ID ABT05017 standard; DNA; 18 BP.
 XX
 AC ABT05017;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE TNFR1 expression modulation related antisense oligo SEQ ID No 47.
 XX
 KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
 KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
 KW human; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200248168-A1.
 XX
 PD 20-JUN-2002.
 XX
 PF 22-OCT-2001; 2001WO-US051224.
 XX
 PR 24-OCT-2000; 2000US-00695451.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Baker BF, Cowser LM, Zhang H, Dean NM;
 XX
 DR WPI; 2002-583481/62.
 XX
 PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
 PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
 PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
 XX
 PS Example 10; Page 45; 121pp; English.
 XX
 CC The invention relates to an antisense compound 8 to 30 nucleotides in
 CC length targeted to nucleic acid molecule encoding tumour necrosis factor
 CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
 CC TNFR1. The antisense compound is useful for inhibiting the expression of
 CC TNFR1 in cells or tissues. The antisense compound is also useful for
 CC treating an animal (preferably human) having a disease or condition
 CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
 CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
 CC the expression of TNFR1. The antisense compound is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC This polynucleotide sequence represents a human oligonucleotide relating
 CC to the TNFR1 of the invention
 XX
 SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 77.3%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 732 GGAGAAACAGAACACCG 748
 |||||
 Db 18 GGAGAAACAGAACACCG 2
 RESULT 7
 AAT16398/C
 ID AAT16398 standard; DNA; 18 BP.
 XX
 AC AAT16398;
 XX
 DT 13-SEP-1996 (first entry)
 XX
 DE Primer #1 for SWS32359 human obesity gene.
 XX
 KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
 KW food intake; energy expenditure; high blood pressure; cholesterol; human;
 KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay; PCR;

KW primer; amplify; polymerase chain reaction; ss.
 XX Synthetic.
 OS GB2292382-A.
 PN 21-FEB-1996.
 XX 17-AUG-1995; 95GB-00016947.
 PD 17-AUG-1994; 94US-00292345.
 PF 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 PR 07-JUN-1995; 95US-00483211.
 XX (UYRQ) UNIV ROCKEFELLER.
 PA Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
 XX Burley SK;
 PI WPI; 1996-099009/11.
 DR Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
 PT reducing wt. in treatment of diabetes, high blood pressure and high
 PT cholesterol and for cosmetic reasons.
 XX Example 10; Page 141; 304pp; English.
 PS AAT16392-T16429 represent amplification primers for the human obesity
 CC polypeptide (OBP) gene sequence (see AAT16373). These sequences were used
 CC to amplify the OBP gene sequence from the YAC contig containing the human
 CC OBP gene, in a series of sequence tagged-site (STS)-specific PCR assays.
 CC There were 19 STSs found within the YAC contig human OBP gene sequence.
 CC This sequence was used in conjunction with AAT16399 to amplify the STS
 CC SWS2359. OBP has effects on both food intake and energy expenditure. OBP
 CC and its analogues are useful for modifying body weight (optionally
 CC combined with known medicaments), for treating diabetes, high blood
 CC pressure or high cholesterol. The OBP coding sequence (and sequences
 CC complementary to it) can be used in gene therapy for modifying body
 CC weight. The protein can be used for reducing weight for health or
 CC cosmetic reasons in obese humans, or to produce leaner food animals.
 CC Antagonists of OBP (including antibodies) are useful for increasing body
 CC weight, e.g. for treating weight loss associated with cancer, or for
 CC cosmetic reasons in humans, or for production of Kobe beef or Foie gras
 CC in domestic animals. OBP antibodies (Ab) can also be used in diagnostic
 CC immunoassays for the presence of OBP. The formation of Ab-OBP complexes
 CC enables in vitro evaluation of levels of OBP in a sample, especially to
 CC detect diseases associated with elevated or decreased levels, and to
 CC monitor treatment of these diseases
 XX Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
 SQ Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 730 CAGGAGAAACAGACAC 746
 DB 18 CAGGAGAAACAGACAC 2
 |||||
 RESULT 8
 AAC62593/c
 ID AAC62593 standard; DNA; 18 BP.
 XX AAC62593;
 AC AAC62593;
 XX 01-FEB-2001 (first entry)
 DT Human OB gene sequence tagged-site-specific PCR primer #7.
 DE Human; mouse; OB gene; obesity; adiposity; body weight; PCR primer; ss.
 KW Human; mouse; OB gene; obesity; adiposity; body weight; PCR primer; ss.
 XX

OS Homo sapiens.
 XX US6124448-A.
 PN 26-SEP-2000.
 XX 07-JUN-1995; 95US-00488208.
 PD 17-AUG-1994; 94US-00292345.
 PF 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 PR (UYRQ) UNIV ROCKEFELLER.
 XX Maffei M, Proenca R, Zhang Y, Friedman JM;
 PI WPI; 2000-601556/57.
 DR Nucleic acid primers and probes useful for detecting mutations in
 XX mammalian OB gene associated with regulation of body weight and
 XX adiposity.
 XX Example 10; Col 80; 153pp; English.
 PS The present sequence is a PCR primer which was used in an invention
 CC relating to the control of body weight of animals including humans.
 CC Nucleic acids of at least 10 nucleotides which are hybridizable to a non-
 CC coding region of an OB nucleic acid have been created. The OB gene plays
 CC a critical role in the regulation of body weight and adiposity. The
 CC nucleic acids may be used as probes or as primers for PCR. They are
 CC useful for evaluating the presence of mutations in the human OB gene or
 CC for evaluating the level of expression of OB mRNA. Defects associated
 CC with OB gene expression result in obese phenotypes
 XX Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
 SQ Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 730 CAGGAGAAACAGACAC 746
 DB 18 CAGGAGAAACAGACAC 2
 |||||
 RESULT 9
 AAA12315/c
 ID AAA12315 standard; DNA; 18 BP.
 XX AAA12315;
 AC AAA12315;
 XX 18-AUG-2000 (first entry)
 DT Human OB DNA PCR primer SWS2359 #1.
 XX OB gene; body weight; obesity; anorectic; adipose tissue; brain; human;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS US6048837-A.
 PN 11-APR-2000.
 PD 07-JUN-1995; 95US-00485942.
 PF 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 PR (UYRQ) UNIV ROCKEFELLER.
 XX Proenca R, Zhang Y, Friedman JM;
 PI

```

XX WPI; 2000-302788/26.
DR
XX Modifying body weight of an animal comprises administering mammalian
PT obesity polypeptide obtained from humans and murine.
XX
XX Example 10; Col 133-134; 153pp; English.
XX
XX This invention describes a novel method for modifying body weight of an
CC animal which comprises administering mammalian obesity (OB) polypeptide.
CC The products of the invention have anorectic activity. The OB polypeptide
CC at a dose of 5 mg/g/day in 300 micro litres of PBS was injected
CC intraperitoneally into mice. Control mice were injected with PBS
CC dialysate of the recombinant protein. The body weight of the mice was
CC noted. The results shows that recombinant the OB polypeptide is capable
CC of reducing a body weight and is found to be effective when it is
CC administered daily. The OB polypeptide acts as a part of the signalling
CC pathway by which adipose tissue communicates with the brain and other
CC organs. (I) is useful for modulating body weight of an animal especially
CC humans. This sequence represents a PCR primer used in the amplification
CC of a human OB protein described in the method of the invention
XX
XX Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
SQ Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACACACAC 746
DB 18 CAGGAGAAACACACAC 2
|||||

RESULT 11
AAC62673/c
ID AAC62673 standard; DNA; 18 BP.
XX
XX AAC62673;
AC
XX
XX 01-FEB-2001 (first entry)
DE
XX
XX Human OB gene sequence tagged-site-specific PCR primer #7.
XX
XX Human; mouse; anabolic; cytostatic; immunostimulant;
KW OB polypeptide inhibitor; body weight; obesity; OB gene; cancer; AIDS;
KW anorexia nervosa; hypertension; heart disease; Type II diabetes;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6124439-A.
XX
XX 26-SEP-2000.
XX
XX 07-JUN-1995; 95US-00488214.
XX
XX 17-AUG-1994; 94US-00292345.
XX
XX 30-NOV-1994; 94US-00347563.
XX
XX 10-MAY-1995; 95US-00438431.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Praelencia R, Zhang Y, Friedman JM;
XX
XX WPI; 2000-611018/58.
XX
XX Novel antibody to mammalian obesity polypeptide useful for diagnosis and
PT treatment of weight loss associated with disorders such as cancer, AIDS.
PT and anorexia nervosa.
XX
XX Example 10; Col 80; 150pp; English.
XX
XX The present sequence is a PCR primer which was used in an invention
CC

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CC relating to the control of body weight of animals including humans.
CC Antibodies against the mammalian obesity (OB) polypeptide have been
CC identified. The antibodies are useful for modulating the activity of OB
CC to control body weight and fat content and/or to treat certain
CC pathological conditions in which there is abnormal depression or
CC elevation of body weight. The antibodies are used to treat weight loss
CC associated with cancer, AIDS and anorexia nervosa. They are useful for
CC the diagnosis of nutritional disorders such as obesity and diseases
CC associated with obesity, such as hypertension, heart disease and Type II
CC diabetes. The kits are used to determine the presence or amount of OB in
CC the blood or plasma of an individual
XX
XX Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
SQ Query Match 70.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 730 CAGGAGAAACACACAC 746
DB 18 CAGGAGAAACACACAC 2
|||||

RESULT 11
ABX89547/c
ID ABX89547 standard; DNA; 18 BP.
XX
XX ABX89547;
AC
XX
XX 08-MAY-2003 (first entry)
DE
XX
XX Human sequence tagged specific PCR primer sWss2359 #1.
XX
XX ss; human; obese polypeptide; body weight; PCR; ob polypeptide; leptin;
KW adipocyte; appetite reduction; cosmetic; primer; fat deposit reduction;
KW improved body appearance; heart disease; obesity; agriculture;
KW nutritional disorder; cancer associated weight loss; type II diabetes;
KW obesity associated disease; AIDS associated weight loss; hypertension;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX US2002107211-A1.
XX
XX 08-AUG-2002.
XX
XX 13-DEC-2000; 2000US-00736084.
XX
XX 07-JUN-1995; 95US-00485943.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Friedman JM, Halaas JL, Gajiwala K, Burley SK, Zhang Y;
XX Praelencia R, Maffei M;
XX
XX WPI; 2002-722695/78.
XX
XX New obese polypeptide useful for inducing reduction of body weight in an
PT animal, for preparing a composition for treating obesity, disease
PT associated with obesity such as hypertension, heart disease or type II
PT diabetes.
XX
XX Example 10; Page 44; 144pp; English.
XX
XX The invention relates to an obese (ob) polypeptide, also known as leptin,
CC expressed predominantly by adipocytes and capable of inducing reduction
CC of body weight in an animal. The polypeptide is useful for monitoring
CC therapeutic treatment of a disease associated with elevated or decreased
CC levels of ob polypeptide in a mammalian subject; for use in
CC radioimmunoassays for measuring fat and/or plasma levels of ob protein or
CC for detecting the presence and level of receptor for ob on tissues, such
CC as hypothalamus; for screening expression libraries to isolate active
CC receptors; for use in cosmetics by improving body appearance by reducing
CC

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CC fat deposits or appetite or both and is used independently or in
 CC conjugation with other cosmetic strategies e.g. surgery for its cosmetic
 CC effect; for identifying agonists or antagonists that affect its activity
 CC and has potential agricultural uses e.g. increasing the body weight of
 CC animals. Nucleic acid encoding the polypeptide is useful for identifying
 CC mutation in ob nucleotide, in gene therapy for obesity and in the
 CC measurement of its encoded RNA and protein in nutritional disorders. A
 CC host cell transfected with a vector expressing the polypeptide is useful
 CC in the preparation of modulators of the polypeptide and its nucleic acid.
 CC An immunogenic fragment of the polypeptide is useful for preparing an
 CC antibody. The antibody is useful for measuring the presence of the
 CC polypeptide in a sample; for evaluating the level of ob polypeptide in a
 CC biological sample to detect or diagnose the presence of a disease
 CC associated with elevated or decreased levels of ob polypeptide in a
 CC mammalian subject; for imaging ob polypeptide in situ. A composition
 CC comprising the polypeptide is useful for reducing body weight of an
 CC animal, in particular humans. A composition comprising an antagonist of
 CC the polypeptide is useful for increasing body weight of an animal.
 CC Compositions containing the polypeptide and the antagonist are useful for
 CC treating obesity, weight loss associated with cancer or AIDS, disease
 CC associated with obesity such as hypertension, heart disease or type II
 CC diabetes. The present sequence represents a human sequence tagged
 CC specific PCR primer
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 730 CAGGAGAAACAGACAC 746
 DB 18 CAGGAGAAACAGACAC 2

RESULT 12
 ABL61421/c
 ID ABL61421 standard; DNA; 18 BP.
 XX
 AC ABL61421;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE Human Ob gene STS sN5S2359 AFVa0652g9 PCR primer #1.
 XX
 KW Ob; human; obese; adiposity; body weight; anorectic; anabolic; PCR;
 KW primer; chromosome 7; STS; sequence tagged site; 7q31.3;
 KW microsatellite marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6350730-B1.
 XX
 PD 26-FEB-2002.
 XX
 PF 07-JUN-1995; 95US-00488223.
 XX
 PR 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 XX
 PI Friedman JM, Zhang Y, Proenca R;
 XX
 DR WPI; 2002-412914/44.
 XX
 PT Modifying the body weight of an animal comprises administering an obese
 PT gene (OB) polypeptide analog.
 XX
 PS Example 10; Col 79-80; 152pp; English.
 XX
 CC This invention describes a novel method of modifying the body weight of

CC an animal comprising administering an obese gene (OB) polypeptide
 CC analogue, capable of modulating body weight and adiposity. The invention
 CC has anorectic and anabolic activity. ABL61415-ABL61468 represent PCR
 CC primers used in the detection of sequence tagged sites (STS's) and
 CC microsatellite markers used in the mapping of the human Ob gene onto
 CC chromosome 7. These genetic markers represent an important tool for
 CC studying the possible role of the Ob gene in inherited forms of human
 CC obesity
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 59;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 730 CAGGAGAAACAGACAC 746
 DB 18 CAGGAGAAACAGACAC 2

RESULT 13
 ABX96407/c
 ID ABX96407 standard; DNA; 18 BP.
 XX
 AC ABX96407;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE Human obese (ob) gene associated PCR primer #7.
 XX
 KW OB polypeptide; obese polypeptide; leptin; body weight; obesity;
 KW weight gain; protein therapy; weight loss; cancer; AIDS; human;
 KW acquired immunodeficiency syndrome; anorexia nervosa; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6471956-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 07-JUN-1995; 95US-00488225.
 XX
 PR 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 XX
 PA (UVRQ) UNIV ROCKEFELLER.
 XX
 PI Friedman JM, Zhang Y, Proenca R;
 XX
 DR WPI; 2003-298093/29.
 XX
 PT New human or mouse OB polypeptide, also referred to as leptin
 PT polypeptide, which is capable of modulating body weight, useful for
 PT treating obesity.
 XX
 PS Example 10; Col 79-80; 153pp; English.
 XX
 CC The invention describes an OB (obese) polypeptide (also referred as
 CC leptin) (I), capable of modulating body weight, comprising amino acids 22
 CC - 167 of a human or mouse OB polypeptide sequence of 167 amino acids
 CC (S1), given in the specification, or amino acids 22 - 166 a human or
 CC mouse OB polypeptide sequence of 166 amino acids (S2), given in the
 CC specification. The OB polypeptide is useful for reducing body weight in
 CC conditions of obesity, and as a target for neutralising antibodies which
 CC results in weight gain (protein therapy), for treating weight loss
 CC associated with cancer, acquired immunodeficiency syndrome (AIDS) or
 CC anorexia nervosa. This sequence represents a primer associated with the
 CC isolation of the human obese (ob) or leptin gene
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGAACAC 746
|||||
Db 18 CAGGAGAAACAGAACAC 2

RESULT 14
AAH60840/c
ID AAH60840 standard; DNA; 19 BP.
XX
AC AAH60840;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin B1 ribozyme binding site #7.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
FN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
FA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
XX Disclosure; Page 96; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAH2415 to AAH6787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 CGAGAAACAGAACACCG 748
|||||
Db 19 CGAGAAACAGAACACCG 3

RESULT 15
AAH60840/c
ID AAH60840 standard; DNA; 19 BP.
XX
AC AAH60840;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cyclin B1 ribozyme binding site SEQ ID NO:3264.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

recognition site; target; ribozyme binding site; eye disease; vulnary;
proliferative disease; skin disease; psoriasis; diabetic retinopathy;
cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
atopic dermatitis; actinic keratosis; squamous cell carcinoma;
basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
PD WPI; 2001-300427/31.
XX
DR Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 309; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 70.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 732 CGAGAAACAGAACACCG 748
|||||
Db 19 CGAGAAACAGAACACCG 3

RESULT 16
AAV14108/c
ID AAV14108 standard; DNA; 18 BP.
XX
AC AAV14108;
XX
DT 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX

DE Probe HBP274 for RT pol region of HBV.
 XX Probe; hepatitis B virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX Synthetic.
 OS Hepatitis B virus.
 XX WO9740193-A2.
 PN 30-OCT-1997.
 PD 21-APR-1997; 97WO-EP002002.
 PF 19-APR-1996; 96EP-00870053.
 PR (INNO-) INNOGENETICS NV.
 XX Stuyver L, Rossau R, Maertens G;
 PI WPI; 1997-535867/49.
 DR Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX Claim 5; Fig 1; 80pp; English.
 XX This sequence represents a probe for the RT pol region of hepatitis B
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (i) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 18 BP; 1 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ Query Match 68.2%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACACAGA 742
 DB 18 GCCAGGAGAACACAGA 4
 RESULT 17
 AAD22805/c
 ID AAD22805 standard; DNA; 22 BP.
 XX AAD22805;
 AC AAD22805;
 XX 26-FEB-2002 (first entry)
 DT Human EMR2 specific nested PCR primer, 3'-1.
 DE Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2;
 KW epidermal growth factor; therapy; acute inflammation; injury; infection;
 KW meningitis; pneumonia; chronic inflammation; chronic tissue damage;
 KW rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;
 KW diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation;
 KW clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis;
 KW haematopoiesis; blood disorder; aneuploidy; agranulocytosis; migration;
 KW myeloid leukaemia; anaemia; vascular malfunction; congenital disease;
 KW wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia;
 KW HHT; tumour; infection; cancer; asthma; anorexia; Parkinson's disease;
 KW bulimia; hypotension; acute heart failure; hypertension; osteoporosis;
 KW urinary retention; angina pectoris; myocardial infarction; allergy;
 KW ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;
 KW schizophrenia; manic depression; delirium; dementia; mental retardation;
 KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS WO200173296-A1.
 PN 25-OCT-2001.
 PD 17-APR-2001; 2001WO-GB001729.
 PF 13-APR-2000; 2000GB-00009181.
 PR (ISIS-) ISIS INNOVATION LTD.
 XX Lin H, Gordon D, McKnight AJ, Stacey M;
 PI WPI; 2002-026015/03.
 DR Novel human epidermal growth factor-like molecule containing mucin-like
 CC hormone receptor-2 polypeptide, useful for treating acute and chronic
 CC inflammation, chronic tissue damages and for wound healing.
 XX Example; Page 49; 118pp; English.
 XX The patent discloses human epidermal growth factor (EGF)-like molecule
 CC containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic
 CC acids encoding them. EMR2 sequences are useful for treating acute
 CC inflammation caused by injury or infection (e.g. meningitis and
 CC pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic
 CC tissue damages, septic shock, atherosclerosis, repair and autoimmune
 CC disease processes, diabetes, Alzheimer's disease, processes such as
 CC killing of targets by degranulation, chemotaxis and leukocyte
 CC recruitment, induction and effector mechanism of innate and acquired
 CC immunity. They are also useful for treating conditions involving
 CC clotting, fibrinolysis, intravascular coagulation, thrombosis and
 CC embolism, wound repair and angiogenesis, haematopoiesis and blood
 CC disorders such as aneuploidy, agranulocytosis, migration, retention and
 CC activation or deactivation of phagocytes, myeloid leukaemia, anaemia,
 CC general disorders of connective tissue (e.g. vascular malfunction, wound
 CC healing) and congenital diseases such as hereditary haemorrhagic
 CC telangiectasia (HHT) and Marfan syndrome. They are also useful for
 CC controlling tumour formation and metastasis, for treating macrophage
 CC giant cells in bacterially-induced granuloma. Sequences of the invention
 CC are useful in the preparation of a medicament for use in a method of
 CC therapy of a condition or disease associated with EMR2 polypeptide and in
 CC the preparation of a diagnostic agent for use in the method of diagnosis
 CC of a condition or disease associated with EMR2 polypeptide. Antibodies
 CC against EMR2 are useful for treating infections such as bacterial,
 CC fungal, protozoan and viral infections, particularly infections caused by
 CC HIV-1 or HIV-2, pain, cancers, asthma, anorexia, Parkinson's disease,
 CC bulimia, hypotension, acute heart failure, hypertension, osteoporosis,
 CC urinary retention, angina pectoris, myocardial infarction, ulcers,
 CC allergies, benign prostatic hypertrophy, psychotic and neurological
 CC disorders including anxiety, schizophrenia, manic depression, delirium,
 CC dementia, severe mental retardation, dyskinesias such as Huntington's
 CC disease or Gilles de la Tourette's syndrome. The present DNA sequence is
 CC nested PCR primer, 3'-1 which is specific for human EMR2 cDNAs
 XX Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
 SQ Query Match 66.4%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 85;

		Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	727 TCCGAGGAGAACAGACACC 747	
Db	22 TCCGAGGAGAACAGACACC 2	
RESULT 18		
AD	AAD22809 standard; DNA; 22 BP.	
XX	AAD22809;	
AC		
XX		
DT	26-FEB-2002 (first entry)	
DE	Human EMR2 specific RT-PCR primer #1.	
XX		
KW	Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2;	
KW	epidermal growth factor; therapy; acute inflammation; injury; infection;	
KW	meningitis; pneumonia; chronic inflammation; chronic tissue damage;	
KW	rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;	
KW	diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation;	
KW	clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis;	
KW	haematopoiesis; blood disorder; aneuploidy; agranulocytosis; migration;	
KW	myeloid leukaemia; anaemia; vascular malfunction; congenital disease;	
KW	wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia;	
KW	HHT; tumour; infection; cancer; asthma; anorexia; Parkinson's disease;	
KW	bulimia; hypotension; acute heart failure; hypertension; osteoporosis;	
KW	urinary retention; angina pectoris; myocardial infarction; allergy;	
KW	ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;	
KW	schizophrenia; manic depression; delirium; dementia; mental retardation;	
KW	dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;	
KW	reverse transcription; RT-PCR primer; ss.	
OS	Homo sapiens.	
XX		
PN	WO200179296-A1.	
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-GB001729.	
XX		
PR	13-APR-2000; 2000GB-00009181.	
XX		
PA	(ISIS-) ISIS INNOVATION LTD.	
PI	Lin H, Gordon D, McKnight AJ, Stacey M;	
XX		
DR	WPI; 2002-026015/03.	
XX		
PT	Novel human epidermal growth factor (EGF)-like molecule containing mucin-like hormone receptor-2 polypeptide, useful for treating acute and chronic inflammation, chronic tissue damages and for wound healing.	
XX		
PS	Example; Page 50; 118pp; English.	
XX		
CC	The patent discloses human epidermal growth factor (EGF)-like molecule containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic acids encoding them. EMR2 sequences are useful for treating acute inflammation caused by injury or infection (e.g. meningitis and pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic tissue damages, septic shock, atherosclerosis, repair and autoimmune disease processes, diabetes, Alzheimer's disease, processes such as killing of targets by degranulation, chemotaxis and leukocyte recruitment, induction and effector mechanism of innate and acquired autoimmunity. They are also useful for treating conditions involving clotting, fibrinolysis, intravascular coagulation, thrombosis and embolism, wound repair and angiogenesis, haematopoiesis and blood disorders such as aneuploidy, agranulocytosis, migration, retention and activation or deactivation of phagocytes, myeloid leukaemia, anaemia, general disorders of connective tissue (e.g. vascular malfunction, wound healing) and congenital diseases such as hereditary haemorrhagic telangiectasia (HHT) and Marfan syndrome. They are also useful for	

CC	controlling tumour formation and metastasis, for treating macrophage giant cells in bacterially-induced granuloma. Sequences of the invention are useful in the preparation of a medicament for use in a method of therapy of a condition or disease associated with EMR2 polypeptide and in the preparation of a diagnostic agent for use in the method of diagnosis of a condition or disease associated with EMR2 polypeptide. Antibodies against EMR2 are useful for treating infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, asthma, anorexia, Parkinson's disease, bulimia, hypotension, acute heart failure, hypertension, osteoporosis, urinary retention, angina pectoris, myocardial infarction, ulcers, allergies, benign prostatic hypertrophy, psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation, dyskinesias such as Huntington's disease or Gilles de la Tourette's syndrome. The present DNA sequence is a reverse transcription (RT)-PCR primer which is specific for human EMR2 cDNA sequences	
XX		
SQ	Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;	
	Query Match	66.4%; Score 14.6; DB 1; Length 22;
	Best Local Similarity	81.0%; Pred. No. 85;
	Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	727 TCCGAGGAGAACAGACACC 747	
Db	22 TCCGAGGAGAACAGACACC 2	
RESULT 19		
AD	AAD22815/c	
ID	AAD22815 standard; DNA; 22 BP.	
XX		
AC	AAD22815;	
XX		
DT	26-FEB-2002 (first entry)	
XX		
DE	Human EMR2 7 transmembrane domain identifying primer #1.	
XX		
KW	Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2; epidermal growth factor; therapy; acute inflammation; injury; infection; meningitis; pneumonia; chronic inflammation; chronic tissue damage; rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease; diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation; clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis; haematopoiesis; blood disorder; aneuploidy; agranulocytosis; migration; myeloid leukaemia; anaemia; vascular malfunction; congenital disease; wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia; HHT; tumour; infection; cancer; asthma; anorexia; Parkinson's disease; bulimia; hypotension; acute heart failure; hypertension; osteoporosis; urinary retention; angina pectoris; myocardial infarction; allergy; ulcer; benign prostatic hypertrophy; neurological disorder; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; transmembrane domain; TW; PCR primer; ss.	
OS	Homo sapiens.	
XX		
PN	WO200179296-A1.	
XX		
PD	25-OCT-2001.	
XX		
PF	17-APR-2001; 2001WO-GB001729.	
XX		
PR	13-APR-2000; 2000GB-00009181.	
XX		
PA	(ISIS-) ISIS INNOVATION LTD.	
PI	Lin H, Gordon D, McKnight AJ, Stacey M;	
XX		
DR	WPI; 2002-026015/03.	
XX		
PT	Novel human epidermal growth factor-like molecule containing mucin-like	

PT hormone receptor-2 polypeptide, useful for treating acute and chronic
 XX inflammation, chronic tissue damages and for wound healing.
 PS Example; Page 51; 118pp; English.
 XX

The patent discloses human epidermal growth factor (EGF)-like molecule
 CC containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic
 CC acids encoding them. EMR2 sequences are useful for treating acute
 CC inflammation caused by injury or infection (e.g. meningitis and
 CC pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic
 CC tissue damages, septic shock, atherosclerosis, repair and autoimmune
 CC disease processes, diabetes, Alzheimer's disease, processes such as
 CC killing of targets by degranulation, chemotaxis and leukocyte
 CC recruitment, induction and effector mechanism of innate and acquired
 CC autoimmunity. They are also useful for treating conditions involving
 CC clotting, fibrinolysis, intravascular coagulation, thrombosis and
 CC embolism, wound repair and angiogenesis, hematopoiesis and blood
 CC disorders such as aneuploidy, granulocytosis, migration, retention and
 CC activation or deactivation of phagocytes, myeloid leukaemia, anaemia,
 CC general disorders of connective tissue (e.g. vascular malfunction, wound
 CC healing) and congenital diseases such as hereditary haemorrhagic
 CC telangiectasia (HHT) and Marfan syndrome. They are also useful for
 CC controlling tumour formation and metastasis, for treating macrophage
 CC giant cells in bacterially-induced granuloma. Sequences of the invention
 CC are useful in the preparation of a medicament for use in a method of
 CC therapy of a condition or disease associated with EMR2 polypeptide and in
 CC the preparation of a diagnostic agent for use in the method of diagnosis
 CC of a condition or disease associated with EMR2 polypeptide. Antibodies
 CC against EMR2 are useful for treating infections such as bacterial,
 CC fungal, protozoan and viral infections, particularly infections caused by
 CC HIV-1 or HIV-2, pain, cancers, asthma, anorexia, Parkinson's disease,
 CC bulimia, hypotension, acute heart failure, hypertension, osteoporosis,
 CC urinary retention, angina pectoris, myocardial infarction, ulcers,
 CC allergies, benign prostatic hypertrophy, psychotic and neurological
 CC disorders including anxiety, schizophrenia, manic depression, delirium,
 CC dementia, severe mental retardation, dyskinesias such as Huntington's
 CC disease or Gilles de la Tourette's syndrome. The present DNA sequence is a
 CC PCR primer which is used for identifying the 7 transmembrane domain (7TM)
 CC of EMR2 transcript
 XX

SQ Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 66.4%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 85;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 727 TCCGAGGAGAGACACACC 747
 | | | | | | | | | | | | | | | | | | | | | |
 Db 22 TCCGAGGAGAGACACACC 747

RESULT 20
 AAA85677/c
 ID AAA85677 standard; DNA; 19 BP.
 AC AAA85677;
 XX

DT 04-DEC-2000 (first entry)
 XX

DE Cyclin B1 ribozyme binding site #6.
 XX

Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX

Mammalia.
 XX

WO200032765-A2.
 FN

08-JUN-2000.
 PD

06-DEC-1999; 99WO-US028772.
 PF

04-DEC-1998; 98US-0110954P.
 PR

XX

(IMMU-) IMMUSOL INC.
 PA
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 XX WPI; 2000-412314/35.
 DR

New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 CC RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 CC PCNA and Cyclin B1.
 PT

Disclosure; Page 96; 109pp; English.
 XX

The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX

SQ Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 65.5%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 86;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGACACCG 748
 | | | | | | | | | | | | | | | | | | | | | |
 Db 19 GAGAAACAGACACCG 748

RESULT 21
 AAAH60839/c
 ID AAAH60839 standard; DNA; 19 BP.
 AC AAAH60839;
 XX

DT 10-SEP-2001 (first entry)
 XX

DE Cyclin B1 ribozyme binding site SEQ ID NO:3263.
 XX

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 CC recognition site; target; ribozyme binding site; eye disease; vulvular;
 CC proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 CC cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 CC matrix metalloproteinase; growth factor; reduction; scarring; cytostatic;
 CC antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 CC antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 CC atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 CC basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 CC sickle cell retinopathy; ss.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

WO200130362-A2.
 PN

03-MAY-2001.
 PD

26-OCT-2000; 2000WO-US029500.
 PF

26-OCT-1999; 99US-0161532P.
 PR

(IMMU-) IMMUSOL INC.
 PA

Robbins JM, Tritz R;
 FI

WPI; 2001-300427/31.
 DR

Treating proliferative skin or eye diseases and scarring, using ribozymes
 CC that cleave RNA encoding cytokines involved in inflammation, matrix
 CC metalloproteinases, growth factors and cell-cycle dependent kinases.
 PT

XX Example 1; Page 309; 408pp; English.

PS The present invention describes a method for treating a proliferative

XX skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnary, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX

XX Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 65.5%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 86;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAACAGACACCG 748

DB 19 GAGAGCAGACACCG 4

|||||

RESULT 22

AAH5941/C

ID AAH5941 standard; DNA; 19 BP.

XX

AC AAH5941;

XX

XX 04-DEC-2000 (first entry)

XX

DE Cdc 25 hs ribozyme binding site #49.

XX

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

KW Mammalia.

OS

XX WO200032765-A2.

PN

XX 08-JUN-2000.

PD

XX

XX 06-DEC-1999; 99WO-US028772.

PF

XX

XX 04-DEC-1998; 98US-0110954P.

PR

XX

XX (IMMU-) IMMUSOL INC.

PA

XX

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

PI

XX

XX WPI; 2000-412314/35.

DR

XX

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves

PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,

PT PCNA and Cyclin B1.

PT

XX

XX Disclosure; Page 100; 109pp; English.

PS

XX

XX The present invention relates to a hairpin or hammerhead ribozyme,

CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase

CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

CC

CC Representative examples of ribozyme recognition sites are given in

CC AAA82415 to AAA86787. The ribozyme of the invention is useful for

CC

CC inhibiting restenosis by introduction of the ribozyme into cells. The

CC ribozyme is resistant to endonuclease activity and hence is efficient in

CC restenosis treatment

XX

XX Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 64.5%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 92;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAGACAC 747

DB 19 CCAGGAGAACAGACAC 1

|||||

RESULT 23

AAH61103/C

ID AAH61103 standard; DNA; 19 BP.

XX

AC AAH61103;

XX

XX 10-SEP-2001 (first entry)

XX

XX Cdc25 hs ribozyme binding site SEQ ID NO:3527.

DE

XX

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

KW recognition site; target; ribozyme binding site; eye disease; vulnary;

KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;

KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

KW matrix metalloproteinase; growth factor; reductase; scarring; cycostatic;

KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;

KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;

KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;

KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;

KW sickle cell retinopathy; ss.

XX

OS Homo sapiens.

OS

XX Synthetic.

XX

XX WO200130362-A2.

PN

XX

XX 03-MAY-2001.

PD

XX

XX 26-OCT-2000; 2000WO-US029500.

PF

XX

XX 26-OCT-1999; 99US-0161532P.

PR

XX

XX (IMMU-) IMMUSOL INC.

PA

XX

XX Robbins JM, Tritz R;

PI

XX

XX WPI; 2001-300427/31.

DR

XX

XX Treating proliferative skin or eye diseases and scarring, using ribozymes

PT that cleave RNA encoding cytokines involved in inflammation, matrix

PT metalloproteinases, growth factors and cell-cycle dependent kinases.

PT

XX

XX Example 1; Page 328; 408pp; English.

PS

XX

XX The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnary, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloïd, adhesion and hypertrophic or hypertrophic burn
 CC scar. AHS7577 to AHS62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 64.5%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 92;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGAACACC 747
 Db 19 CCAGGAGAAACAAACACC 1

RESULT 24
 AAD30255
 ID AAD30255 standard; DNA; 21 BP.

XX AAD30255;
 XX
 DT 17-MAY-2002 (first entry)

XX Human PKD1 gene mutation detecting nested PCR primer, 5FL.

XX Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
 KW acquired cystic disease; transgenic animal; PCR primer; ss.

XX Homo sapiens.

XX WO200206529-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022035.

XX 13-JUL-2000; 2000US-0218261P.

PR 13-APR-2001; 2001US-0283691P.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Germino GG, Watnick TJ, Phakdeekitcharoen B;

XX WPI; 2002-179805/23.

XX Novel primer for diagnosing polycystic kidney disease-associated
 PT disorder, comprises regions having sequence that selectively hybridizes
 PT to polycystic kidney disease gene sequence.

XX Claim 6; Page 100; 192pp; English.

XX The present invention relates to compositions and methods useful for the
 CC identification and detection of polycystic kidney disease (PKD1) gene
 CC mutations. The invention also relates to primers comprising a 5' region
 CC having a sequence that selectively hybridizes to a PKD1 gene sequence and
 CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having
 CC a sequence that selectively hybridizes to a PKD1 gene sequence and not to
 CC a PKD1 homologue sequence. Primer pairs of the invention are useful for
 CC detecting the presence or absence of a mutation in a PKD1 polynucleotide
 CC in a sample, for identifying a subject at risk for a PKD1-associated
 CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
 CC acquired cystic disease and for diagnosing a PKD1-associated disorder in
 CC a subject. They are useful for selectively amplifying a region of a PKD1
 CC gene. PKD1 DNA fragments are useful detecting the presence of a mutant
 CC PKD1 polynucleotide in a sample, as a probe for an amplification
 CC reaction, in hybridisation or amplification assays of biological samples
 CC to detect abnormalities of PKD1 expression and for engineering transgenic
 CC animals. The present sequence is a PCR primer used to detect mutation in
 CC human PKD1 gene

XX Sequence 21 BP; 7 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 64.5%; Score 14.2; DB 1; Length 21;
 Best Local Similarity 84.2%; Pred. No. 96;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGAACACC 746
 Db 3 GCCAGGAGGAGCAGAACCC 21

RESULT 25
 AAV14110/C
 ID AAV14110 standard; DNA; 18 BP.

XX AAV14110;

XX 27-AUG-2003 (revised)

DT 19-MAY-1998 (first entry)

XX Probe HBP276 for RT pol region of HBV.

XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.

XX Synthetic.

XX Hepatitis B virus.

XX WO9740193-A2.

XX 30-OCT-1997.

XX 21-APR-1997; 97WO-EF002002.

XX 19-APR-1996; 96EP-00870053.

XX (INNO-) INNOGENETICS NV.

XX Stuyver L, Rossau R, Maertens G;

XX WPI; 1997-535867/49.

XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.

XX Claim 5; Fig 1; 80pp; English.

XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (I) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (I) with a combination of at least
 CC 2 nucleotide probes, which are applied to known locations on a solid
 CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACAG 5
RESULT 26
AAV02721
ID AAV02721 standard; DNA; 18 BP.
AC AAV02721;
XX 19-MAY-1998 (first entry)
DT Human Class I HLA gene probe GE2-183.
XX Human leukocyte antigen class I gene; allele testing; probe; donor;
KW tissue matching; recipient; graft rejection; class typing; ds.
XX Synthetic.
OS Homo sapiens.
XX WO9723645-A1.
XX 03-JUL-1997.
XX 04-JAN-1996; 96WO-US000362.
XX 04-JAN-1996; 96WO-US000362.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
PA Yang SY, Cereb N;
PI WPI; 1997-351080/32.
DR DNA-based human leukocyte antigen class I gene typing method - useful for
PT tissue matching and prevention of graft versus host disease.
PT Disclosure; Page 10; 89pp; English.
XX AAV02716-V02738 are hybridisation probes used in a novel method for
CC testing tissue samples to determine the allelic type of a human leukocyte
CC antigen (HLA) class I gene in the sample. The HLA Class I gene is
CC selected from among HLA-A, -B and -C genes. The method comprises of
CC treating the tissue sample to obtain nucleic acid polymers suitable for
CC amplification then combining these polymers with a first primer which
CC hybridises with a portion of intron 1 or intron 3 of the HLA Class I gene
CC and a second primer which hybridises with a different portion of the HLA
CC Class I gene under conditions suitable for amplification to obtain an
CC amplified product. The product is then evaluated to determine the allelic
CC type of the HLA-Class I gene. The method is useful for tissue matching
CC HLA class I antigens between donors and recipients and hence for
CC preventing graft versus host disease
XX
SQ Sequence 18 BP; 7 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 62.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;
QY 731 AGGAGAAACAGAACACC 747
Db 2 AGGAGACACGGAACACC 18
RESULT 27
AA11105
ID AA11105 standard; DNA; 18 BP.
XX AA11105;
AC
DT 28-JUL-2000 (first entry)
XX
Hybridisation probe GE2-183 for typing HLA Class I genes.
Tissue sample testing; allelic typing; human leukocyte antigen;
PCR primer; probe; hybridisation; intron; amplification; ss;
allelic variation; non-classical HLA class I gene; exon.
Homo sapiens.
US6030775-A.
29-FEB-2000.
22-DEC-1995; 95US-00577081.
22-DEC-1995; 95US-00577081.
(CERE/) CERE3 N.
(YANG/) YANG S Y.
Cereb N, Yang SY;
WPI; 2000-223159/19.
Testing a tissue sample to determine the allelic type of a human
leukocyte antigen class I gene comprises amplification of nucleic acid
polymers with primers which flank a region including an allelic variation
of the HLA class I gene.
Disclosure; Col 8; 90pp; English.
The invention relates to a method (I) for testing a tissue sample to
determine the allelic type of a human leukocyte antigen (HLA) class I
gene in the sample, where the HLA class I gene is selected from HLA-A,
HLA-B or HLA-C, by: (a) treating the tissue sample to obtain nucleic acid
polymers suitable for amplification; (b) combining the nucleic acid
polymers with a primer which hybridizes with a portion of intron 1 or
intron 3 of the HLA class I gene, and a second primer which hybridizes
with a different portion of the HLA class I gene and performing
CC amplification, where the primers flank a region including at least one
CC site of allelic variation in at least one of exons 2 or 3 of the HLA
CC class I gene and where the first primer is a locus specific primer which
CC hybridizes with intron 1 or 3 of only one of the HLA class I genes; and
CC (c) evaluating the amplified product to determine the allelic type of the
CC HLA class I gene. The method is useful for testing a tissue sample to
CC determine the allelic type of a classical or non-classical HLA class I
CC gene in the sample. The sequences AAA1039-A1122 represent consensus
CC sequences of introns and exons of the HLA genes and primers and probes
CC used to isolate and analyse the HLA genes
SQ Sequence 18 BP; 7 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 62.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;
QY 731 AGGAGAAACAGAACACC 747
Db 2 AGGAGACACGGAACACC 18
RESULT 28
AAZ57075/c
ID AAZ57075 standard; DNA; 20 BP.
XX AAZ57075;
AC
XX 19-MAY-2000 (first entry)
DT Murine melanocortin receptor MC3-R amplifying primer.
XX
Medicament; agonist; melanocortin receptor type 3; ACTH; PMN; MC3-R;
KW adrenocorticotrophic hormone; neutrophil chemoattractant; antigen;
KW polymorphonuclear cell; septic shock; skin disorder; antiarthritic;

KW melanocortin receptor; anti-inflammatory; anti-inflammatory; PCR primer; ss.
 OS Mus sp.
 XX
 XX WO200005263-A2.
 PN
 XX
 XX PD 03-FEB-2000.
 XX
 XX PF 22-JUL-1999; 99WO-GB002392.
 XX
 XX PR 24-JUL-1998; 98GB-00016234.
 XX
 XX PA (HARV-) HARVEY RES LTD WILLIAM.
 XX
 XX PI Perretti M, Getting S, Flower R;
 XX WPI; 2000-182651/16.
 XX
 XX DR Inhibition of neutrophil chemoattractant production, inhibition of
 PT polymorphonuclear cell accumulation or reduction/treatment of
 PT inflammation using compounds comprising the peptide sequence HFRW.
 XX
 XX PS Disclosure; Page 8; 20pp; English.
 XX
 XX CC The invention relates to the use of a compound comprising an amino acid
 CC sequence His-Phe-Arg-Tip (HFRW) in the manufacture of a medicament and/or
 CC an agonist of melanocortin receptor type 3 (MC3-R) where the compound is
 CC not adrenocorticotrophic hormone (ACTH)1-39. The compounds are used to
 CC inhibit neutrophil chemoattractant production, polymorphonuclear cell
 CC (PMN) accumulation or reduction/treatment of inflammation. Especially,
 CC these compounds are agonists of the MC3-R. The inflammatory response/
 CC disease is selected from gout, gouty arthritis, rheumatoid arthritis,
 CC asthma, reperfusion injury or damage, stroke, myocardial infarction,
 CC septic shock, or a skin disorder. Sequences AA257073-80 represent PCR
 CC primers used for amplifying murine melanocortin receptors
 XX
 XX SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 62.7%; Score 13.8; DB 1; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 732 GGAGAAACAGACACCG 748
 DB 19 GGAGAAACAGAGACAG 3
 RESULT 29
 ABT05166/c
 ID ABT05166 standard; DNA; 20 BP.
 XX
 XX AC ABT05166;
 XX
 XX DT 11-OCT-2002 (first entry)
 XX
 XX DE TNFR1 expression modulation related antisense oligo SEQ ID No 196.
 XX
 XX KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
 KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
 KW mouse; murine; ds.
 XX
 XX OS Mus sp.
 XX
 XX PN WO200248169-A1.
 XX
 XX PD 20-JUN-2002.
 XX
 XX PF 22-OCT-2001; 2001WO-US051224.
 XX
 XX PR 24-OCT-2000; 2000US-00695451.
 XX
 XX PA (ISIS-) ISIS PHARM INC.
 XX

PI Baker BF, Cowse LM, Zhang H, Dean NM;
 XX WPI; 2002-593481/62.
 XX
 XX PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
 PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
 PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
 XX
 XX PS Example 21; Page 61; 121pp; English.
 XX
 XX CC The invention relates to an antisense compound 8 to 30 nucleotides in
 CC length targeted to nucleic acid molecule encoding tumour necrosis factor
 CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
 CC TNFR1. The antisense compound is useful for inhibiting the expression of
 CC TNFR1 in cells or tissues. The antisense compound is also useful for
 CC treating an animal (preferably human) having a disease or condition
 CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
 CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
 CC the expression of TNFR1. The antisense compound is useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC This polynucleotide sequence represents a mouse oligonucleotide relating
 CC to the TNFR1 of the invention
 XX
 XX SQ Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 61.8%; Score 13.6; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 727 TGCCAGGAGAAACAGACAC 746
 DB 20 TGTAGGAGACTCAGACAC 1
 RESULT 30
 AAV14107/c
 ID AAV14107 standard; DNA; 18 BP.
 XX
 XX AC AAV14107;
 XX
 XX DT 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX
 XX DE Probe HBP273 for RT pol region of HBV.
 XX
 XX KW Probe; hepatitis B virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX
 XX OS Synthetic.
 OS Hepatitis B virus.
 XX
 XX PN WO9740193-A2.
 XX
 XX PD 30-OCT-1997.
 XX
 XX PF 21-APR-1997; 97WO-EP02002.
 XX
 XX PR 19-APR-1996; 96EP-00870053.
 XX
 XX PA (INNO-) INNOGENETICS NV.
 XX
 XX PI Stuyver L, Rossau R, Maertens G;
 XX WPI; 1997-535867/49.
 XX
 XX DR Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX
 XX PS Claim 5; Fig 1; 80pp; English.
 XX
 XX CC This sequence represents a probe for the RT pol region of hepatitis b

virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudine and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4

RESULT 31
AAV14104/c
ID AAV14104 standard; DNA; 18 BP.
XX AC AAV14104;
XX 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX Probe HBPr270 for RT pol region of HBV.
XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target; mutation detection; ss.
XX Synthetic.
OS Hepatitis B virus.
XX WO9740193-A2.
XX 30-OCT-1997.
XX 21-APR-1997; 97WO-EP002002.
XX 19-APR-1996; 96EP-00870053.
XX (INNO-) INNOGENETICS NV.
XX Stuyver L, Rossau R, Maertens G;
XX WPI; 1997-535867/49.
XX Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
XX Claim 5; Fig 1; 80pp; English.
XX This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudine and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

CC suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudine and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACAGA 4

RESULT 32
AAV14106/c
ID AAV14106 standard; DNA; 18 BP.
XX AC AAV14106;
XX 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX Probe HBPr272 for RT pol region of HBV.
XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target; mutation detection; ss.
XX Synthetic.
OS Hepatitis B virus.
XX WO9740193-A2.
XX 30-OCT-1997.
XX 21-APR-1997; 97WO-EP002002.
XX 19-APR-1996; 96EP-00870053.
XX (INNO-) INNOGENETICS NV.
XX Stuyver L, Rossau R, Maertens G;
XX WPI; 1997-535867/49.
XX Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
XX Claim 5; Fig 1; 80pp; English.
XX This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudine and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
 DB 18 GCCATGAGAAACAGA 4

RESULT 33
 AAX77255/c
 ID AAX77255 standard; DNA; 20 BP.

XX AC AAX77255;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 04-AUG-1999 (first entry)
 DE Hepatitis B virus genomic DNA amplifying primer BF108.
 XX
 XX Polymerase chain reaction; nested PCR; viral; mutation detection;
 KW lamivudine resistance; hepatitis B virus; PCR primer; ss.

XX Synthetic.
 XX Hepatitis B virus.
 XX JP11127860-A.
 XX
 XX 18-MAY-1999.
 XX 28-OCT-1997; 97JP-00296042.
 XX 28-OCT-1997; 97JP-00296042.
 XX (SAYA/) SAYAMA K.
 XX WPI; 1999-350321/30.

PT A highly sensitive detection method for detecting lamivudine resistant
 PT hepatitis B virus - using nested PCR.

XX Example; Page 6; 11pp; Japanese.
 XX The invention provides a highly sensitive method for detecting variation
 CC of viruses using a 2-step polymerase chain reaction (nested PCR) regime.
 CC The method comprises: (1) amplification of a predetermined region of
 CC viral DNA in the first round of PCR; (2) treatment of the amplified
 CC product with a restriction enzyme capable of cleavage of a product
 CC derived from the wild type virus, (3) amplification of the viral DNA with
 CC a second round of PCR using a primer designed to introduce a mismatch
 CC base, to form a restriction enzyme recognition site in the amplified
 CC product from the viral mutant, (4) treatment of the amplified product
 CC with a restriction enzyme capable of cleavage of the amplified product
 CC derived from the viral mutant, (5) detection of mutation of viruses by
 CC investigation of the restriction pattern. The method allows simple and
 CC highly sensitive detection of mutation in viral genomes using 2-step
 CC nested PCR method in a short period of time. Sequences AAX77255-263
 CC represent PCR primers used for the detection of lamivudine resistant
 CC hepatitis B virus by the method of the invention. (Updated on 27-AUG-2003
 CC to correct OS field.)
 XX
 XX Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
 DB 17 GCCAGGAGAAACGGA 3

RESULT 34
 AAA85942/c
 ID AAA85942 standard; DNA; 19 BP.

XX AC AAA85942;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Cdc 25 hs ribozyme binding site #50.
 XX
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX Mammalia.
 XX WO200032765-A2.
 XX
 XX 08-JUN-2000.
 XX
 XX 06-DEC-1999; 99WO-US028772.
 XX
 XX 04-DEC-1998; 98US-0110954P.
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX WPI; 2000-412314/35.
 XX
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.

XX Disclosure; Page 100; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 XX Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAGACAC 746
 DB 18 CCAGGAGAAACAAAC 1

RESULT 35
 AAA85940/c
 ID AAA85940 standard; DNA; 19 BP.

XX AC AAA85940;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Cdc 25 hs ribozyme binding site #48.
 DE
 XX

CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoariatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscikling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;
 Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 730 CAGGAGAAACAGAACACC 747
 |||||
 Db 19 CAGGAGAAACAAACC 2
 RESULT 38
 AAH61104/c
 ID AAH61104 standard; DNA; 19 BP.
 XX
 AC AAH61104;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cdc25 hs ribozyme binding site SEQ ID NO:3528.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoariatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 XX 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 XX that cleave RNA encoding cytokines involved in inflammation, matrix
 XX metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 XX Example 1; Page 328; 408pp; English.
 XX
 XX The present invention describes a method for treating a proliferative
 XX skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoariatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscikling,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAGAACAC 746
 |||||
 Db 18 CCAGGAGAAACAAAC 1
 RESULT 39
 AAH60841/c
 ID AAH60841 standard; DNA; 19 BP.
 XX
 AC AAH60841;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cyclin B1 ribozyme binding site SEQ ID NO:3265.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoariatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antiscikling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 XX 26-OCT-1999; 99US-0161532P.
 XX
 XX (IMMU-) IMMUSOL INC.
 XX
 XX Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 XX that cleave RNA encoding cytokines involved in inflammation, matrix
 XX metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 XX Example 1; Page 309; 408pp; English.
 XX
 XX The present invention describes a method for treating a proliferative
 XX skin or eye disease and scarring. The method involves administering a

CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulvar, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AA457577 to AA462099 represent sequences used in the
 CC exemplification of the present invention

XX SQ Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 728 GCCAGGAGAAACAGAAACA 745
 Db 18 GCGGGGAGAGCAGAAACA 1

RESULT 40

AAZ05107

ID AAZ05107 standard; DNA; 20 BP.

XX AC AAZ05107;

XX DT 07-OCT-1999 (first entry)

XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 XX paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 XX bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX OS Synthetic.

XX OS Chlamydia trachomatis.

XX FN WO9928475-A2.

XX PD 10-JUN-1999.

XX PF 27-NOV-1998; 98WO-IB001939.

XX PR 28-NOV-1997; 97FR-00015041.

XX PR 17-DEC-1997; 97FR-00016034.

XX PR 04-NOV-1998; 98US-0107077P.

XX PA (GEST) GENSET.

XX PI Griffais R;

XX DR WPI; 1999-371125/31.

XX PT Genome sequence of Chlamydia trachomatis.

XX PS Disclosure; Page 1743; 1755pp; English.

XX CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also

CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis; cervicitis; salpingitis; perihepatitis; bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

XX SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 729 CCAGGAGAAACAGAAACAC 746

Db 1 CCAGGAGAGCTAAGAAACAC 18

RESULT 41

ABV80008/c

ID ABV80008 standard; DNA; 17 BP.

XX AC ABV80008;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 1254.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

XX KW human testis expressed Patched like protein; testis; adrenal; liver;

XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 XX for identifying agonist and antagonist and specific binding partners, and
 XX for treating subjects having defects in HTPL.

XX PS Example 2; Page 228; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 58.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 727 TCCAGGAGAAACACA 742
 ||||| |||||
 Db 17 TCCAGGAGAAACACA 2
 RESULT 42
 ABV80009/c
 ID ABV80009 standard; DNA; 17 BP.
 XX
 AC ABV80009;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPL scanning oligonucleotide SEQ ID 1255.
 XX
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US0000663.
 PR 30-JAN-2001; 2001WO-US0000664.
 PR 30-JAN-2001; 2001WO-US0000665.
 PR 30-JAN-2001; 2001WO-US0000667.
 PR 30-JAN-2001; 2001WO-US0000668.
 PR 30-JAN-2001; 2001WO-US0000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 XX
 PS Example 2; Page 228; 718pp; English.
 XX
 CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 58.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 727 TCCAGGAGAAACACA 742
 ||||| |||||
 Db 16 TCCAGGAGAAACACA 1
 RESULT 43
 AAZ88792
 ID AAZ88792 standard; DNA; 19 BP.
 XX
 AC AAZ88792;
 XX
 DT 18-MAY-2000 (first entry)
 XX
 DE Human HLA Cw*07 Gene PCR primer Cw*07 forward.
 XX
 KW Human; HLA; tumor cell; major histocompatibility complex; MHC; vaccine;
 KW prophylaxis; treatment; lymphocyte; HLA; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200004918-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-DE002280.
 XX
 PR 21-JUL-1999; 98DE-01032840.
 XX
 PA (KERR/) KERKMAN-TUCEK A.
 XX
 PI Kerkman-Tucek A;
 XX
 DR WPI; 2000-182538/16.
 XX
 PT Tumor cells expressing human MHC I and II genes, methods of producing
 PT these and vaccines for immunotherapy of tumors.
 XX
 PS Example 3; Page 8; 17pp; German.
 XX
 CC This invention describes novel tumor cells (I), with a combination of
 CC major histocompatibility (MHC) I and II genes occurring in humans. The
 CC tumor cells, tumor cell library or vaccine described in the invention can
 CC be used for the prophylaxis or treatment of tumor diseases. AAZ88790-
 CC Z88805 represent PCR primers used to amplify the human lymphocyte HLA
 CC molecules described in the method of the invention.
 XX
 SQ Sequence 19 BP; 7 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 58.2%; Score 12.8; DB 1; Length 19;
 Best Local Similarity 87.5%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAGAC 744
 ||||| |||||

Db 4 CCGGAGACAGAC 19

RESULT 44
ABK15585/c
ID ABK15585 standard; cDNA; 19 BP.
XX
XX AC ABK15585;
XX AC
XX DT 08-MAY-2002 (first entry)
XX
DE DE Melanocortin 4 receptor (MC4R) isolation, reverse PCR primer.
XX
XX Melanocortin 4 receptor; MC4R; G-protein coupled receptor; appetite;
KW metabolic disorder; cachexia; anorexia; weaning-induced inappetence;
KW growth; diabetes; cancer; renal failure; cardiac disease; endotoxaemia;
KW fever; hepatic lipidosis; infection; inflammation; post partum sow;
KW dairy cow; livestock; poultry; shipping stress; crowding stress; obesity;
KW vaccine; PCR; primer; ss.
XX
XX Felidae.
OS Canidae.
XX
XX EP1167386-A1.
PN
XX 02-JAN-2002.
PD
XX 26-JUN-2001; 2001EP-00305509.
XX
PF 26-JUN-2000; 2000US-0213909P.
PR
XX (PFI2) PFIZER PROD INC.
PA
XX Hickman MA, Houseknecht KL, Robertson AS;
PI WPI; 2002-156598/21.
XX
XX Novel canine or feline melanocortin 4 receptor polypeptide for screening
PT modulator compounds useful for treating cachexia, anorexia, diabetes and
PT cancer.
XX
XX Disclosure; Page 10; 73pp; English.
XX
XX The invention describes a substantially pure canine or feline
CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be
CC used in the treatment of appetite-related or metabolic disorders
CC including cachexia, anorexia or weaning-induced inappetence and growth
CC leg, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,
CC fever, hepatic lipidosis, infection or inflammation, in a post partum
CC sow, dairy cow, companion animal, livestock animal, poultry animal,
CC animal suffering from shipping or crowding stress, lactating animal,
CC obese animal or a gravid animal. (I) is useful in the generation of
CC antibodies, as reagents in diagnostic assays, identification of other
CC cellular gene products involved in the regulation of appetite in animals,
CC as reagents in assays for screening for compounds that can be used in the
CC treatment of appetite disorders in animals. A ligand of MC4R is useful
CC for elaborating the biological function of MC4R gene product and for
CC ameliorating appetite disorders and metabolic disorders, in animals. This
CC sequence represents the reverse primer used with primer ABK15584 to
CC isolate feline and canine melanocortin 4 receptor (MC4R) clones, a G-
CC protein coupled receptor described in the method of the invention
XX
XX Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
SQ

Query Match 57.3%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. NO. 1.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps

RESULT 45
ABK15582/c
ID ABK15582 standard; cDNA; 19 BP.
XX AC
XX AC ABK15582;
XX DT 08-MAY-2002 (first entry)
XX DE Melanocortin 4 receptor (MC4R) detection, reverse PCR primer.
XX KW
XX KW Melanocortin 4 receptor; MC4R; G-protein coupled receptor; appetite;
XX KW metabolic disorder; cachexia; anorexia; weaning-induced inappetence;
XX KW growth; diabetes; cancer; renal failure; cardiac disease; endotoxaemia;
XX KW fever; hepatic lipidosis; infection; inflammation; post partum sow;
XX KW dairy cow; livestock; poultry; shipping stress; crowding stress; obesity;
XX KW vaccine; PCR; primer; ss.
XX OS Felidae.
XX OS Canidae.
XX XX
XX PN EPI167386-AL.
XX PD 02-JAN-2002.
XX PF 26-JUN-2001; 2001EP-00305509.
XX PR 26-JUN-2000; 2000US-0213909P.
XX XX (PFIZ) PFIZER PROD INC.
XX FA
XX PI Hickman MA, Houseknecht KL, Robertson AS;
XX DR WPI; 2002-156598/21.
XX XX
XX PT Novel canine or feline melanocortin 4 receptor polypeptide for screening
XX PT modulator compounds useful for treating cachexia, anorexia, diabetes and
XX PT cancer.
XX PS Example 1; Page 27; 73pp; English.
XX CC
XX CC The invention describes a substantially pure canine or feline
XX CC melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be
XX CC used in the treatment of appetite-related or metabolic disorders
XX CC including cachexia, anorexia or weaning-induced inappetence and growth
XX CC lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia,
XX CC fever, hepatic lipidosis, infection or inflammation, in a post partum
XX CC sow, dairy cow, companion animal, livestock animal, poultry animal,
XX CC animal suffering from shipping or crowding stress, lactating animal,
XX CC obese animal or a gravid animal. (I) is useful in the generation of
XX CC antibodies, as reagents in diagnostic assays, identification of other
XX CC cellular gene products involved in the regulation of appetite in animals,
XX CC as reagents in assays for screening for compounds that can be used in the
XX CC treatment of appetite disorders in animals. A ligand of MC4R is useful
XX CC for elaborating the biological function of MC4R gene product and for
XX CC ameliorating appetite disorders and metabolic disorders, in animals. This
XX CC sequence represents the reverse primer used with primer ABK15581 to
XX CC isolate feline and canine melanocortin 4 receptor (MC4R) clones, a G-
XX CC protein coupled receptor described in the method of the invention
XX XX
XX SQ Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 57.3%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Fred. No. 1.6e-02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0

Qy 728 GCCAGGAGAAACAGAACAC 746
 |||||
Db 19 GCCAGGAGCTACAGATCAC 1

RESULT 46
AAS56856/c
ID AAS56856 standard; DNA; 16 BP.

XX AC AAS56856;
 XX XX
 XX DT 16-JAN-2002 (first entry)
 XX XX
 XX DE Validation ribozyme DNA sequence #30.
 XX XX
 XX KW Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
 XX KW cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
 XX KW inhibitor dominant negative 4; breast basic conserved protein 1; BBC1;
 XX KW BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX FN WO200170982-A2.
 XX XX
 XX PD 27-SEP-2001.
 XX XX
 XX PF 23-MAR-2001; 2001WO-US009559.
 XX XX
 XX PR 23-MAR-2000; 2000US-00536058.
 XX XX
 XX PA (IMMU-) IMMUSOL INC.
 XX PA (BEGE/) BEGER C.
 XX PI Begger C, Barber J, Wong-Staal F;
 XX XX
 XX DR WPI; 2001-611503/70.
 XX XX
 XX PT Novel polypeptides that are the regulators of BRCA-1, useful for treating
 XX PT cancer and diagnosing the presence of neoplastic cells in biological
 XX PT sample.
 XX PS Disclosure; Fig 8; 97pp; English.
 XX XX
 XX CC Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators,
 XX CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA
 XX CC and primers used in the methods of the invention. Hybridisation of
 XX CC ribozymes to their targets results in cleavage of the RNA target. The
 XX CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-
 XX CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The
 XX CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor
 XX CC dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1),
 XX CC CHLR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and
 XX CC diagnosing cancer and other proliferative disorders. The severity of an
 XX CC incidence of cancer can be lessened by regulating tumour proliferation
 XX CC through modulation of BRCA-1 expression. The sequences of the invention
 XX CC are useful in the development of anti-cancer drugs
 XX XX
 XX SQ Sequence 16 BP; 0 A; 2 C; 6 G; 8 T; 0 U; 0 Other;
 XX XX
 XX Query Match 56.4%; Score 12.4; DB 1; Length 16;
 XX Best Local Similarity 92.9%; Pred. No. 1.6e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX XX
 XX QY 734 AGAACACAGACACC 747
 XX Db |||||
 XX 15 AGAACACAGACACC 2
 XX XX
 XX RESULT 47
 XX AAF56034/c
 XX ID AAF56034 standard; DNA; 17 BP.
 XX AC AAF56034;
 XX XX
 XX DT 18-APR-2001 (first entry)
 XX XX
 XX DE HBV DNA polymerase gene L528M mutation probe HBP-293.
 XX XX
 XX KW HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
 XX KW mutation detection; probe; ss.

OS Hepatitis B virus.
 XX XX
 XX FN WO200104358-A2.
 XX XX
 XX PD 18-JAN-2001.
 XX XX
 XX PF 05-JUL-2000; 2000WO-EP006306.
 XX XX
 XX PR 08-JUL-1999; 99EP-00870148.
 XX PR 13-JUL-1999; 99US-0143546P.
 XX XX
 XX PA (INNO-) INNOGENETICS NV.
 XX XX
 XX PI Stuyver L, Maertens G, Van Geyt C;
 XX XX
 XX DR WPI; 2001-139370/14.
 XX XX
 XX PT Monitoring anti-HBV drug resistance by genetic detection of mutations in
 XX PT DNA polymerase of HBV in patient's sample, involves hybridizing the
 XX PT polynucleic acids of the sample with a probe and detecting the hybrid.
 XX XX
 XX PS Claim 2; Page 9; 64pp; English.
 XX XX
 XX CC The present sequence is a probe used in a method for monitoring anti-
 XX CC hepatitis B virus (HBV) drug resistance in a patient by genetic detection
 XX CC of any one of mutations L528M, M552V/I and/or V/L/M551 in HBV DNA
 XX CC polymerase in a biological sample from the patient. The method is useful
 XX CC in the field of genetic detection of anti-HBV drug resistance during HBV
 XX CC therapy. The method is rapid, reliable and precise
 XX XX
 XX SQ Sequence 17 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 XX XX
 XX Query Match 56.4%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 1.6e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX XX
 XX QY 728 GCCAGGAGAAACAG 741
 XX Db |||||
 XX 14 GCCAGGAGAAACGG 1
 XX XX
 XX RESULT 48
 XX ABV80011/c
 XX ID ABV80011 standard; DNA; 17 BP.
 XX AC ABV80011;
 XX XX
 XX DT 03-JAN-2003 (first entry)
 XX XX
 XX DE Human HTPL scanning oligonucleotide SEQ ID 1257.
 XX XX
 XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 XX KW human testis expressed patched like protein; testis; adrenal; liver;
 XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX FN EP1229046-A2.
 XX XX
 XX PD 07-AUG-2002.
 XX XX
 XX PF 26-JAN-2002; 2002EP-00001167.
 XX XX
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 23-MAY-2001; 2001US-00864761.
 XX PR 09-OCT-2001; 2001US-0327898P.
 XX XX

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PA (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 228; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 56.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACA 740
Db 14 TGCCAGGTGAAACA 1
RESULT 49
ABV80010/C
ID ABV80010 standard; DNA; 17 BP.
AC ABV80010;
XX
XX 03-JAN-2003 (first entry)
XX
XX Human HTPL scanning oligonucleotide SEQ ID 1256.
XX
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EP1229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000653.
XX
XX 30-JAN-2001; 2001WO-US000654.
XX
XX 30-JAN-2001; 2001WO-US000655.
XX
XX 30-JAN-2001; 2001WO-US000656.
XX
XX 30-JAN-2001; 2001WO-US000657.
XX
XX 30-JAN-2001; 2001WO-US000658.
XX
XX 30-JAN-2001; 2001WO-US000659.
XX
XX 23-MAY-2001; 2001US-00864761.
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PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 228; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
XX Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 56.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAACA 740
Db 15 TGCCAGGTGAAACA 2
RESULT 50
AAQ69166/C
ID AAQ69166 standard; DNA; 18 BP.
XX
XX AAQ69166;
XX
XX 25-MAR-2003 (revised)
XX
XX 14-FEB-1995 (first entry)
XX
XX PCR primer LDGF1 UTR-5'.
XX
XX Leucocyte derived growth factor 2; mitogenic; chemotactic; PDGF;
XX receptors; platelet derived growth factor; coagulation; inflammation;
XX immune response; cell growth; coagulation; amplification; ss.
XX
XX Synthetic.
XX
XX WO9416070-A1.
XX
XX 21-JUL-1994.
XX
XX 07-JAN-1994; 94WO-US000300.
XX
XX 07-JAN-1993; 93US-00001177.
XX
XX 07-JAN-1994; 94US-00179656.
XX
XX (UYSP-) UNIV SOUTH FLORIDA.
XX
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PI Grotendorst GR, Iida N;
 XX WPI; 1994-249217/30.
 XX
 XX New leukocyte derived growth factor 2 - having mitogenic and/or
 PT chemotactic activity, partic. for connective tissue cells, used esp. for
 PT wound healing.
 XX
 XX Disclosure; Page 24; 58pp; English.
 XX
 XX The sequence is that of a PCR primer used for the amplification of a
 CC leukocyte derived growth factor 2 having mitogenic and/or chemotactic
 CC activity. LDGF2 reacts with PDGF receptors and can be used in wound
 CC healing, coagulation, inflammation, immune responses and cell growth. See
 CC also AAQ69162-73. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 XX Sequence 18 BP; 1 A; 4 C; 3 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 56.4%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGAAC 745
 DB 16 GCAGAAACAGAAC 3
 RESULT 51
 AAV14112/c
 ID AAV14112 standard; DNA; 18 BP.
 XX
 XX AAV14112;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX
 DE Probe HBPr278 for RT pol region of HBV.
 XX
 XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX
 XX Synthetic.
 OS Hepatitis B virus.
 XX
 XX WO9740193-A2.
 PN
 PD 30-OCT-1997.
 XX
 XX 21-APR-1997; 97WO-EP002002.
 XX
 XX 19-APR-1996; 96EP-00870053.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Stuyver L, Rossau R, Maertens G;
 PI WPI; 1997-535867/49.
 XX
 XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX
 XX Claim 5; Fig 1; 80pp; English.
 XX
 XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (i) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the

CC support and hybridise specifically to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the
 CC differential hybridisation signal(s). The composition can be used to
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample.
 CC Specifically genotype, preCore mutations, vaccine escape mutations and RT
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 XX Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 56.4%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAG 741
 DB 18 GCCATGAGAACAG 5
 RESULT 52
 AAV14109/c
 ID AAV14109 standard; DNA; 18 BP.
 XX
 XX AAV14109;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 19-MAY-1998 (first entry)
 XX
 DE Probe HBPr275 for RT pol region of HBV.
 XX
 XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
 KW preCore region; HBsAg region; genotype specific target;
 KW mutation detection; ss.
 XX
 XX Synthetic.
 OS Hepatitis B virus.
 XX
 XX WO9740193-A2.
 PN
 PD 30-OCT-1997.
 XX
 XX 21-APR-1997; 97WO-EP002002.
 XX
 XX 19-APR-1996; 96EP-00870053.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Stuyver L, Rossau R, Maertens G;
 PI WPI; 1997-535867/49.
 XX
 XX Detection and/or genetic analysis of hepatitis B virus - specifically
 PT genotype, preCore mutations, vaccine escape mutations and RT gene
 PT mutations selected by treatment with drugs.
 XX
 XX Claim 5; Fig 1; 80pp; English.
 XX
 XX This sequence represents a probe for the RT pol region of hepatitis b
 CC virus (HBV). This sequence can be used in the method of the invention for
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
 CC The method comprises: (a) optionally releasing, isolating or
 CC concentrating polynucleic acids (i) in the sample, and amplifying the
 CC relevant part of a suitable HBV gene in the sample with at least 1
 CC suitable primer pair; (b) hybridising (i) with a combination of at least
 CC 2 nucleotide probes, which are applied to mutant target sequences chosen from
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
 CC genotype specific target sequences, or their complements or U for T
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring
 CC the HBV genotype and/or mutants present in the sample from the

CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 18 BP; 1 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 56.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACGG 5

RESULT 53
ABT11223/c
ID ABT11223 standard; DNA; 19 BP.
XX
AC ABT11223;
XX
DT 12-DEC-2002 (first entry)
XX
DE TRC8 related PCR primer SEQ ID No 28.
XX
KW TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3.2;
KW FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT;
KW human chromosomal translocation; PCR; primer; ss.
XX
OS Homo sapiens.
XX
FN US2002106656-A1.
XX
PD 08-AUG-2002.
XX
PF 02-JUL-2001; 2001US-00899833.
XX
PR 12-MAR-1998; 98US-0077723P.
PR 12-MAR-1999; 99US-00268140.
XX
PA (GEMM/) GEMMILL R M.
PA (DRAB/) DRABKIN H A.
XX
PI Gemmill RM, Drabkin HA;
XX
WPI; 2002-712395/77.
XX
PT Novel Translocation in Renal cancer from Chromosome 8 genes, useful for
PT detection of tumors, comprises rearrangements in the t(3;8)(p14.2;q24.1)
PT chromosomal translocation which occurs in renal and thyroid carcinomas.
XX
PS Claim 9; Page 10; 49pp; English.
XX
CC The invention relates to an isolated TRC8 (Translocation in Renal cancer
CC from Chromosome 8) nucleic acid molecule, encoding a polypeptide
CC comprising a sequence of 664 amino acids fully defined in the
CC specification and comprising a sequence located in the 5' flanking region
CC to the coding region of TRC8 and a sequence which occurs in certain
CC sporadic renal cell carcinomas. The methods are useful for detecting the
CC presence of the TRC8 gene in a biological sample, detecting alterations
CC to the gene, such as a 3;2 human chromosomal translocation, and fused DNA
CC containing the fused site of TRC8/FHIT. A nucleic acid probe is useful
CC for detecting the 3;8 human chromosomal translocation, by contacting the
CC nucleic acid probe with a biological sample to be tested, and determining
CC whether the nucleic acid probe specifically hybridises to the TRC8FHIT or
CC FHIT/TRC8 fusion DNA. This polynucleotide sequence represents a TRC8
CC related PCR primer of the invention
XX
SQ Sequence 19 BP; 2 A; 3 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 56.4%; Score 12.4; DB 1; Length 19;

Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACA 740
Db 16 TGCCAGGAGAAACA 3

RESULT 54
ABK10445/c
ID ABK10445 standard; DNA; 19 BP.
XX
AC ABK10445;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human TRC8 coding region SSCP PCR primer 4F.
XX
KW Human; ss; translocation in renal cancer from chromosome 8; 4F; TRC8;
KW fragile histidine triad; FHIT; renal cell carcinoma; t(3; 8);
KW single-stranded conformational polymorphism; thyroid tumour; PCR; primer;
KW SSCP.
XX
OS Homo sapiens.
XX
FN US6268176-B1.
XX
PD 31-JUL-2001.
XX
PF 12-MAR-1999; 99US-00268140.
XX
PR 12-MAR-1998; 98US-0077723P.
XX
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Gemmill RM, Drabkin HA;
XX
WPI; 2002-224110/28.
XX
PT New TRC8 (Translocation in Renal Cancer from Chromosome 8) polypeptide,
PT useful for diagnosing tumors, particularly for determining TRC8 gene
PT expression in samples.
XX
PS Example 5; Col 17; 45pp; English.
XX
CC The invention relates to a polypeptide (which is the product of the
CC expression in a host cell of a DNA) TRC8 (Translocation in Renal Cancer
CC from Chromosome 8). Also included are a polypeptide product of the
CC expression in a host cell of a DNA, comprising (a) culturing a host cell
CC containing a vector comprising a nucleic acid molecule encoding the
CC polypeptide comprising TRC8 and (b) recovering the polypeptide. The gene
CC encoding TRC8 is located in the chromosomal translocation region t(3;8),
CC resulting in a fusion with the fragile histidine triad gene, FHIT. This
CC region is associated with renal and thyroid tumors (especially renal
CC cell carcinoma, RCC). The polypeptide is useful for diagnosing tumors,
CC particularly for determining if the TRC8 gene is expressed in samples.
CC The present sequence is an single-stranded conformational polymorphism
CC (SSCP) PCR primer used to identify tumour specific mutations in TRC8 in
CC sporadic renal cell carcinoma samples
XX
SQ Sequence 19 BP; 2 A; 3 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 56.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 727 TGCCAGGAGAAACA 740
Db 16 TGCCAGGAGAAACA 3

RESULT 55
AAZ70293/c

ID AAZ70293 standard; DNA; 18 BP.
 AC AAZ70293;
 XX
 XX 10-SEP-2001 (first entry)
 XX
 XX Human biallelic marker upstream amplification primer SEQ ID NO:4649.
 DE
 XX Human genome; biallelic marker; high density disequilibrium map;
 XX Genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9954500-A2.
 XX
 XX 28-OCT-1999.
 XX
 XX 21-APR-1999; 99WO-IB000822.
 XX
 XX 21-APR-1998; 98US-0082614P.
 PR
 PR 23-NOV-1998; 98US-01097322.
 XX
 XX (GEST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI
 XX WPI; 2000-013267/01.
 DR
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 PT
 XX
 XX Claim 8; Page 1222; 2745pp; English.
 PS
 XX AAZ5654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 XX Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 55.5%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 1.8e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGACACC 747
 DE |||||
 Db 17 AGGAGAAACAGAGGAAAC 1
 RESULT 56
 AAZ36131/C
 ID AAZ36131 standard; DNA; 17 BP.
 XX
 XX AAZ36131;
 AC
 XX 26-JUL-2000 (first entry)
 DT
 XX Human genomic SNP allele specific oligonucleotide SEQ ID NO:188.
 DE
 XX

KW Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200018960-A2.
 XX
 XX 06-APR-2000.
 PD
 XX 24-SEP-1999; 99WO-US022283.
 PF
 XX 25-SEP-1998; 98US-0101757P.
 PR
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX Landers JE, Jordan B, Housman DE, Charest A;
 PI
 XX WPI; 2000-293181/25.
 DR
 XX Detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs.
 PT
 XX Disclosure; Page 59; 111pp; English.
 PS
 XX A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a SNP
 CC allele. The method can be used to characterise a tumour, to generate a
 CC genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be used
 CC to perform linkage analysis. AAZ35944 to AAZ35947 represent sequences
 CC used in the exemplification of the present invention. AAZ35948 to
 CC AAZ36632 represent nucleotide sequences containing SNPs
 XX
 XX Sequence 17 BP; 1 A; 2 C; 5 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 54.5%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 736 AAACAGACACC 747
 Db 13 AAACAGACACC 2
 RESULT 57
 AAF16608
 ID AAF16608 standard; DNA; 17 BP.
 XX
 XX AAF16608;
 AC
 XX 13-MAR-2001 (first entry)
 DT
 XX Gastric acid production inhibiting oligonucleotide SEQ ID NO: 95.
 DE
 XX Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
 KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antitense;
 KW DNA-RNA hybrid; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200071164-A1.
 PN
 XX 30-NOV-2000.
 PD
 XX 24-MAY-2000; 2000WO-AU000498.
 PF
 XX

PR 24-MAY-1999; 99AU-00000510.
XX (TACH/) TACHAS G.
XX Tachas G;
PI WPI; 2001-025093/03.
DR Treating gastric acid disturbance by administering an oligonucleotide
XX PT which modulates the activity of a polypeptide involved in gastric acid
XX production or secretion.
XX Example 3; Page 149; 164pp; English.
XX The present invention provides oligonucleotides, and methods for their
XX use, which are useful in modulating the action of proteins involved in
XX gastric acid production. The target protein is preferably the histamine
XX H2 receptor or one of the proteins which form part of the gastric proton
XX pump. The sequences and methods of the invention are useful in the
XX treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
XX duodenal ulcers and other gastric acid disturbances, most of which are
XX caused by Helicobacter pylori.
XX Sequence 17 BP; 10 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
SQ Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGACACCG 748
DB ||||| ||||| |||||
3 AGGAACAGACACAG 17
RESULT 59
ABV80007/c
ID ABV80007 standard; DNA; 17 BP.
XX AC ABV80007;
XX DT 03-JAN-2003 (first entry)
XX DE Human HTPL scanning oligonucleotide SEQ ID 1253.
XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX KW human testis expressed Patched like protein; testis; adrenal; liver;
XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX OS Homo sapiens.
XX PN EP1229046-A2.
XX PD 07-AUG-2002.
XX PF 28-JAN-2002; 2002EP-00001167.
XX PR 30-JAN-2001; 2001WO-US0000663.
XX PR 30-JAN-2001; 2001WO-US0000664.
XX PR 30-JAN-2001; 2001WO-US0000665.
XX PR 30-JAN-2001; 2001WO-US0000667.
XX PR 30-JAN-2001; 2001WO-US0000668.
XX PR 30-JAN-2001; 2001WO-US0000669.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 09-OCT-2001; 2001US-0327898P.
XX PA (AEOM-) AEOMICA INC.
XX PI Zhan J;
XX DR WPI; 2002-676582/73.
XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX Example 2; Page 228; 718pp; English.
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention
SQ Sequence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 53.6%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
DB ||||| ||||| |||||
17 GCCAGGTGAACACA 3
RESULT 59
ACC54250/c
ID ACC54250 standard; DNA; 17 BP.
XX AC ACC54250;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #3017.
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 737; 798pp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated

CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 Db 15 CTGGAGAAACAGATC 1

RESULT 60
 ABT35836/c
 ID ABT35836 standard; DNA; 17 BP.

AC ABT35836;
 XX
 DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 1473.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

XX Homo sapiens.

OS WO2003025175-A2.

PN 27-MAR-2003.

PD 17-SEP-2002; 2002WO-IB004208.

PF 17-SEP-2001; 2001FR-00011978.

PR (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

PI WPI; 2003-313353/30.

DR New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

XX Disclosure; Page 205; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids, and
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and

CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX

SQ Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 Db 15 CAGGAGACACAGATC 1

RESULT 61
 ACD50569/c
 ID ACD50569 standard; RNA; 17 BP.

XX ACD50569;

XX 23-SEP-2003 (first entry)

DE HBV hammerhead ribozyme substrate sequence #137.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis B virus.

PN WO200281494-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002WO-US009187.

PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296878P.

PR 24-OCT-2001; 2001US-0330599P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.

PS Example 1; Page 138; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 0 A; 5 C; 4 G; 0 T; 8 U; 0 Other;
 Query Match 53.6%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAAACAGA 742
 DB 16 GCCAAGAGAAACGGA 2
 RESULT 62
 ACDS0568/c
 ID ACDS0568 standard; RNA; 17 BP.
 XX
 AC ACDS0568;
 XX
 DT 23-SEP-2003 (first entry)
 XX
 DE HBV hammerhead ribozyme substrate sequence #136.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX

DR WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PS
 XX Example 1; Page 138; 387pp; English.
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyne sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 1 A; 5 C; 4 G; 0 T; 7 U; 0 Other;
 Query Match 53.6%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAAACAGA 742
 DB 17 GCCAAGAGAAACGGA 3
 RESULT 63
 ACDS1996/c
 ID ACDS1996 standard; RNA; 17 BP.
 XX
 AC ACDS1996;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HBV inozyme substrate sequence #177.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 XX

PI Stuyver L, Rossau R, Maertens G;
XX WPI; 1997-535867/49.
XX
XX Detection and/or genetic analysis of hepatitis B virus - specifically
PT genotype, preCore mutations, vaccine escape mutations and RT gene
PT mutations selected by treatment with drugs.
XX
XX Claim 5; Page 32; 80pp; English.
XX
XX This sequence represents a probe for the RT pol region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to mutant target sequences chosen from
CC support and hybridise specifically to mutant target sequences on a solid
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and inferring
CC the HBV genotype and/or mutants present in the sample from the
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 18 BP; 1 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4
|||||
AAV14105;
AAV14105 standard; DNA; 18 BP.

RESULT 66
AAV14105/c
ID AAV14105 standard; DNA; 18 BP.
AC AAV14105;
XX
XX 27-AUG-2003 (revised)
DT 19-MAY-1998 (first entry)
XX
XX Probe HBPz271 for RT pol region of HBV.
DE
XX
XX Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
KW preCore region; HBsAg region; genotype specific target;
KW mutation detection; ss.
XX
XX Synthetic.
OS Hepatitis B virus.
XX
XX WO9740193-A2.
FN
XX
XX 30-OCT-1997.
PD
XX
XX 21-APR-1997; 97WO-EP002002.
PF
XX
XX 19-APR-1996; 96EP-00870053.
PR
XX (INNO-) INNOGENETICS NV.
PA
XX
XX Stuyver L, Rossau R, Maertens G;
PI
XX
XX WPI; 1997-535867/49.
XX
XX Detection and/or genetic analysis of hepatitis B virus - specifically

PT genotype, preCore mutations, vaccine escape mutations and RT gene
XX mutations selected by treatment with drugs.
XX
XX Claim 5; Fig 1; 80pp; English.
XX
XX This sequence represents a probe for the RT pol region of hepatitis b
CC virus (HBV). This sequence can be used in the method of the invention for
CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
CC The method comprises: (a) optionally releasing, isolating or
CC concentrating polynucleic acids (I) in the sample, and amplifying the
CC relevant part of a suitable HBV gene in the sample with at least 1
CC suitable primer pair; (b) hybridising (I) with a combination of at least
CC 2 nucleotide probes, which are applied to mutant target sequences on a solid
CC support and hybridise specifically to mutant target sequences chosen from
CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
CC genotype specific target sequences, or their complements or U for T
CC homologues; (c) detecting the hybrids formed in step (b), and inferring
CC the HBV genotype and/or mutants present in the sample from the
CC differential hybridisation signal(s). The composition can be used to
CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
CC specifically genotype, preCore mutations, vaccine escape mutations and RT
CC gene mutations selected by treatment with drugs, e.g. lamivudine and
CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4
|||||
AAV14105;
AAV14105 standard; DNA; 18 BP.

RESULT 67
AAV14105/c
ID AAV14105 standard; DNA; 18 BP.
AC AAV14105;
XX
XX 15-JUL-1999 (first entry)
DT
XX
XX HIV-1 Group O env PCR primer SEQ ID NO:42.
DE
XX
XX HIV; human immunodeficiency virus; antigen; detection; antibody;
KW differentiation; Group O; env; immunogen; immunoassay; ss.
KW
XX
XX Synthetic.
OS Human immunodeficiency virus 1.
OS
XX
XX WO9909179-A2.
FN
XX
XX 25-FEB-1999.
PD
XX
XX 17-AUG-1998; 98WO-US017014.
PF
XX
XX 15-AUG-1997; 97US-00911824.
PR
XX
XX (ABBO) ABBOTT LAB.
PA
XX
XX Hackett JR, Yamaguchi J, Golden AM, Brennan CA, Hickman RK;
PI
XX
XX WPI; 1999-190167/16.
DR
XX
XX New isolated HIV-1 Group O env polypeptides - used for the detection of
PT anti-HIV antibodies and for the production of antibodies for use in
PT detection, purification and therapy.
XX
XX Example 3; Page 69; 138pp; English.
XX
XX The present invention describes (A) an isolated HIV-1 Group O env
CC polypeptide. Also described are: (1) an isolated HIV-1 Group O env

CC polypeptide comprising an immunoreactive portion of a polypeptide as in (A); (2) a polynucleotide (PN) encoding a polypeptide as in (A) or (1);
 CC (3) an antigen construct comprising a first HIV-1 Group O env polypeptide
 CC fused to a second HIV-1 Group O env polypeptide; (4) an antigen construct
 CC comprising a fusion of at least one HIV-1 Group O env polypeptide with at
 CC least one HIV-1 Group M env polypeptide; (5) an antigen construct
 CC comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env
 CC polypeptide, and at least one additional HIV-1 polypeptide; (6) an
 CC antigen construct comprising a first HIV-2 env polypeptide fused to a
 CC second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as
 CC in (3)-(6); (8) an expression vector comprising a PN as in (7); (9) a
 CC host cell transformed by an expression vector as in (8); and (10) an
 CC immunoassay kit for the detection of antibodies to HIV-1 comprising an
 CC antigen construct as in (3)-(6). The antigen constructs can be used for
 CC the detection of anti-HIV-1 antibodies in test samples. They can also be
 CC used as immunogens to produce antibodies. The antibodies can be used to
 CC purify HIV polypeptides, for therapy and for detection of HIV
 CC polypeptides
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 DB 3 CAGCAGGAACAGAAC 17

RESULT 68
 AAX37184
 ID AAX37184 standard; DNA; 18 BP.
 XX
 AC AAX37184;
 XX
 XX
 DT 06-JUL-1999 (first entry)
 XX
 DE PCR primer Seq ID No: 42.
 XX
 XX HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;
 KW antibody; assay; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9909410-A2.
 PN
 XX
 PD 25-FEB-1999.
 XX
 PF 07-AUG-1999; 98WO-US016506.
 XX
 PR 15-AUG-1997; 97US-00912129.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 XX Vallari AS, Hackett JR, Hickman RK, Varitek V, Necklaws EC;
 PI Golden AM, Brennan CA, Devare SG;
 XX
 DR WPI; 1999-190224/16.

XX New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 - can
 PT be used in field assay, requiring no electricity and less specialised
 PT equipment.
 XX
 PS Example; Page 50; 104pp; English.
 XX
 CC The invention relates to a rapid assay for simultaneous detection and
 CC differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The
 CC method comprises (a) contacting the sample with a strip containing at
 CC least one immobilised capture reagent per analyte and on which the sample
 CC moves from the proximal to the distal end by capillary action, under
 CC conditions sufficient to form capture reagent/analyte complexes, and (b)
 CC determining the presence of analyte(s) by detecting a visible colour

CC change at the capture reagent site on the strip wherein the capture
 CC reagent for HIV-1 group O comprises a polypeptide shown in AA06977-80
 CC and AA06983-84; and that for HIV-1 group M comprises a polypeptide shown
 CC in AA06982; and that for HIV-2 comprises the polypeptide shown in
 CC AA06981. The invention is used to screen patients for antibodies to HIV-
 CC 1 types O and M, and HIV-2. The invention will be particularly useful in
 CC places and situation where equipment and/or electricity is not available.
 CC The invention provides a screening method which is faster and requires
 CC less equipment than prior art methods
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 53.6%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAAC 744
 |||||
 DB 3 CAGCAGGAACAGAAC 17

RESULT 69
 AAF73900/c
 ID AAF73900 standard; DNA; 15 BP.
 XX
 AC AAF73900;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Human SLC6A4 allele-specific oligonucleotide primer #20.
 XX
 KW Solute carrier family 6 neurotransmitter transporter; seotonin 4; SLC6A4;
 KW genotyping; allele specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200109161-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000WO-US020638.
 XX
 PR 29-JUL-1999; 99US-0148290P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
 PI
 XX WPI; 2001-123317/13.

XX New isolated polynucleotide comprising a polymorphic variant for the
 PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
 PT gene for identifying drugs for treating disorders related to expression
 PT of the protein.
 XX
 PS Claim 12; Page 21; 152pp; English.
 XX
 CC The present invention relates to a polymorphic variant of a reference
 CC sequence for the solute carrier family 6 neurotransmitter transporter,
 CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
 CC complementary to the first sequence. The invention is used in producing a
 CC recombinant organism that can be used to express SLC6A4 for protein
 CC structure analysis and binding studies. A composition comprising a
 CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
 CC gene
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 51.8%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACAG 741


```

XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX DR WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 128; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX CC treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AA67275 to AA75752 represent specific examples
XX CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 9 A; 1 C; 3 G; 0 T; 4 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAAC 745
DB 2 GAGAAAUAGAAC 14
RESULT 73
ABV80012/c
ID ABV80012 standard; DNA; 17 BP.
XX AC ABV80012;
XX DT 03-JAN-2003 (first entry)
XX DE Human HTPL scanning oligonucleotide SEQ ID 1258.
XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX KW human testis expressed Patched like protein; testis; adrenal; liver;
XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX OS Homo sapiens.
XX PN EP1229046-A2.
XX PD 07-AUG-2002.
XX PF 28-JAN-2002; 2002EP-00001167.
XX PR 30-JAN-2001; 2001WO-US000653.
XX PR 30-JAN-2001; 2001WO-US000654.
XX PR 30-JAN-2001; 2001WO-US000655.
XX PR 30-JAN-2001; 2001WO-US000656.
XX PR 30-JAN-2001; 2001WO-US000657.
XX PR 30-JAN-2001; 2001WO-US000658.
XX PR 30-JAN-2001; 2001WO-US000659.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 09-OCT-2001; 2001US-0327898P.
XX PA (ABOM-) ABOMICA INC.
XX PI Zhan J;
XX DR WPI; 2002-676582/73.
XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
XX PT for identifying agonist and antagonist and specific binding partners, and
XX PT for treating subjects having defects in HTPL.
XX PS Example 2; Page 228; 718pp; English.
XX CC The present invention relates to human testis expressed patched like
XX CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
XX CC has two isoforms, with a few single base pair differences between the
XX CC two. One of the single base pair changes introduces a premature stop
XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX CC shares an overall structure organisation with the Patched protein. The
XX CC shared structural features strongly imply that HTPL plays a role similar
XX CC to that of Patched, and is a potential tumour suppressor. HTPL is
XX CC important in regulating male germ cell development, and the HTPL gene was
XX CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX CC useful for diagnosing a disorder caused by mutation in HTPL, and in
XX CC therapy and manufacture of a medicament for treatment or prevention of
XX CC such disorder associated with decreased expression or activity of human
XX CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX CC clinically useful diagnostic markers and potential therapeutic agents for
XX CC male infertility and cancer. The present oligonucleotide was used in an
XX CC example from the invention
XX SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCCAGGAGAAC 739
DB 13 TGCCAGGTGAAC 1
RESULT 74
ACC53821/c
ID ACC53821 standard; DNA; 17 BP.
XX AC ACC53821;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2588.
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (WOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Anson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 638; 798pp; French.

```

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX

SQ Sequence 17 BP; 1 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 730 CAGGAGAAACAGCA 742
| | | | | | | | | |
Db 17 CAGGAGAAACAGCA 5

RESULT 75
ABT38554/c
ID ABT38554 standard; DNA; 17 BP.
XX
AC ABT38554;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4191.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 523; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SQ Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 51.8%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 733 GAGAAACAGCA 745
| | | | | | | | | |
Db 17 GTGAAACAGCA 5

RESULT 76
AAI64977
ID AAI64977 standard; DNA; 16 BP.
XX
AC AAI64977;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human Creml protein coding sequence exon 25/intron 25 junction.
XX
KW Human; Creml; repeat; transcriptional control factor; Rb;
KW retinoblastoma protein; intron-exon junction; ds.
XX
OS Homo sapiens.
XX
PN CN1303861-A.
XX
PD 18-JUL-2001.
XX
PF 07-JAN-2000; 2000CN-00111426.
XX
PR 07-JAN-2000; 2000CN-00111426.
XX
PA (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.
XX
PI Zhu X, Yan X, Qian M;
XX WPI; 2001-566148/64.
XX
XX New retinoblastoma protein binding protein, its preparation and
PT application.
XX
PS Disclosure; Fig 3B; 35pp; Chinese.
XX
XX The present invention relates to the coding sequence of human Creml,
CC which is a protein containing a repetitive 86 amino acid motif. The
CC protein is a transcriptional control factor, and is a conjugate of
CC retinoblastoma protein (Rb). The present sequence is the an intron-exon
CC junction in the coding sequence of the invention
XX

SQ Sequence 16 BP; 4 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 50.9%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 727 TGCAGGAGAAACAGCA 742
| | | | | | | | | |
Db 1 TGCAGGAGAGTCAGCA 16

RESULT 77
AAT16993
ID AAT16993 standard; DNA; 17 BP.
XX

```

AC AAT16993;
XX
DT 10-JUL-1996 (first entry)
XX
DE E-Dex integrin inhibitor 1 PCR primer No. 1771.
XX
KW Integrin inhibitor; E-Dex; neutrophil; leukocyte; trans-migration;
KW cell adhesion; tick-derived antiinflammatory protein; Ixodes pacificus;
KW Amblyomma americanum; polymerase chain reaction; PCR; primer; ss.
XX
OS Synthetic.
XX
FN WO9605304-A1.
XX
PD 22-FEB-1996.
XX
PF 08-AUG-1995; 95WO-US010138.
XX
PR 09-AUG-1994; 94US-00287730.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bard F, Yednock TA, Keim PS, Basi GS;
XX
DR WPI; 1996-139700/14.
XX
PT Tick derived anti-inflammatory proteins E-Dex and Y/A-Dex - used to
PT inhibit leukocyte trans-migration and in the treatment of inflammatory
PT disease.
XX
PS Example; Fig 3A; 76pp; English.
XX
CC Degenerate sense PCR primers (AAT16990-94) are based on the 5' end of a
CC sequence coding for a peptide fragment of novel tick-derived
CC antiinflammatory protein E-Dex (see also AAR81794). They were used with
CC antisense primers (AAT16995-99) complementary to the 3' end of the
CC sequence for the RT-PCR amplification of tick salivary gland mRNA.
CC Partial cDNA clones were obt'd. and used to screen a cDNA library to
CC obtain a full-length cDNA clone (AAT16988) coding for E-Dex
XX
SQ Sequence 17 BP; 8 A; 1 C; 4 G; 1 T; 0 U; 3 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAAC 744
DB 2 ARGARARAGAAC 15

RESULT 78
AA73286/c
ID AA73286 standard; RNA; 17 BP.
XX
AC AA73286;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #719.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
FN WO9715662-A2.
XX
PD 01-MAY-1997.
XX

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PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-000584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability--useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 146; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGAGAACAGAA 743
DB 16 GCCAGAGACACGTAA 1

RESULT 79
AA73641/C
ID AAC73641 standard; DNA; 17 BP.
XX
AC AAC73641;
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #143 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
FN WO2000058516-A2.
XX
PD 05-OCT-2000.
XX
PR 27-MAR-2000; 2000WO-US0008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT

```

PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
PS Example 7; Page 63; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
SQ Sequence 17 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACACGAA 743
Db 16 GCCATGAGAGCAGGA 1

RESULT 80
AAH95688
ID AAH95688 standard; RNA; 17 BP.
XX
AC AAH95688;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human Chk1 ribozyme substrate SEQ ID NO: 1113.
XX
KW Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
KW RNA cleavage; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157206-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003504.
XX
PR 03-FEB-2000; 2000US-0179983P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (FATT/) FATTAEY A R.
XX
PI Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
XX WPI; 2001-496922/54.
DR
XX
PT Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT molecules, which downregulate expression of a checkpoint kinase-1 gene,
PT useful for treating colorectal, lung, breast or prostate cancers.
XX
PS Claim 4; Page 80; 115pp; English.
XX
CC The present invention provides nucleic acid molecules capable of
CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC gene. These may be antisense or ribozyme sequences, and are useful in the
CC treatment of diseases associated with conditions affected by Chk1 levels,
CC including cancer. The present sequence is an oligonucleotide described in
CC the exemplification of the invention
XX
SQ Sequence 17 BP; 10 A; 2 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 731 AGGAGAAACACACAC 746
Db 2 AGGAGAAACAAUAAAC 17

RESULT 81
AAH45387/c
ID AAH45387 standard; DNA; 17 BP.
XX
AC AAH45387;
XX
DT 11-SEP-2001 (first entry)
XX
DE Corynebacterium thermoaminogenes lysa PCR primer #2.
XX
KW Heat-resistant; lysin biosynthesis; enzyme; coryneform;
KW aspartate-semialdehyde dehydrogenase; lysa; PCR primer; ss.
XX
OS Corynebacterium thermoaminogenes.
XX
PN JP2001120270-A.
XX
PD 08-MAY-2001.
XX
PF 01-NOV-1999; 99JP-00311148.
XX
PR 01-NOV-1999; 99JP-00311148.
XX
PA (AJIN) AJINOMOTO KK.
XX
DR WPI; 2001-364760/38.
XX
PT A heat-resistant lysin biosynthetic system enzyme gene of a high
PT temperature-resistant coryneform microbe.
XX
PS Example 2; Page 7; 27pp; Japanese.
XX
CC The invention relates to a gene from a high temperature-resistant
CC coryneform microbe that encodes a heat-resistant lysin biosynthetic
CC enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and
CC can be used for growing amino acid-producing microbes. The present
CC sequence is a primer which was used to amplify DNA encoding a heat-
CC resistant lysin biosynthetic enzyme of the invention
XX
SQ Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACACGAA 743
Db 17 GCCACGAGGATCAGAA 2

RESULT 82
ABL31707
ID ABL31707 standard; DNA; 17 BP.
XX
AC ABL31707;
XX
DT 21-MAR-2002 (first entry)
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 1196.
XX
KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX
OS Homo sapiens.

PN W0200192572-A1.
 XX 06-DEC-2001.
 XX 01-JUN-2001; 2001WO-JP004662.
 XX 01-JUN-2000; 2000JP-00164798.
 XX (NISH) NISSHINBO IND INC.
 XX (SYST-) SYSTEM RES INC.
 XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 XX WPI; 2002-122074/16.
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplanting between them.
 XX Claim 10; Page 320; 345pp; Japanese.
 XX The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ASL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as alloantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene
 CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 50.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 729 CCAGGAGAACAGAC 744
 DB 1 CCGGAGATACAGATC 16
 RESULT 83
 ID ADB03778/c
 XX ADB03778 standard; DNA; 17 BP.
 XX ADB03778;
 AC ADB03778;
 DT 20-NOV-2003 (first entry)
 DE Human MD27 scanning oligonucleotide SEQ ID 4764.
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS EP1281758-A2.
 PN 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 XX 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.

XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX Example 8; SEQ ID NO 4764; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1. MD24 is encoded at chromosome 6p21.3-22.2.
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;
 SQ Query Match 50.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAGAA 743
 DB 16 GCCAGGAGAGAGGGA 1
 RESULT 84
 ID ADB03777/c
 XX ADB03777 standard; DNA; 17 BP.
 XX ADB03777;
 AC ADB03777;
 DT 20-NOV-2003 (first entry)
 DE Human MD27 scanning oligonucleotide SEQ ID 4763.
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS EP1281758-A2.
 PN 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 XX 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.

PS Example 8; SEQ ID NO 4763; 103pp; English.

XX The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder,

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX

XX Sequence 17 BP; 0 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.5e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAACAGAA 743

Db 17 GCCAGGAGAGAGAGCA 2

RESULT 85

ABZ60021

ID ABZ60021 standard; RNA; 17 BP.

AC ABZ60021;

XX

XX 21-MAR-2003 (first entry)

DE Human K-Ras DNzyme substrate #133.

DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;

KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

OS

XX WO200297114-A2.

PN

XX 05-DEC-2002.

PD

XX 29-MAY-2002; 2002WO-US016840.

EF

XX 29-MAY-2001; 2001US-0294140P.

PR 06-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA

XX Mcswiggen J;

PI

XX WPI; 2003-140484/13.

DR

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX

XX Claim 58; Page 87; 185pp; English.

PS The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and anti-

CC rheumatic activity. The nucleic acid molecules are useful for reducing

CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are

CC also useful for treating breast, ovarian, colorectal, lung, prostate,

CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences

CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ6531, ABZ6520 - ABZ6524,

CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human

CC ribozymes of the invention

XX

XX Sequence 17 BP; 9 A; 4 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 50.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.5e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 730 CAGGAGAACAGAA 745

Db 1 CAGGAGACACAAACA 16

RESULT 86

AAT54804/C

ID AAT54804 standard; RNA; 15 BP.

XX

XX AAT54804;

AC

XX 25-MAR-2003 (revised)

DT 07-APR-1997 (first entry)

XX

XX Mouse re1A hammerhead ribozyme target sequence (nt. position 93).

DE

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

KW gene expression; downregulation; interleukin-5; IL-5; ICM-1;

KW intercellular adhesion molecule; rel A; tumour necrosis factor;

KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

KW translocation; chronic myelogenous leukaemia; CML; cancer;

KW Philadelphia chromosome; inflammation; autoimmune disease;

KW atherosclerosis; myocardial infarction; stroke; restenosis;

KW transplant rejection; rheumatoid arthritis; psoriasis;

KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;

KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;

XX ss.

XX Mus musculus.

OS

XX WO9523225-A2.

PN

XX 31-AUG-1995.

PD

XX 23-FEB-1995; 95WO-IB000156.

PF

XX 23-FEB-1994; 94US-00201109.

PR 29-MAR-1994; 94US-00218934.

PR 04-APR-1994; 94US-00227955.

PR 07-APR-1994; 94US-00224483.

PR 15-APR-1994; 94US-00227958.

PR 15-APR-1994; 94US-00228041.

PR 18-MAY-1994; 94US-00245736.

PR 06-JUL-1994; 94US-00271280.

PR 15-AUG-1994; 94US-00291433.

PR 16-AUG-1994; 94US-00292620.

PR 19-AUG-1994; 94US-00293520.

PR 02-SEP-1994; 94US-00300000.

PR 08-SEP-1994; 94US-00303039.

PR 23-SEP-1994; 94US-00311486.

PR 28-SEP-1994; 94US-00311749.

PR 28-SEP-1994; 94US-00314397.

PR 03-OCT-1994; 94US-00316771.

PR 07-OCT-1994; 94US-00319492.

PR 11-OCT-1994; 94US-00321993.

PR 04-NOV-1994; 94US-00334847.

PR 10-NOV-1994; 94US-00337608.

PR 28-NOV-1994; 94US-00345516.

PR 16-DEC-1994; 94US-00357577.

```

PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 225; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
CC nucleotide base position indicated in the DE line. The relA gene product
CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
CC specifically in the induction of inflammatory responses. Regions of the
CC mRNA that do not form secondary folding structures and that contain
CC potential hammerhead and hairpin ribozyme cleavage sites were identified
CC by computer analysis. Ribozymes directed against these mRNA sequences
CC were designed and synthesised with modifications that improve their
CC nuclease resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit relA expression, making them potentially
CC useful for treating rheumatoid arthritis, restenosis and asthma as well
CC as for increasing tolerance to transplanted tissues. The potential
CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
CC that uses are limited to local delivery, acute indications or ex vivo
CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 15 BP; 1 A; 6 C; 2 G; 0 T; 6 U; 0 Other;
SQ

```

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 731 AGGAGAAACAGAAC 744
Db 14 AGGGGAAACAGATC 1

```

RESULT 87
AAZ63818/c
ID AAZ63818 standard; RNA; 15 BP.
XX
XX AAZ63818;
XX
XX 28-MAR-2000 (first entry)
XX
XX Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 1861.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX Hepatitis C virus.
XX
XX WO9955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX
XX 18-SEP-1998; 98US-0100842P.
XX
XX 25-FEB-1999; 99US-00257608.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PT

Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
WPI; 2000-062023/05.
Novel ribozymes for the treatment of diseases and conditions related to
hepatitis C infection.
Claim 1; Page 71; 123pp; English.
The present sequence represents the preferred target sequence of an
enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
the Hepatitis C virus (HCV) RNA sequence at the base position given in
the descriptor line. The HCV sequence was screened for optimal ribozyme
target sites using a computer folding algorithm and regions of the mRNA
which did not form secondary folding structures and contained potential
ribozyme cleavage sites were identified. Ribozymes were synthesised to
target these sites and their activities optimised by either varying the
length of the binding arms or by modification to prevent degradation and/or
nucleases. The ribozymes of the invention inhibit gene expression and/or
viral replication, and are used to treat diseases associated with
Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
hepatocellular carcinoma. The ribozymes may be used in combination with
interferon to treat HCV infection, other infectious diseases, autoimmune
diseases, and cancer
Sequence 15 BP; 2 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 735 GAAACAGACACCG 748
Db 15 GAAACAGTACACTG 2

```

RESULT 88
AAFS0111/c
ID AAFS0111 standard; DNA; 15 BP.
XX
XX AAFS0111;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #1071.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO2000078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

PS Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAA 743
DB 14 CAGAGGTACAGAA 1

RESULT 89
AAF50110/C
ID AAF50110 standard; DNA; 15 BP.
XX AC AAF50110;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #1070.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.

XX OS Homo sapiens.
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

PS Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 49.1%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAA 743
DB 15 CAGAGGTACAGAA 2

RESULT 90
ABX00871/C
ID ABX00871 standard; RNA; 15 BP.
XX AC ABX00871;
XX DT 23-DEC-2002 (first entry)
XX DE Hepatitis C virus substrate #653 for HCV hammerhead ribozyme #653.
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX KW type I interferon; interferon alpha; interferon beta; cytosatic;
XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX OS Hepatitis C virus.
XX PN US2002082225-A1.
XX PD 27-JUN-2002.
XX PF 23-MAR-1999; 99US-00274553.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX DR New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX PT replication and are useful to treat hepatitis C virus infections and
XX PT cirrhosis, liver failure or hepatocellular carcinoma.
XX PS Claim 1; Page 40; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which

CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/paipsDIDEntry.html
 XX
 XX Sequence 15 BP; 2 A; 4 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 49.1%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGTACACTG 748
 Db 15 GAAACAGTACACTG 2

RESULT 91
 ABV72560/C
 ID ABV72560 standard; DNA; 15 BP.
 XX
 AC ABV72560;
 XX
 DT 12-FEB-2003 (first entry)
 XX
 DE Consensus sequence of methanol regulated promoters of yeast.
 XX
 KW Yeast; alcohol oxidase 1; AOX1; AOX2; promoter; formaldehyde; methanol;
 KW protein production; peroxisome biogenesis; ss.
 XX
 OS Synthetic.
 XX
 PN WO200281650-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 05-APR-2002; 2002WO-US012851.
 XX
 PR 05-APR-2001; 2001US-0281861P.
 XX
 PA (UNNE-) UNIV NEBRASKA.
 XX
 PI Inan M, Meagher MM, Benson AK;
 XX
 DR WPI; 2003-058528/05.
 XX

PT Novel alcohol oxidase 1 regulatory nucleotide sequences useful for
 PT enhancing expression of genes of interest in a variety of host cells,
 PT especially yeast cells.
 XX
 PS Disclosure; Fig 6; 66pp; English.

XX The present sequence represents a consensus sequence of methanol
 CC regulated promoters of methylotrophic yeast. The specification describes
 CC 5' regulatory sequences within the alcohol oxidase 1 (AOX1) promoter
 CC region. AOX1 catalyses the oxidation of methanol to formaldehyde. The
 CC AOX1 promoter is an inducible promoter, primarily induced by methanol and
 CC starvation, and repressed in response to glucose and ethanol. The AOX1 5'
 CC regulatory sequences can be used to produce expression cassettes and
 CC vectors, which are useful for protein production. The regulatory
 CC sequences are useful to increase expression of genes of interest in a
 CC variety of host cells, in a research setting to further characterize
 CC promoter function and to study peroxisome biogenesis. They are also

CC useful as probes
 XX
 SQ Sequence 15 BP; 1 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 49.1%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAG 741
 Db 15 GCCAGGAGAACAG 2
 RESULT 92
 AAF56033/C
 ID AAF56033 standard; DNA; 16 BP.
 XX
 AC AAF56033;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE HBV DNA polymerase gene L528M mutation probe HBPr270.
 XX
 KW HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
 KW mutation detection; probe; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200104358-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 05-JUL-2000; 2000WO-EP006306.
 XX
 PR 08-JUL-1999; 99EP-00870148.
 PR 13-JUL-1999; 99US-0143546P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Stuyver L, Maertens G, Van Geyt C;
 XX
 DR WPI; 2001-138370/14.
 XX
 PT Monitoring anti-HBV drug resistance by genetic detection of mutations in
 PT DNA polymerase of HBV in patient's sample, involves hybridizing the
 PT polynucleic acids of the sample with a probe and detecting the hybrid.
 XX
 PS Claim 2; Page 9; 64pp; English.
 XX
 CC The present sequence is a probe used in a method for monitoring anti-
 CC hepatitis B virus (HBV) drug resistance in a patient by genetic detection
 CC of any one of mutations L528M, M552V/I and/or V/L/M555I in HBV DNA
 CC polymerase in a biological sample from the patient. The method is useful
 CC in the field of genetic detection of anti-HBV drug resistance during HBV
 CC therapy. The method is rapid, reliable and precise
 XX
 SQ Sequence 16 BP; 0 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 49.1%; Score 10.8; DB 1; Length 16;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAACAG 741
 Db 14 GCCAGGAGAACAG 1
 RESULT 93
 AAS98698
 ID AAS98698 standard; DNA; 15 BP.
 XX
 AC AAS98698;
 XX

XX 26-MAR-2002 (first entry)
XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #64.
XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytostatic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
KW genotype; human; allele specific oligonucleotide; ASO; primer; ss.
XX Homo sapiens.
XX WO200179225-A2.
XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US012044.
XX 12-APR-2000; 2000US-0196411P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Chew A, Choi JY, Koshy B;
XX WPT; 2002-075058/10.
XX Novel polymorphic variants of colony stimulating factor 1 receptor useful
PT in studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases e.g. inflammatory disorders.
XX Claim 15; Page 16; 164pp; English.
XX The invention describes a novel isolated polynucleotide (I) comprising a
CC sequence which is a polymorphic variant (PV) of a reference sequence for
CC colony stimulating factor 1 receptor (CSF1R) gene, found on the
CC polypeptide are useful for improving the discovery and development of
CC drugs for treating diseases associated with CSF1R activity e.g. disorders
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC and the haplotypes can be used to validate CSF1R as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC be used in developing diagnostic tests and therapeutic treatments. (I) is
CC useful in studying the expression and function of CSF1R, and in
CC expressing CSF1R protein for use in screening for candidate drugs to
CC treat diseases related to CSF1R activity and in studying the effect of
CC the variation on the biological activity of CSF1R as well as on the
CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC useful in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A transgenic animal is useful in studying expression of the
CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is an allele specific
CC oligonucleotide primer used for detecting CSF1R gene polymorphisms,
CC described in the method of the invention
XX SQ Sequence 15 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 1 Other;
Query Match 48.2%; Score 10.6; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 2.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 5 AGGAGAAACRG 15
RESULT 94
ABI99104/c
ID ABI99104 standard; DNA; 15 BP.
XX 27-FEB-2002 (first entry)
XX Human PCDH2 ASO PCR primer SEQ ID NO 61.
XX Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
KW allele-specific oligonucleotide; ASO; PCR primer; ss.
XX Homo sapiens.
XX WO200194361-A2.
XX 13-DEC-2001.
XX 06-JUN-2001; 2001WO-US019321.
XX 06-JUN-2000; 2000US-0209564P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Kliem SE, Koshy B, Tanguay DA;
XX WPI; 2002-097928/13.
XX New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
PT useful in expressing PCDH2 protein for screening candidate drugs to treat
PT diseases related to PCDH2 activity.
XX Claim 16; Page 14; 127pp; English.
XX The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
CC comprising determining which of the haplotypes given in the specification
CC defines one or both copies of the individual's PCDH2 gene. The
CC polymorphisms are within a 30244 base pair sequence (ABA05413), fully
CC defined in the specification. The polymorphic variants are useful in
CC studying the expression and function of PCDH2, in expressing PCDH2
CC protein for use in screening for candidate drugs to treat diseases such
CC as cancer, related to PCDH2 activity, in studying the effect of the
CC variation on the biological activity of PCDH2 and the binding affinity of
CC candidate drugs targeting PCDH2. The haplotyping methods are useful in
CC validating PCDH2 as a candidate target for treating a specific condition
CC or disease predicted to be associated with PCDH2 activity or in the
CC design of clinical trials of candidate drugs for treating a specific
CC condition or disease associated with PCDH2 activity. The present sequence
CC is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
CC the invention
XX SQ Sequence 15 BP; 0 A; 3 C; 2 G; 9 T; 0 U; 1 Other;
Query Match 48.2%; Score 10.6; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 2.9e+02;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
DB 15 GAGAAACAGAA 5
RESULT 95
AAI56920
ID AAI56920 standard; DNA; 12 BP.
XX AAI56920;
XX 16-OCT-2003 (revised)
DT 15-JUL-1999 (first entry)
XX HIV-1 proviral DNA fragment 3.
DE DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;
XX

KW vital DNA-binding agent; solid support; primer; ss.
 OS Human immunodeficiency virus 1.
 XX WO9531434-A1.
 XX 23-NOV-1995.
 XX 12-MAY-1995; 95WO-US006379.
 XX 13-MAY-1994; 94US-00242664.
 XX (SLOAN) SLOAN KETTERING INST CANCER RES.
 XX (ZWBI-) ZW BIOMEDICAL RES AG.
 XX Watanabe KA, Ren W, Weil R;
 XX WPI; 1996-010846/01.
 XX

XX Derivatized solid supports and reagents for oligonucleotide synthesis -
 PT and new oligonucleotide phosphoramidate conjugates.
 PT

PS Disclosure; Page 43; 68pp; English.
 XX

XX This invention describes novel derivatized solid supports of formula S'-L
 CC -Z-CH₂CH₂-R, where: S' = a solid support; L = a bond or an (in)organic
 CC linker; Z = SO₂ or S-S; R = OH, an H-phosphate, alkanephosphonate,
 CC phosphotriester, phosphite triester, phosphite diester, phosphorothioate,
 CC phosphorodithioate, phosphoramidate or phosphoramidite group, OR1, SR1,
 CC an optionally substituted or modified nucleotide (N'), or an
 CC oligonucleotide of formula (N')GR₂; G = 1-200; R₁ = a protecting group;
 CC R₂ = an H-phosphate, alkanephosphonate, phosphotriester, phosphite
 CC triester, phosphite diester, phosphorothioate, phosphorodithioate,
 CC phosphoramidate or phosphoramidite group, OH, OR1, SR1 or
 CC OP(OCH₂CH₂CN)OCH₂CH₂CH₂CH₂OR1. Also mentioned are compounds of formula
 CC R₃CH₂CH₂CH₂CH₂R₄, where: R₃ = a protecting group; and R₄ = OH or an H-
 CC phosphate, alkanephosphonate, phosphotriester, phosphite triester,
 CC phosphite diester, phosphorothioate, phosphorodithioate, phosphoramidate
 CC or phosphoramidite group. Also claimed are new phosphoramidates, a
 CC process for preparing an oligonucleotide 5'-phosphate, a process for
 CC preparing a solid support useful for preparation of an oligonucleotide 3'-
 CC phosphate, a process for preparing an oligonucleotide 3'-phosphate and a
 CC process for preparing an oligonucleotide 3',5'-diphosphate. The
 CC oligonucleotide 3'- and/or 5'-phosphates may be used to prepare DNA-
 CC targeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNA-
 CC cleaving or -binding agents. The process for preparing oligonucleotide
 CC 3',5'-diphosphates is simple and suitable for use in automatic DNA
 CC synthesizers. This sequence represents a fragment of the HIV-1 provirus
 CC genome, used to describe the method of the invention. (Updated on 16-Oct-
 XX 2003 to standardise OS field)
 XX

SQ Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 2.8e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742

Db 1 AGGAGAAACAGA 12

RESULT 96

ABI03318

ID ABI03318 standard; DNA; 12 BP.

XX

AC ABI03318;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 303291 for detecting SNP TSC0020423.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT

PS Claim 1; SEQ ID NO 303291; 29pp + Sequence Listing; German.
 XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 2.8e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGACACC 747

Db 1 AAACATACACC 12

RESULT 97

ABI54034

ID ABI54034 standard; DNA; 12 BP.

XX

AC ABI54034;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 354007 for detecting SNP TSC0006126.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 354007; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 7 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACGAGAAC 744
Db 1 GAGAAAGAGAAC 12
RESULT 98
ABH94559/C
ID ABH94559 standard; DNA; 12 BP.
XX
XX ABH94559;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 294552 for detecting SNP TSC0016175.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 294552; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 735 GAAACGAGAAC 746
Db 12 GAAACAAACAC 1
RESULT 99
ABH40265
ID ABH40265 standard; DNA; 13 BP.
XX
XX ABH40265;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 240242 for detecting SNP TSC0058589.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 240242; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
SQ

```

Query Match      47.3%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
    |||||
Db 2 AAACCGAACACC 13

RESULT 100
ABF73171
ID ABF73171 standard; DNA; 13 BP.
XX
AC ABF73171;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 173168 for detecting SNP TSC0006888.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 173168; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match      47.3%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
    |||||
Db 2 AAACATACACC 13

RESULT 101
ABF73170/c
ID ABF73170 standard; DNA; 13 BP.
XX
AC ABF73170;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 173167 for detecting SNP TSC0058589.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX

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XX ABF73170;
AC
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 173167 for detecting SNP TSC0006888.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 173167; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

Query Match      47.3%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
    |||||
Db 12 AAACATACACC 1

RESULT 102
ABH40264/c
ID ABH40264 standard; DNA; 13 BP.
XX
AC ABH40264;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 240241 for detecting SNP TSC0058589.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX

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CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 13 AAACAAACATC 2

RESULT 561
ABF56045/C
ID ABF56045 standard; DNA; 13 BP.
XX AC ABF56045;
XX AC
DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 156042 for detecting SNP TSC0039372.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 156042; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 13 AAACAAACATC 2

RESULT 562
ABH3790
ID ABH3790 standard; DNA; 13 BP.
XX AC ABH3790;
XX AC
DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 233767 for detecting SNP TSC0057055.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 233767; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 7 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACCA 745
Db 2 AGAAACGGAAGA 13

RESULT 563
ABH34756/C
ID ABH34756 standard; DNA; 13 BP.
XX AC ABH34756;

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XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 87428; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAAACAGAACCA 745
XX Db 2 AAAAAACACACCA 13
XX
XX RESULT 559
XX ABH24319
XX ID ABH24319 standard; DNA; 13 BP.
XX AC ABH24319;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 224296 for detecting SNP TSC0054650.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 224296; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 736 AAACAGACACAC 747
XX Db 1 AAACCCACACAC 12
XX
XX RESULT 560
XX ABF49924/C
XX ID ABF49924 standard; DNA; 13 BP.
XX AC ABF49924;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 149921 for detecting SNP TSC0037827.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 149921; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BF; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 734 AGAACAGAACCA 745
Db 2 AAAACACACCA 13

RESULT 556
ABC07303
ID ABC07303 standard; DNA; 13 BP.
XX
AC ABC07303;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 7294 for detecting SNP TSC0002134.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 7294; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BF; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 734 AGAACAGAACCA 745
Db 2 AAAACACACCA 13

RESULT 557
ABC09300/c
ID ABC09300 standard; DNA; 13 BP.
XX
AC ABC09300;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 9291 for detecting SNP TSC0002459.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 9291; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BF; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 AAACAGAACACC 747
Db 12 AAACATAAACCC 1

RESULT 558
ABC87411
ID ABC87411 standard; DNA; 13 BP.
XX
AC ABC87411;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 87428 for detecting SNP TSC0021983.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

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XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 1509; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
 XX Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAACCA 745
 Db | | | | | | | | | |
 12 AAAACATAACCA 1
 RESULT 554
 ABC01519
 ID ABC01519 standard; DNA; 13 BP.
 XX AC ABC01519;
 XX DT 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 1510 for detecting SNP TSC0000521.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 1510; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
 XX Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAACCA 745
 Db | | | | | | | | | |
 2 AAAACATAACCA 13
 RESULT 555
 ABC29855
 ID ABC29855 standard; DNA; 13 BP.
 XX AC ABC29855;
 XX DT 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 29872 for detecting SNP TSC0008971.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 29872; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at

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QY 736 AAACAGAACACC 747
Db 1 AAACACCACACC 12
RESULT 551
ABH48475
ID ABH48475 standard; DNA; 13 BP.
AC ABH48475;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 248452 for detecting SNP TSC0060719.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 248452; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, AB00010-ABF9989, ABH0010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 736 AAACAGAACACC 747
Db 1 AAACAAAACACC 12
RESULT 552
ABH54080/C
ID ABH54080 standard; DNA; 13 BP.
XX
XX ABH54080;
AC
XX
XX 22-FEB-2002 (first entry)
XX
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 736 AAACAGAACACC 747
Db 1 AAACAAAACACC 12
RESULT 553
ABH54080/C
ID ABC01518 standard; DNA; 13 BP.
XX
XX ABC01518;
AC
XX
XX 20-FEB-2002 (first entry)
XX
XX
XX Oligonucleotide SEQ ID NO 1509 for detecting SNP TSC0000521.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX

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DE Oligonucleotide SEQ ID NO 254057 for detecting SNP TSC0061944.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 254057; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, AB00010-ABF9989, ABH0010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 735 GAACAGAACACC 746
Db 12 GAACATAATAC 1
RESULT 553
ABC01518/c
ID ABC01518 standard; DNA; 13 BP.
XX
XX ABC01518;
AC
XX
XX 20-FEB-2002 (first entry)
XX
XX
XX Oligonucleotide SEQ ID NO 1509 for detecting SNP TSC0000521.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX

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XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 32973; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
 DB 13 ATAAACATAACA 2

RESULT 549

ABC87410/C

ID ABC87410 standard; DNA; 13 BP.

AC ABC87410;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 87427 for detecting SNP TSC0021983.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PP 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 87427; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
 DB 12 ATAAACATAACA 1

RESULT 550

ABH42939

ID ABH42939 standard; DNA; 13 BP.

AC ABH42939;

DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 242916 for detecting SNP TSC0000966.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PP 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 242916; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX AC ABH42938;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 242915 for detecting SNP TSC0000966.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPFIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 242915; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other;

XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 736 AACACGACACACC 747
XX DB 13 AACACGACACACC 2
|||||
|||||

XX RESULT 547
XX ABH48474/c
XX ID ABH48474 standard; DNA; 13 BP.
XX AC ABH48474;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 248451 for detecting SNP TSC0060719.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

PN WO200177384-A2.
XX 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPFIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 248451; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 736 AACACGACACACC 747
XX DB 13 AACACGACACACC 2
|||||
|||||

XX RESULT 548
XX ABC32956/c
XX ID ABC32956 standard; DNA; 13 BP.
XX AC ABC32956;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 32973 for detecting SNP TSC0010416.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPFIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 2 AAACAGAACACC 13
 ||||| |||||

RESULT 544
 ABH02515
 ID ABH02515 standard; DNA; 13 BP.
 XX AC ABH02515;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 202492 for detecting SNP TSC0049770.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 202492; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 2 AAACAGAACACC 13
 ||||| |||||

RESULT 545
 ABH42937
 ID ABH42937 standard; DNA; 13 BP.
 XX AC ABH42937;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 242914 for detecting SNP TSC0000966.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 242914; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;

QY 736 AAACAGAACACC 747
 Db 1 AAACAGAACACC 12
 ||||| |||||

RESULT 546
 ABH42938/C
 ID ABH42938 standard; DNA; 13 BP.

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 82397; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGACAC 747
DB 12 AAACCGAAAC 1
|||||
RESULT 542
ABF30658/C
ID ABF30658 standard; DNA; 13 BP.
XX
XX AC ABF30658;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 130655 for detecting SNP TSC0032625.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX

PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 130655; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAACAGAAC 745
DB 12 ACAACCAAAAC 1
|||||
RESULT 543
ABH19407
ID ABH19407 standard; DNA; 13 BP.
XX
XX AC ABH19407;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 219384 for detecting SNP TSC0008134.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 219384; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAACACAC 747
 |||||
 Db 2 AACAACATCAC 13

RESULT 539
 ABC23145
 ID ABC23145 standard; DNA; 13 BP.
 XX AC
 XX ABC23145;
 XX DT 20-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 23162 for detecting SNP TSC0004665.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.

XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 23162; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 9 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAC 745
 |||||
 Db 2 ACAACAACAC 13

RESULT 540
 ABC06154/C
 ID ABC06154 standard; DNA; 13 BP.
 XX AC
 XX ABC06154;
 XX DT 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 6145 for detecting SNP TSC0001931.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.

XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 6145; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAC 745
 |||||
 Db 13 AAAACAACAC 2

RESULT 541
 ABC82380/C
 ID ABC82380 standard; DNA; 13 BP.
 XX AC
 XX ABC82380;
 XX DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 82397 for detecting SNP TSC0020796.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 253818; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;
Qy 736 AAACAGAACACC 747
Db 1 AAAAAAACACC 12
RESULT 537
ABH54081
ID ABH54081 standard; DNA; 13 BP.
AC ABH54081;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 254058 for detecting SNP TSC0061944.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.
XX Claim 1; SEQ ID NO 254058; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 2; Indels 0; Gaps 0;
Qy 735 GAAACAGAACACC 746
Db 2 GAAACATAATAC 13
RESULT 538
ABC94297
ID ABC94297 standard; DNA; 13 BP.
AC ABC94297;
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 94314 for detecting SNP TSC0023541.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 94314; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAGAACCA 745
 1 ATAAACATAACA 12
 ||||| |||||
 RESULT 534
 ABH42798/C
 ID ABH42798 standard; DNA; 13 BP.
 AC
 XX ABH42798;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 242775 for detecting SNP TSC0059232.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 242775; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 12 AAACAAAAAAC 1
 ||||| |||||
 RESULT 535
 ABH43252/C
 ID ABH43252 standard; DNA; 13 BP.
 AC
 XX ABH43252;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 253818 for detecting SNP TSC0061883.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD

DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 243229 for detecting SNP TSC0059331.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 243229; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 12 AAACAAAAAAC 1
 ||||| |||||
 RESULT 536
 ABH53841
 ID ABH53841 standard; DNA; 13 BP.
 AC
 XX ABH53841;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 253818 for detecting SNP TSC0061883.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 XX 18-OCT-2001.
 PD

XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 202493; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACC 747
Db 12 AAAAAAACACC 1
|||||
RESULT 532
ABF82674/C
ID ABF82674 standard; DNA; 13 BP.
XX
AC ABF82674;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 182671 for detecting SNP TSC0045147.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 182671; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACGACACC 747
Db 12 AAAAAAACACC 1
|||||
RESULT 533
ABH34757
ID ABH34757 standard; DNA; 13 BP.
XX
AC ABH34757;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 234734 for detecting SNP TSC0057297.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 234734; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;

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ABF39592/c
ID  ABF39592 standard; DNA; 13 BP.
XX
AC  ABF39592;
XX
DT  21-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 139589 for detecting SNP TSC0034952.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
WI  WIPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 139589; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 13 BP; 0 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
XX
    Query Match      40.0%; Score 8.8; DB 1; Length 13;
    Best Local Similarity 83.3%; Pred. No. 5e+02;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  729 CCAGCGAAGAAC 740
DB  13 CCAGCGAAGAAC 2
    ||| |||||
    ||| |||||

RESULT 530
ABH25372/c
ID  ABH25372 standard; DNA; 13 BP.
XX
AC  ABH25372;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 225349 for detecting SNP TSC0054939.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;

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OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
WI  WIPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 225349; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
XX
    Query Match      40.0%; Score 8.8; DB 1; Length 13;
    Best Local Similarity 83.3%; Pred. No. 5e+02;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  734 AGAAGACAGAAC 745
DB  13 ATAAACAAACAA 2
    ||| |||||
    ||| |||||

RESULT 531
ABH02516/c
ID  ABH02516 standard; DNA; 13 BP.
XX
AC  ABH02516;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 202493 for detecting SNP TSC0049770.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;

```

```
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
  Query Match      40.0%; Score 8.8; DB 1; Length 13;
  Best Local Similarity 83.3%; Pred. No. 5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 734 AGAACAGAAC 745
  Db 1 ATRACATAACA 12
  ||||| |||||
  RESULT 527
ABC37924
ID ABC37924 standard; DNA; 13 BP.
XX
AC ABC37924;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 37941 for detecting SNP TSC0011780.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR WO200177384-A2.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 37941; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
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XX
SQ Sequence 13 BP; 6 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
  Query Match      40.0%; Score 8.8; DB 1; Length 13;
  Best Local Similarity 83.3%; Pred. No. 5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 732 GGAGAAACAGAA 743
  Db 2 GGAGAAAGGAGAA 13
  ||||| |||||
  RESULT 528
ABF27769
ID ABF27769 standard; DNA; 13 BP.
XX
AC ABF27769;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 127766 for detecting SNP TSC0031989.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 127766; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
  Query Match      40.0%; Score 8.8; DB 1; Length 13;
  Best Local Similarity 83.3%; Pred. No. 5e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 735 GAAACAGAACAC 746
  Db 2 GAAACCGAAAC 13
  ||||| |||||
  RESULT 529
```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 240239; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 736 AACACAGACACC 747
 DB 12 AACCAACACCC 1
 RESULT 525
 ABC48960
 ID ABC48960 standard; DNA; 13 BP.
 XX ABC48960;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 48977 for detecting SNP TSC0013898.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX Claim 1; SEQ ID NO 32974; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 48977; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 5 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 733 GAGAAACAGAAC 744
 DB 1 GAGAAACGTAC 12
 RESULT 526
 ABC32957
 ID ABC32957 standard; DNA; 13 BP.
 XX ABC32957;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 32974 for detecting SNP TSC0010416.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 32974; 29pp + Sequence Listing; German.

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 729 CCAGGAGAAACA 740
Db 13 CCAGGAGAAACA 2

RESULT 522
ABH29485
ID ABH29485 standard; DNA; 13 BP.
XX AC ABH29485;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 229462 for detecting SNP TSC0055973.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 229462; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 5 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 729 CCAGGAGAAACA 740

Db 1 CCACGACAAACA 12

RESULT 523
ABF59006/c
ID ABF59006 standard; DNA; 13 BP.
XX AC ABF59006;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 159003 for detecting SNP TSC0040037.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 159003; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 734 AGAAACAGAAACA 745
Db 13 AGAAACAGAAACA 2

RESULT 524
ABH40262/c
ID ABH40262 standard; DNA; 13 BP.
XX AC ABH40262;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 240239 for detecting SNP TSC0058589.

XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 29871; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABJ0010-ABJ82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
 XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
 XX Best Local Similarity 83.3%; Pred. No. 5e+02;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 734 AGAAACAGAACCA 745
 DB 12 AAAAAACAAACA 1
 RESULT 520
 ABF23388/c
 ID ABF23388 standard; DNA; 13 BP.
 XX AC ABF23388;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 123385 for detecting SNP TSC0030855.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 29871; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABJ0010-ABJ82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
 XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
 XX Best Local Similarity 83.3%; Pred. No. 5e+02;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 734 AGAAACAGAACCA 745
 DB 12 AAAAAACAAACA 1
 RESULT 520
 ABF23388/c
 ID ABF23388 standard; DNA; 13 BP.
 XX AC ABF23388;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 123385 for detecting SNP TSC0030855.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 29871; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABJ0010-ABJ82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
 XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
 XX Best Local Similarity 83.3%; Pred. No. 5e+02;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 123385; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABJ0010-ABJ82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
 XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
 XX Best Local Similarity 83.3%; Pred. No. 5e+02;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 734 AGAAACAGAACCA 745
 DB 12 AAAAAACAAACA 1
 RESULT 521
 ABH29482/c
 ID ABH29482 standard; DNA; 13 BP.
 XX AC ABH29482;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 229459 for detecting SNP TSC0055973.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 05-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 229459; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010


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Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAGAGAAACACC 747
   ||||| |||||
Db 2 AAGAGAAACACC 13

RESULT 517
ABH41118
ID ABH41118 standard; DNA; 13 BP.
XX AC ABH41118;
XX AC
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 241095 for detecting SNP TSC0059805.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 241095; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
   ||||| |||||
Db 2 AAGAGAAAGAGA 13

RESULT 518
ABC24673
ID ABC24673 standard; DNA; 13 BP.
XX AC
```

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AC ABC24673;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 24690 for detecting SNP TSC0005920.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 24690; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 10 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match      40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAACA 745
   ||||| |||||
Db 2 AAAAACAATAACA 13

RESULT 519
ABC29854/c
ID ABC29854 standard; DNA; 13 BP.
XX AC ABC29854;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 29871 for detecting SNP TSC0008971.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
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XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 173769; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 9 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAACCA 745
 DB 1 AGAAATAGAAAA 12
 RESULT 515
 ABF82673
 ID ABF82673 standard; DNA; 13 BP.
 AC ABF82673;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 182670 for detecting SNP TSC0045147.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 182670; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 9 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAACCA 745
 DB 1 AGAAATAGAAAA 12
 RESULT 515
 ABF82673
 ID ABF82673 standard; DNA; 13 BP.
 AC ABF82673;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 182670 for detecting SNP TSC0058589.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 240238; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AAACAGAACACC 747
 DB 2 AAACATAAACACC 13
 RESULT 516
 ABH40261
 ID ABH40261 standard; DNA; 13 BP.
 AC ABH40261;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 240238 for detecting SNP TSC0058589.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 240238; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

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RESULT 512
ABH19990/C
XX ABH19990 standard; DNA; 13 BP.
XX
XX AC ABH19990;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 219967 for detecting SNP TSC0053525.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 219967; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 737 AACAGACACCG 748
XX Db 12 AACACACTCCG 1
XX
XX RESULT 513
ABF48664/C
XX ABF48664 standard; DNA; 13 BP.
XX
XX AC ABF48664;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 148661 for detecting SNP TSC0037536.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX
```

```
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 148661; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAACACAGACA 745
XX Db 13 AAAACATAACA 2
XX
XX RESULT 514
ABF73772
XX ABF73772 standard; DNA; 13 BP.
XX
XX AC ABF73772;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 173769 for detecting SNP TSC0043273.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
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XX Oligonucleotide SEQ ID NO 107386 for detecting SNP TSC0026896.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 107386; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAACACAGACCA 745
DB 2 ATAAACAAACCA 13
RESULT 508
ABC82381
ID ABC82381 standard; DNA; 13 BP.
XX
XX ABC82381;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 82398 for detecting SNP TSC0020796.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 82398; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 5e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGACACCC 747
DB 2 AAACGAAACCC 13
RESULT 509
ABC37925/c
ID ABC37925 standard; DNA; 13 BP.
XX
XX ABC37925;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 37942 for detecting SNP TSC0011780.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

XX WO200177384-A2.
 PN
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 20494; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AACAGAACACC 747
 DB |||||
 2 AAAAAAACACC 13
 RESULT 503
 ABC48961/c
 ID ABC48961 standard; DNA; 13 BP.
 XX
 AC ABC48961;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 48978 for detecting SNP TSC0013898.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 20494; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AACAGAACACC 747
 DB |||||
 2 AAAAAAACACC 13
 RESULT 504
 ABC24672/c
 ID ABC24672 standard; DNA; 13 BP.
 XX
 AC ABC24672;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 24689 for detecting SNP TSC0005920.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 24689; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACGATAC 744
 DB |||||
 13 GAGAAACGATAC 2

DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 48978; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACGATAC 744
 DB |||||
 13 GAGAAACGATAC 2
 RESULT 504
 ABC24672/c
 ID ABC24672 standard; DNA; 13 BP.
 XX
 AC ABC24672;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 24689 for detecting SNP TSC0005920.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 24689; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 5 C; 2 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 733 GAGAAACGATAC 744
 DB |||||
 13 GAGAAACGATAC 2

```

SQ Sequence 13 BP; 10 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 13;
  Best Local Similarity 83.3%; Pred. No. Se+02; 2; Indels 0; Gaps 0;
  Matches 10; Conservative 0; Mismatches 0;

QY 734 AGAAGAACAGACA 745
  | | | | | | | |
Db 2 ATAAACAAATAGA 13

RESULT 500
ABF43128
ID ABF43128 standard; DNA; 13 BP.
XX
AC ABF43128;
XX
DT 21-FEB-2002 (first entry)
XX
Oligonucleotide SEQ ID NO 143125 for detecting SNP TSC0035899.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 143125; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 13;
  Best Local Similarity 83.3%; Pred. No. Se+02; 2; Indels 0; Gaps 0;
  Matches 10; Conservative 0; Mismatches 0;

QY 731 AGGAGAAACAGACA 742
  | | | | | | | |
Db 1 AAGAGAAATAGA 12

RESULT 501
ABF43129/c
ID ABF43129 standard; DNA; 13 BP.
XX
AC ABF43129;
XX
DT 21-FEB-2002 (first entry)
XX
Oligonucleotide SEQ ID NO 143126 for detecting SNP TSC0049770.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 143126; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 13;
  Best Local Similarity 83.3%; Pred. No. Se+02; 2; Indels 0; Gaps 0;
  Matches 10; Conservative 0; Mismatches 0;

QY 731 AGGAGAAACAGACA 742
  | | | | | | | |
Db 13 AAGAGAAATAGA 2

RESULT 502
ABH02517
ID ABH02517 standard; DNA; 13 BP.
XX
AC ABH02517;
XX
DT 22-FEB-2002 (first entry)
XX
Oligonucleotide SEQ ID NO 202494 for detecting SNP TSC0049770.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX OS

```


XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 9290; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACAGAACACC 747
Db 2 AACACAGAACACC 13
RESULT 498
ABC64866/C
ID ABC64866 standard; DNA; 13 BP.
XX
AC ABC64866;
XX
XX 21-FEB-2002 (first entry)
DT
XX
DE Oligonucleotide SEQ ID NO 64883 for detecting SNP TSC0017098.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 64883; 29pp + Sequence Listing; German.
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACAGAACACC 747
Db 12 AACACAGAACACC 1
RESULT 499
ABF24769
ID ABF24769 standard; DNA; 13 BP.
XX
AC ABF24769;
XX
XX 21-FEB-2002 (first entry)
DT
XX
DE Oligonucleotide SEQ ID NO 124766 for detecting SNP TSC0031192.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 124766; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

DB 13 AGAAGCAGCACA 2

RESULT 495
ABC76054/C
ID ABC76054 standard; DNA; 13 BP.

XX AC ABC76054;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 76071 for detecting SNP TSC0019478.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 76071; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGACACACC 747
DB 12 AAACCTACACC 1

RESULT 496
ABC09298/C
ID ABC09298 standard; DNA; 13 BP.

XX AC ABC09298;
XX 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 9289 for detecting SNP TSC0002459.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.
XX WO200177384-A2.
XX 19-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 9289; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGACACACC 747
DB 12 AAACACAAACC 1

RESULT 497
ABC09299
ID ABC09299 standard; DNA; 13 BP.

XX AC ABC09299;
XX 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 9290 for detecting SNP TSC0002459.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.
XX WO200177384-A2.
XX 19-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.

AA56496 standard; DNA; 13 BP.
AC AAX56496;
XX
XX
XX 27-JUL-1999 (first entry)
XX
XX Locked nucleoside analogue oligomer.
XX
XX Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
KW PCR application; strand displacement oligomer; polymerase; substrate;
KW nucleotide based drug; diagnostic probe; antisense therapy; antiviral;
KW antitumour; ss.
XX
XX Synthetic.
OS
XX
XX WO9914226-A2.
XX
XX 25-MAR-1999.
XX
XX 14-SEP-1998; 98WO-DK000393.
XX
XX 12-SEP-1997; 97DK-00001054.
XX
XX 19-DEC-1997; 97DK-00001492.
XX
XX 16-JAN-1998; 98DK-00000061.
XX
XX 03-MAR-1998; 98DK-00000286.
XX
XX 29-APR-1998; 98DK-00000585.
XX
XX 05-JUN-1998; 98US-0008309F.
XX
XX 08-JUN-1998; 98DK-00000750.
XX
XX 28-JUL-1998; 98DK-00000982.
XX
XX (EXIQ-) EXIQON AS.
XX
XX Wengel J, Nielsen P;
PI
XX WPI; 1999-337376/28.
XX
XX New oligonucleotides containing polycyclic, locked nucleoside analogs,
PT useful e.g. as diagnostic probes or in antisense therapy.
XX
XX Example 161; Page 186; 269pp; English.
XX
XX The present invention describes novel modified oligonucleotides (I)
CC containing at least one locked nucleoside analog (LNA). Monomeric LNA's
CC (II) are also described. (I) are used: (i) to bind to target sequences in
CC double-stranded DNA or RNA (by strand displacement or triplex formation);
CC (ii) as ribozymes; (iii) as therapeutic antisense, antigenic or gene
CC activating agents, specifically for recruitment of RNase H; (iv)
CC diagnostically for isolation, purification, detection, identification,
CC quantitation or capture of (synthetic) nucleic acid, e.g. as probes or
CC primers; (v) as aptamers for therapy, diagnosis, RNA-mediated catalytic
CC processes and for specific binding to antibodies, drugs etc., including
CC resolution of enantiomers; (vi) for labeling, then separating, cells; and
CC (vii) to hybridize to non-coding RNA. LNA are used in synthesis of (I);
CC as therapeutic and diagnostic agents; to equalize the melting point of;
CC unmodified reference oligonucleotides and as enzyme substrates. Typical
CC therapeutic applications are as antiviral and antitumour agents. (I) have
CC increased specificity and/or affinity, i.e. higher melting point (Tm),
CC for complementary RNA or DNA than oligomers not containing LNA, and are
CC more resistant to nuclease. The present sequence represents an oligomer
CC used in an example from the present invention
XX
XX Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8.6; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACACGACACC 747
|||||
Db 12 AACACGACACC 1

RESULT 494

AAA62335/c
ID AAA62335 standard; cDNA; 13 BP.
XX
XX
XX AAA62335;
AC
XX
XX 06-NOV-2000 (first entry)
DT
XX
XX Mouse wild-type agouti cDNA exon junction.
DE
XX
XX Mouse; agouti; chromosome 2; coat colour; diabetes; hyperamylinaemia;
KW tumour; obesity; bulimia; anorexia; transgenic mouse; lethal yellow; ss.
KW
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH Key 1..7
FT exon /*tag= a
FT FT /number= 1
FT exon 8..13
FT FT /*tag= b
FT FT /number= 2
XX
XX US6080550-A.
XX
XX 27-JUN-2000.
XX
XX 22-JUN-1998; 98US-00102977.
XX
XX 21-MAY-1993; 93US-00064385.
XX
XX 05-JUN-1995; 95US-00462732.
XX
XX 23-JUL-1997; 97US-00899134.
XX
XX (LOCK) LOCKHEED MARTIN ENERGY RES CORP.
XX
XX Woychik RP;
PI
XX
XX WPI; 2000-451204/39.
XX
XX Detecting Agouti protein, useful for screening for the risk of developing
PT e.g. diabetes or obesity in animals, by contacting a biological sample
PT with antibodies specific for the protein and detecting the resulting
PT immune complex.
XX
XX Example 10; Fig 9B; 28pp; English.
XX
XX The present sequence is the junction between the first and second exons
CC of the wild-type agouti cDNA. The agouti locus is located on mouse
CC chromosome 2. It regulates the differential production of black and
CC yellow pigment granules which give rise to the agouti coat colour of the
CC mouse. The cDNA sequence of the lethal yellow allele, which confers an
CC all-yellow phenotype in the heterozygous condition, diverges from the
CC wild-type sequence at the junction between the first and second exons.
CC The agouti locus also contributes to essential developmental processes
CC unrelated to pigmentation. For example, the lethal yellow allele is
CC associated with obesity, diabetes and the development of tumours in a
CC wide variety of tissues. Embryonic lethality and hyperamylinaemia may
CC also be associated with certain agouti alleles. The agouti gene may
CC therefore be used to produce transgenic mice which can be used as animal
CC models for the study of such disorders. Potential therapeutic agents to
CC treat these disorders and others, such as bulimia or anorexia, may be
CC tested using the animal models. Oligonucleotide probes derived from the
CC agouti cDNA sequence may be used for the detection of the agouti gene and
CC mutations in the gene. Antibodies to the agouti gene product may be used
CC as therapeutic and diagnostic agents
XX
XX Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGACA 745
|||||

SQ Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAAACA 740
 DB 2 CCTGGAGAGACA 13

RESULT 491
 AAV81348/c
 ID AAV81348 standard; cDNA; 13 BP.
 XX
 AC AAV81348;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Mouse agouti wild type exon 1/2 junction.
 XX
 KW Mouse; agouti; locus; neonatal skin cell; mutant; inversion; deletion;
 KW mutation; alternative splicing; breakpoint; detection; amplification;
 KW hybridisation; ss.
 XX
 OS Mus sp.
 XX
 FN US5843652-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 05-JUN-1995; 95US-00463387.
 XX
 PR 21-MAY-1993; 93US-00064385.
 XX
 PA (LOCK) LOCKHEED MARTIN ENERGY SYSTEMS INC.
 XX
 FI Woychik RP;
 XX
 DR WPI; 1999-044565/04.
 XX
 PT Detection of Agouti gene by amplification or hybridisation assay - for
 PT diagnosis of diabetes or obesity.
 XX
 PS Claim 10; Fig 9B; 31pp; English.
 XX
 CC The inversion relates to the isolation of the mouse agouti locus cDNA
 CC sequence (AAV81341) from neonatal skin cells. Several mutant sequences
 CC were also isolated: the ISI-Gso and a (SMNU) mutations. The ISI-Gso
 CC mutation contains an inversion which causes the 3' half of the gene to be
 CC juxtaposed with the 1d gene in the opposite transcriptional orientation. Also
 CC the a(SMNU) mutation contains an intragenic 2.8 kb genomic deletion. Also
 CC isolated was a lethal yellow mutant A(y) which contains an alternatively
 CC splice 1st exon sequence (see AAV81342-V81350 for the sequences around
 CC the mutation breakpoints). This sequence represents the wild type
 CC sequence across the exon I and exon II junction. The agouti cDNA is
 CC claimed to be useful in method for detecting the agouti gene by
 CC amplification or hybridisation
 XX
 SQ Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGACA 745
 DB 13 AGAAGACAGACA 2

RESULT 492
 AAX56464/c
 ID AAX56464 standard; DNA; 13 BP.

XX
 AC AAX56464;
 XX
 DT 27-JUL-1999 (first entry)
 XX
 DE Locked nucleoside analogue oligomer FP2.
 XX
 KW Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
 KW PCR application; strand displacement oligomer; polymerase; substrate;
 KW nucleotide based drug; diagnostic probe; antisense therapy; antiviral;
 KW antitumour; ss.
 XX
 OS Synthetic.
 XX
 FN WO9914226-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 14-SEP-1998; 98WO-DK000393.
 XX
 PR 12-SEP-1997; 97DK-00001054.
 PR 19-DEC-1997; 97DK-00001492.
 PR 16-JAN-1999; 98DK-00000061.
 PR 03-MAR-1999; 98DK-000000286.
 PR 29-APR-1998; 98DK-00000585.
 PR 05-JUN-1998; 98US-0088309P.
 PR 08-JUN-1998; 98DK-00000750.
 PR 28-JUL-1998; 98DK-00000982.
 XX
 PA (EXIQ-) EXIQON AS.
 XX
 PI Wengel J, Nielsen P;
 XX
 XX WPI; 1999-337376/28.
 XX
 PT New oligonucleotides containing polycyclic, locked nucleoside analogs,
 PT useful e.g. as diagnostic probes or in antisense therapy.
 XX
 PS Example 137; Page 152; 269pp; English.
 XX
 CC The present invention describes novel modified oligonucleotides (I)
 CC containing at least one locked nucleoside analog (LNA). Monomeric LNA's
 CC (II) are also described. (I) are used: (i) to bind to target sequences in
 CC double-stranded DNA or RNA (by strand displacement or triplex formation);
 CC (ii) as ribozymes; (iii) as therapeutic antisense, antigene or gene
 CC activating agents, specifically for recruitment of RNase H; (iv)
 CC diagnostically for isolation, purification, detection, identification,
 CC quantitation or capture of (synthetic) nucleic acid, e.g. as probes or
 CC primers; (v) as aptamers for therapy, diagnosis, RNA-mediated catalytic
 CC processes and for specific binding to antibodies, drugs etc.; including
 CC resolution of entanomers; (vi) for labeling, then separating, cells; and
 CC (vii) to hybridize to non-coding RNA. LNA are used in synthesis of (I);
 CC as therapeutic and diagnostic agents; to equalize the melting point of
 CC unmodified reference oligonucleotides and as enzyme substrates. Typical
 CC therapeutic applications are as antiviral and antitumour agents. (I) have
 CC increased specificity and/or affinity, i.e. higher melting point (Tm).
 CC for complementary RNA or DNA than oligomers not containing LNA, and are
 CC more resistant to nuclease. The present sequence represents an oligomer
 CC used in an example from the present invention
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
 DB 12 AAACAGAACACC 1

RESULT 493
 AAX56496/c

XX PI Kool ET;
 XX WPI; 1997-245044/22.
 XX New C-5 thiol-substituted nucleoside derivatives - whose presence in
 PT oligonucleotide(s) allows formation of covalent cross-links between non-
 PT complementary DNA domains.
 XX
 XX Example 11; Page 101; 122pp; English.
 XX
 XX The present sequence represents a complementary target sequence for a
 CC bridged oligonucleotide derivative (AAV06762). The invention relates to C
 CC -5 thiol-substituted nucleoside derivatives which can be incorporated
 CC into an RNA or DNA strand during synthesis of oligonucleotides. These
 CC compounds can be in the form of cross-linked linear, cross-linked hairpin
 CC or bridged circular oligonucleotides. The oligonucleotides may be used
 CC for detection and isolation of target nucleic acids, or for targeting
 CC drugs to specific cell types (e.g. for treatment of Alzheimer's disease,
 CC beta-thalassemia, osteogenesis imperfecta, arthritis, sickle cell anaemia
 CC or viral infections). The presence of the nucleoside derivatives in a
 CC linear oligonucleotide allows the formation of covalent crosslinks
 CC between non-complementary DNA domains
 XX
 XX Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGAA 743
 DB 1 GAAGAAAAGAA 12
 RESULT 489
 AAV42361/C
 ID AAV42361 standard; cDNA; 13 BP.
 XX
 AC AAV42361;
 XX
 XX 02-OCT-1998 (first entry)
 DT
 XX Transition point of exon 1 from exon 2 in agouti locus of chromosome 2.
 DE
 XX Agouti locus; mouse chromosome 2; hair colour; embryonic lethality;
 KW obesity; diabetes; tumour development; transgenic mouse model; ss.
 XX
 OS Mus sp.
 XX
 XX US5789651-A.
 XX
 XX 04-AUG-1998.
 PD
 XX
 XX 05-JUN-1995; 95US-00465293.
 PF
 XX
 XX 21-MAY-1993; 93US-00064385.
 PR
 XX (WARM) MARTIN MARIETTA ENERGY SYSTEMS.
 PA
 XX Woychik RP;
 XX
 XX WPI; 1998-446202/38.
 DR
 XX Transgenic mouse containing agouti gene - exhibiting diabetes, obesity,
 PT hyperamylinemia or tumours.
 XX
 XX Disclosure; Fig 9B; 30pp; English.
 PS
 XX AAV42361-62 represent the transition point of exon 1 from exon 2 in
 CC agouti locus of chromosome 2 of mice (see AAV42361 for wild type
 CC sequence). The mutations for homozygous lethal yellow (AAV42362) and
 CC heterozygous lethal yellow (AAV42362) occur here. The agouti gene is

CC responsible for hair colour in mice, as well as embryonic lethality,
 CC obesity, diabetes, and the development of tumours in a wide variety of
 CC tissues. A transgene encoding the agouti gene product is used to
 CC transform the germ and somatic cells to produce a transgenic mouse. The
 CC transgene includes an operable linkage a promoter necessary for
 CC transcription of the transgene in the mouse, and where the agouti gene
 CC product is ectopically expressed in the mouse at levels sufficient for
 CC the mouse to exhibit insulin-independent diabetes, obesity,
 CC hyperamylinemia or tumours. The mouse is used in animal models for the
 CC study of diabetes, obesity and tumours, and for the testing of potential
 CC therapeutic agents against these diseases
 XX
 XX Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAGACAGACA 745
 DB 13 AGAAGACAGACA 2
 RESULT 490
 AAV16594
 ID AAV16594 standard; DNA; 13 BP.
 XX
 AC AAV16594;
 XX
 XX 12-JUN-1998 (first entry)
 DT
 XX Probe H30 used to identify HLA-DR sequences.
 DE
 XX DR region; major histocompatibility complex; HLA-DR; HLA-typing;
 KW HLA-DR beta consensus sequence; allelic polymorphism;
 XX HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX US5702885-A.
 PN
 XX
 XX 30-DEC-1997.
 PD
 XX
 XX 08-APR-1993; 93US-00057957.
 PF
 XX
 XX 27-JUN-1990; 90US-00544218.
 PR
 XX (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 XX Gorski JA, Baxter-Lowe LA;
 XX
 XX WPI; 1998-076408/07.
 DR
 XX
 XX Oligo:nucleotide probes and primers and methods for HLA typing -
 PT particularly for tissue typing for bone marrow transplants.
 XX
 XX Disclosure; Col 20; 20pp; English.
 PS
 XX Probes AAV1651-624 are used to identify differences in the DR region of
 CC human major histocompatibility complex (HLA-DR). The specification
 CC describes a method for HLA-typing, which includes an oligonucleotide
 CC probe which undergoes sequence-specific hybridisation with an HLA-DR beta
 CC consensus sequence at positions 61-64. The probe contains a labelling
 CC substance other than a nucleotide sequence, which facilitates detection
 CC of the probe. The HLA sequence of a subject is PCR amplified, and a probe
 CC that recognises an allelic polymorphism at a selected HLA locus is
 CC contacted with the amplified product. This first probe recognises a HLA-
 CC DR beta-allelic polymorphism. A second (different) probe is brought into
 CC contact with a second sample of the amplified DNA in a separate reaction,
 CC and hybridisation detected. The probes and primers are used for HLA
 CC typing, e.g. for tissue, especially bone marrow, transplants
 XX

KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX Homo sapiens.
 OS
 PN US2003190617-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 06-MAR-2002; 2002US-00091281.
 XX
 PR 06-MAR-2002; 2002US-00091281.
 XX
 PA (SIEE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 PI Raymond V, Morissette J, Si E;
 XX
 DR WPI; 2003-864168/80.
 XX
 CC New nucleic acid sequences of the optineurin gene are useful to detect
 XX polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognosis and treat glaucoma and related
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 393; 159pp; English.
 XX
 CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADEI3890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 XX
 SQ Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACAGAGACA 745
 DB 1 AAAAAACAAAAA 12
 |||||
 RESULT 487
 AAX79398
 ID AAX79398 standard; DNA; 13 BP.
 XX
 AC AAX79398;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE HLA-DR typing probe H30.
 XX

KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
 KW major histocompatibility complex; bone marrow transplant; primer;
 KW amplification; polymerase chain reaction; probe; polymorphism;
 KW sequence-specific oligonucleotide probe hybridisation; ss.
 XX
 OS Synthetic.
 XX
 PN US5468611-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 08-APR-1993; 93US-00045530.
 XX
 PR 27-JUN-1990; 90US-00544218.
 XX
 PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 PI Gorski JA, Baxter-Lowe LA;
 XX
 DR WPI; 1996-010091/01.
 XX
 CC Improved method for HLA typing - by DNA amplification and sequence-
 PT specific oligonucleotide hybridisation, used to select bone marrow
 PT donors.
 XX
 PS Disclosure; Col 19-20; 20pp; English.
 XX
 CC A novel method of typing the human leukocyte antigen (HLA) of the major
 CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
 CC transplants, involves determining if the donor tissue HLA-DR alleles are
 CC selected from the gp.: HLA-DRW52C, DR12a.b, DR3a.n, DR5a.e, DRNew1, DRa-
 CC DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-
 CC c. The method uses PCR to amplify these regions followed by sequence-
 CC specific oligonucleotide probe hybridisation (SSOPH) using the probes-
 CC AAX79365-X79429. SSOPH allows detection of polymorphisms that predict
 CC differences at a single amino acid level thus reducing errors and
 CC improving the chance of successfully matching tissues
 XX
 SQ Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 729 CCAGGAGAGACA 740
 DB 2 CCTGGAGAGACA 13
 |||||
 RESULT 488
 AAV06763
 ID AAV06763 standard; DNA; 13 BP.
 XX
 AC AAV06763;
 XX
 DT 02-JUN-1998 (first entry)
 XX
 DE Target oligonucleotide for bridged DNA ligand.
 XX
 KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
 KW circular; bridged; hairpin; detection; target sequence; ss.
 XX
 OS Synthetic.
 XX
 PN WO9714708-A1.
 XX
 PD 24-APR-1997.
 XX
 PF 29-MAR-1996; 96WO-US0004525.
 XX
 PR 04-OCT-1995; 95US-0004778P.
 XX
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 736 AACACAGAACACC 747
|||||
DB 1 AACCTAACACC 12

RESULT 484

AAS20481/C
ID AAS20481 standard; DNA; 12 BP.

XX AAS20481;

XX 20-MAR-2002 (first entry)

XX Oligonucleotide used to prepare a DNA triplex affinity gel.

XX ss; DNA purification; triple helix; plasmid purification;

XX DNA triplex affinity chromatography.

XX Synthetic.

XX WO200192511-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US017122.

XX 26-MAY-2000; 2000US-00580923.

XX (AVET) AVENTIS PHARMA SA.

XX Crouzet J, Scherman D, Wils P, Blanche F, Cameron B;

XX WPI; 2002-097772/13.

XX Purifying double-stranded (ds) DNA from a solution containing dsDNA and
XX other components, comprises passing the solution through a support
XX comprising a covalently coupled oligonucleotide able to form a triple
XX helix with the dsDNA.

PS Claim 1; Page 25; 40pp; English.

XX This invention comprises a method of purifying double-stranded DNA from a
XX solution containing the double-stranded DNA mixed with other components,
XX comprising passing the solution through a support comprising a covalently
XX coupled oligonucleotide capable of forming a triple helix with the double
XX -stranded DNA by hybridisation with a specific sequence present in the
XX double-stranded DNA. The method is useful for purifying double-stranded
XX DNA contained in a solution and mixed with other components. The new
XX method is a simple, rapid and effective method for DNA purification, and
XX makes it possible to obtain especially high purities with high yields.
XX The method enables DNA to be purified from complex mixtures comprising
XX other nucleic acids, proteins, endotoxins, nucleases and the like. The
XX supports may be readily recycled, and the DNAs obtained display improved
XX properties to pharmaceutical safety. Further, the method entails only one
XX step contrary to prior art. The present sequence represents an
XX oligonucleotide which can be used to prepare a DNA triplex affinity gel
XX used to purify ColEI derived plasmids by triple-helix affinity
XX chromatography

XX Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 731 AGGAGAAACAGA 742
|||||
DB 12 AGGAAAAAAGA 1

RESULT 485

ADD71434/C
ID ADD71434 standard; DNA; 12 BP.

XX ADD71434;

XX 15-JAN-2004 (first entry)

XX Stimulus-responsive DNA organization oligonucleotide #4.

XX ss; stimulus-responsive DNA organization; supercoil; rotation;
XX external stimulus; medical micromachines; artificial muscle.

XX Synthetic.

XX WO2003072772-A1.

XX 04-SEP-2003.

XX 28-AUG-2002; 2002WO-JP008656.

XX 27-FEB-2002; 2002JP-00051927.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Yui N, Ootani T;

XX WPI; 2003-679952/64.

XX Stimulus-responsive DNA organization of highly compatible functional
XX material undergoing reversible formation/dissociation of supercoil or
XX rotation in response to external stimulus, useful as e.g. artificial
XX muscles.

PS Example 3; SEQ ID NO 5; 29pp; Japanese.

XX The invention relates to a stimulus-responsive DNA organization
XX undergoing formation/dissociation of a supercoil or rotation in response
XX to an external stimulus and comprises a number of plasmid DNAs ligated in
XX it. The DNA organization is applicable in various materials and body
XX parts or medical micromachines e.g. artificial muscles. This sequence
XX represents an oligonucleotide used in the method of the invention.

SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 731 AGGAGAAACAGA 742
|||||
DB 12 AGGAAAAAAGA 1

RESULT 486

ADE14282
ID ADE14282 standard; DNA; 12 BP.

XX ADE14282;

XX 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #391.

XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;

XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 281819; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AAACAGACACACC 747
 Db 12 AAACAAATACC 1
 ||||| |||||
 RESULT 482
 ABI08687
 ID ABI08687 standard; DNA; 12 BP.
 AC ABI08687;
 DT 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 308660 for detecting SNP TSC0023145.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 PD 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PT methylation status.
 XX Claim 1; SEQ ID NO 308660; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 736 AAACAGACACACC 747
 Db 1 AAACACACACACC 12
 ||||| |||||
 RESULT 483
 ABI15833
 ID ABI15833 standard; DNA; 12 BP.
 AC ABI15833;
 DT 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 315806 for detecting SNP TSC0027111.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 PD 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 315806; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence


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Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 732 GGAGAAACAGAA 743
Db 12 GGAGAAATAGAA 1

RESULT 479
ABI26708/c
ID ABI26708 standard; DNA; 12 BP.
AC ABI26708;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 326681 for detecting SNP TSC0033222.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 326681; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 736 AAACAGAACACC 747
Db 12 AAACAAATCACC 1

RESULT 480
ABH81408
ID ABH81408 standard; DNA; 12 BP.
AC ABH81408;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 281819 for detecting SNP TSC0010087.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
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DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 281401 for detecting SNP TSC0009722.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 281401; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 736 AAACAGAACACC 747
Db 1 AAATAAACACC 12

RESULT 481
ABH81826/c
ID ABH81826 standard; DNA; 12 BP.
XX
AC ABH81826;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 281819 for detecting SNP TSC0010087.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
```

XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 365188; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH99989
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACGAGACA 745
 Db 1 ACAACCGAGACA 12
 | | | | | | | | | |
 | | | | | | | | | |
 RESULT 477
 AB123702
 ID AB123702 standard; DNA; 12 BP.
 AC AB123702;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 323675 for detecting SNP TSC0031537.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 323675; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH99989
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACGAGACA 745
 Db 1 ACAACCGAGACA 12
 | | | | | | | | | |
 | | | | | | | | | |
 RESULT 477
 AB123702
 ID AB123702 standard; DNA; 12 BP.
 AC AB123702;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 323675 for detecting SNP TSC0031537.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 323675; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH99989
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 734 AGAAACGAGACA 745
 Db 1 ATAAACATAACA 12
 | | | | | | | | | |
 | | | | | | | | | |
 RESULT 478
 AB147510/C
 ID AB147510 standard; DNA; 12 BP.
 AC AB147510;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 347483 for detecting SNP TSC0045131.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 347483; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH99989
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;

ABI46968
ID ABI46968 standard; DNA; 12 BP.
XX AC ABI46968;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 346941 for detecting SNP TSC0044842.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WI 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 346941; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
Db 1 AAACAGAACACC 12
RESULT 475
ABI67539
ID ABI67539 standard; DNA; 12 BP.
XX AC ABI67539;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 367512 for detecting SNP TSC0056383.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WI 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 367512; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AAACAGAACACC 747
Db 1 AAACAGAACACC 12
RESULT 476
ABI65215
ID ABI65215 standard; DNA; 12 BP.
XX AC ABI65215;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 365188 for detecting SNP TSC0054956.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 12 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGA 742
Db 1 AAGAGAAATAGA 12
|||||

RESULT 472
ABI23606/c
ID ABI23606 standard; DNA; 12 BP.
XX
AC ABI23606;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 323579 for detecting SNP TSC0031466.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 323579; 29pp + Sequence Listing; German.
XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX
SQ Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
Db 12 GTAGAAAAGAA 1
|||||

RESULT 473
ABI30553/c
ID ABI30553 standard; DNA; 12 BP.
XX
AC ABI30553;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 330526 for detecting SNP TSC0035562.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 330526; 29pp + Sequence Listing; German.
XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACC 747
Db 12 AACATAAACC 1
|||||

RESULT 474

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX 18-OCT-2001.
FD
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271109; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAGAGAGA 12
|||||
RESULT 470
ABI44609
ID ABI44609 standard; DNA; 12 BP.
XX
XX AC ABI44609;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 344582 for detecting SNP TSC0043623.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX

PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 344582; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 731 AGGAGAAACAGA 742
Db 1 AGGAGAAAAA 12
|||||
RESULT 471
ABI77488
ID ABI77488 standard; DNA; 12 BP.
XX
XX AC ABI77488;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 377461 for detecting SNP TSC0062342.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 377461; 29pp + Sequence Listing; German.
PS

XX 18-OCT-2001.
XX
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX FA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 298959; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 736 AAACAGACACC 747
Db 1 AAACATAAAC 12
XX
XX RESULT 465
XX ABI08983/C
XX ID ABI08983 standard; DNA; 12 BP.
XX
XX AC ABI08983;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 308956 for detecting SNP TSC0023294.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 308956; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 732 GGAGAAACAGAA 743
Db 12 GGATAAACAGAA 1
XX
XX RESULT 466
XX ABI47139
XX ID ABI47139 standard; DNA; 12 BP.
XX
XX AC ABI47139;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 347112 for detecting SNP TSC0044915.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 347112; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

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Query Match      40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAAC 745
Db 12 AGAAACAGAAC 1

RESULT 462
ABH97184 standard; DNA; 12 BP.
AC ABH97184;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 269724 for detecting SNP TSC0001860.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX ABH69747;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 269724 for detecting SNP TSC0001860.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 269724; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match      40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 733 GAGAAACAGAAC 744
XX Db 12 GATAAACCAAC 1
XX
XX RESULT 463
XX ABH97184
XX ID ABH97184 standard; DNA; 12 BP.
XX
XX Query Match      40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 733 GAGAAACAGAAC 744
XX Db 12 GATAAACCAAC 1
XX
XX RESULT 463
XX ABH97184
XX ID ABH97184 standard; DNA; 12 BP.
XX
XX Query Match      40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAAACAGAAC 745
XX Db 12 AGAAACAGAAC 12
XX
XX RESULT 464
XX ABH98966
XX ID ABH98966 standard; DNA; 12 BP.
XX
XX AC ABH98966;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 298959 for detecting SNP TSC0018363.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX

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AC ABH97184;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 297177 for detecting SNP TSC0017472.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 297177; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match      40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 734 AGAAACAGAAC 745
XX Db 1 ACAAACACCAAC 12
XX
XX RESULT 464
XX ABH98966
XX ID ABH98966 standard; DNA; 12 BP.
XX
XX AC ABH98966;
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 298959 for detecting SNP TSC0018363.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX

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XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 330934; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGAGAGACA 745
Db 1 AGAAGAGAGAAA 12
|||||
RESULT 460
ABH86305
ID ABH86305 standard; DNA; 12 BP.
XX AC ABH86305;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 286298 for detecting SNP TSC0012661.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 286298; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 AACACAGAACAC 747
Db 1 AACACAAACCCC 12
|||||
RESULT 461
ABI72010/C
ID ABI72010 standard; DNA; 12 BP.
XX AC ABI72010;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 371983 for detecting SNP TSC0059099.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 371983; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

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RESULT 457
ABI25965
ID ABI25965 standard; DNA; 12 BP.
XX
AC ABI25965;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 325938 for detecting SNP TSC0032808.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Pieperbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 325938; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACACCG 748
Db 1 AACAAAAAACCG 12
|||||
|||||

RESULT 458
ABI48399
ID ABI48399 standard; DNA; 12 BP.
XX
AC ABI48399;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 348372 for detecting SNP TSC0045565.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Pieperbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 325938; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 737 AACAGAACACCG 748
Db 1 AACAAAAAACCG 12
|||||
|||||

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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Pieperbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 348372; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AACAGAACACCG 747
Db 1 AACATTACACCG 12
|||||
|||||

RESULT 459
ABI30861
ID ABI30861 standard; DNA; 12 BP.
XX
AC ABI30861;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 330834 for detecting SNP TSC0035783.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX

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XX Claim 1; SEQ ID NO 270303; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 1 AAAAAACAGAACACA 12

RESULT 455
ABI11213/c
ID ABI11213 standard; DNA; 12 BP.
XX
AC ABI11213;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 311186 for detecting SNP TSC0024345.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 311186; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACA 746
Db 12 GAAACAGAACACA 1

RESULT 456
ABI22547/c
ID ABI22547 standard; DNA; 12 BP.
XX
AC ABI22547;
XX
XX 22-FEB-2002 (first entry)
DT
DE Oligonucleotide primer SEQ ID NO 322520 for detecting SNP TSC0030916.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 322520; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
SQ Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAACAGAACACA 745
Db 12 ATAAACAGAACACA 1

XX Oligonucleotide primer SEQ ID NO 316187 for detecting SNP TSC0027326.
DE DE
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316187; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 736 AAACAGAACACC 747
Db 1 AAACAAAAACCC 12
RESULT 453
AB117624
ID AB117624 standard; DNA; 12 BP.
XX AC AB117624;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 317597 for detecting SNP TSC0028131.
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317597; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 736 AAACAGAACACC 747
Db 1 AAACAAAAACCC 12
RESULT 453
AB117624
ID AB117624 standard; DNA; 12 BP.
XX AC AB117624;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 317597 for detecting SNP TSC0028131.
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317597; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 731 AGGAGAGACAGA 742
Db 1 AGGAGAGATAGA 12
RESULT 454
ABH70326
ID ABH70326 standard; DNA; 12 BP.
XX AC ABH70326;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 270303 for detecting SNP TSC0002082.
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAA 738
DB 1 TGTAGGAGAAA 12

RESULT 450
ABI03566/c
ID ABI03566 standard; DNA; 12 BP.
XX
AC ABI03566;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 303539 for detecting SNP TSC0020522.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 303539; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGAGACACC 747
DB 12 AAACGAGACCCC 1

RESULT 451
ABH84329/c
ID ABH84329 standard; DNA; 12 BP.
XX
AC ABH84329;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 284322 for detecting SNP TSC0011780.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 284322; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 6 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
DB 12 GGAGAGGAGAA 1

RESULT 452
ABI16214
ID ABI16214 standard; DNA; 12 BP.
XX
AC ABI16214;
XX
DT 22-FEB-2002 (first entry)

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XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 333457; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 10 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 734 AGAAGACAGACA 745
XX Db 1 AGAAGACAGAAA 12
XX RESULT 448
XX ABIS3341
XX ID ABIS3341 standard; DNA; 12 BP.
XX AC ABIS3341;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 353314 for detecting SNP TSC0048447.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317361; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 10 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 734 AGAAGACAGACA 745
XX Db 1 AGAAGACAGAAA 12
XX RESULT 448
XX ABIS3341
XX ID ABIS3341 standard; DNA; 12 BP.
XX AC ABIS3341;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 317361 for detecting SNP TSC0027952.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317361; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 736 AAACAGACACC 747
XX Db 1 AAATACACACC 12
XX RESULT 449
XX ABII7388
XX ID ABII7388 standard; DNA; 12 BP.
XX AC ABII7388;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 317361 for detecting SNP TSC0027952.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317361; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

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SQ Sequence 12 BP; 6 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAACAGAACAC 746
D 1 GAACAGAACAC 12
  ||||| |||
  ||||| |||

RESULT 445
ABH79549
ID ABH79549 standard; DNA; 12 BP.
XX AC ABH79549;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 279542 for detecting SNP TSC0007469.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
  designed to detect single-nucleotide polymorphisms and cytosine
  methylation status.
XX Claim 1; SEQ ID NO 279542; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
  and cytosine methylation status in chemically pretreated genomic DNA. The
  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
  range of diseases including immune system, gastrointestinal, respiratory,
  central nervous system, cardiovascular and metabolic disorders. The
  oligomers are also used for detecting cell type differentiation. ABC00010
  -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
  represent the oligomers described in the invention. NOTE: The sequence
  data for this patent did not form part of the printed specification, but
  was obtained in electronic format from WIPO at
  ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 747
D 1 AAACAGAACAC 12
  ||||| |||
  ||||| |||

RESULT 446
AB107767
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ID XX AB107767 standard; DNA; 12 BP.
AC XX AB107767;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 307740 for detecting SNP TSC0022659.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
  designed to detect single-nucleotide polymorphisms and cytosine
  methylation status.
XX Claim 1; SEQ ID NO 307740; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
  and cytosine methylation status in chemically pretreated genomic DNA. The
  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
  range of diseases including immune system, gastrointestinal, respiratory,
  central nervous system, cardiovascular and metabolic disorders. The
  oligomers are also used for detecting cell type differentiation. ABC00010
  -ABG9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
  represent the oligomers described in the invention. NOTE: The sequence
  data for this patent did not form part of the printed specification, but
  was obtained in electronic format from WIPO at
  ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
  Query Match 40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743
D 1 GGAGAAATAAAA 12
  ||||| |||
  ||||| |||

RESULT 447
AB133484
ID AB133484 standard; DNA; 12 BP.
XX AC AB133484;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 333457 for detecting SNP TSC0037554.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```


Db 1 GGAGAAAAGGAA 12

RESULT 440

AB122903/c

ID AB122903 standard; DNA; 12 BP.

XX AC AB122903;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 322876 for detecting SNP TSC0031092.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 322876; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 0 A; 1 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 746

Db 12 GAAACAAAAC 1

RESULT 441

ABH76378

ID ABH76378 standard; DNA; 12 BP.

XX AC ABH76378;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 276371 for detecting SNP TSC0004169.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 276371; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 GAAACAGAACAC 745

Db 1 AAAACAAAAC 12

RESULT 442

ABI01710/c

ID ABI01710 standard; DNA; 12 BP.

XX AC ABI01710;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 301683 for detecting SNP TSC0019609.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 367441; 29pp + Sequence Listing; German.

XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGAAACACC 747

DB 12 AAAAAAACACC 1

RESULT 438

ABI75557

ID ABI75557 standard; DNA; 12 BP.

XX ABI75557;

XX
XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 375530 for detecting SNP TSC0061310.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 375530; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGAAACACC 747

DB 1 AAAAAAACACC 12

RESULT 439

ABI80821

ID ABI80821 standard; DNA; 12 BP.

XX ABI80821;

XX
XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 380794 for detecting SNP TSC0000528.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 380794; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAA 743

|||||

XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 268591; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 727 TGCCAGGAGAAA 738
Db 1 TGTAAGGAGAAA 12
||| |||||
RESULT 431
ABH89478
ID ABH89478 standard; DNA; 12 BP.
XX AC ABH89478;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 289471 for detecting SNP TSC0013949.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 268591; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 727 TGCCAGGAGAAA 738
Db 1 TGTAAGGAGAAA 12
||| |||||

PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 289471; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 40.0%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 4.9e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 734 AGAAACAGAAACA 745
Db 1 ATAAACAAACA 12
||| |||||
RESULT 432
ABI66990
ID ABI66990 standard; DNA; 12 BP.
XX AC ABI66990;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 366963 for detecting SNP TSC0005306.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 366963; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAAC 745
Db 12 AAAAAACATAACA 1

RESULT 428
ABI43959/c
ID ABI43959 standard; DNA; 12 BP.
XX
AC ABI43959;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343932 for detecting SNP TSC0005420.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 371355; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGAAC 745
Db 12 AAAAAACGACA 1

RESULT 429
ABI71382/c
ID ABI71382 standard; DNA; 12 BP.
XX
AC ABI71382;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 371355 for detecting SNP TSC0058727.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 371355; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match      40.0%; Score 8.8; DB 1; Length 12;
  Best Local Similarity 83.3%; Pred. No. 4.9e+02;
  Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747
Db 12 AAACACACATC 1

RESULT 430
ABH68614
ID ABH68614 standard; DNA; 12 BP.
XX
AC ABH68614;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 268591 for detecting SNP TSC0001238.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

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XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 347162; 29pp + Sequence Listing; German.
XX SQ Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AAACGAGACACC 747
Db 1 AAACCCACACC 12
|||||
1 AAACCCACACC 12

RESULT 426
ABI52196
ID ABI52196 standard; DNA; 12 BP.
XX AC ABI52196;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352169 for detecting SNP TSC0047706.
XX SN SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

PS Claim 1; SEQ ID NO 352169; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAAGACAGAAC 745
Db 1 ACAACCAAAACA 12
|||||
1 ACAACCAAAACA 12

RESULT 427
ABH81189/C
ID ABH81189 standard; DNA; 12 BP.
XX AC ABH81189;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 281182 for detecting SNP TSC0009516.
XX SN SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 281182; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

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QY 736 AATACAGACACC 747
Db 1 AATACAAACAC 12

RESULT 423
ABI31059
ID ABI31059 standard; DNA; 12 BP.
XX
AC ABI31059;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 331032 for detecting SNP TSC0035932.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 331032; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 AATACAGACACC 747
Db 1 AATACAAACACC 12

RESULT 424
ABI12029
ID ABI12029 standard; DNA; 12 BP.
XX
AC ABI12029;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 347162 for detecting SNP TSC0044938.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 331032; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

DE Oligonucleotide primer SEQ ID NO 312002 for detecting SNP TSC0024799.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 312002; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAAGACACA 745
Db 1 AATAACACACA 12

RESULT 425
ABI47189
ID ABI47189 standard; DNA; 12 BP.
XX
AC ABI47189;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 347162 for detecting SNP TSC0044938.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

```


XX SQ Sequence 12 BP; 9 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 734 AGAAACAGACACA 745
Db 1 AAAAAAGAGACACA 12
RESULT 421
AAA06946/C
ID AAA06946 standard; RNA; 12 BP.
XX AC AAA06946;
XX DT 03-JUL-2000 (first entry)
XX DE Human XIAP IRES wild-type polypyrimidine tract.
XX KW X-linked inhibitor of apoptosis protein; XIAP; IRES;
KW internal ribosome entry site; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy; polypyrimidine tract; ss.
XX OS Homo sapiens.
XX FN WO200005366-A2.
XX PD 03-FEB-2000.
XX PF 22-JUL-1999; 99WO-IB001415.
XX PR 24-JUL-1998; 98US-00121979.
XX PR 14-JUN-1999; 99US-00332319.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Korneluk RG, Holcik M, Liston P;
XX WPI; 2000-338644/29.
XX New isolated X-linked inhibitor of apoptosis internal ribosome entry
site, used to develop agents for treating, e.g. cancer.
XX Example IV; Fig 5A; 87pp; English.
XX The invention relates to the identification of modulators of cap-
independent translation and apoptosis. The method comprises exposing a
test compound to an X-linked inhibitor of apoptosis protein (XIAP)
internal ribosome entry site (IRES) reporter cistron, and determining the
amount of translation from the XIAP IRES reporter cistron exposed to the
compound relative to the translation from the unexposed XIAP IRES
reporter cistron. A relative increase in translation from the exposed
XIAP IRES reporter cistron indicates a compound that increases XIAP IRES-
dependent (cap independent) translation. XIAP protein plays a critical
role in the regulation of apoptosis by suppressing activation of
downstream caspase-3 and caspase-7. Compounds identified by the method
which decrease XIAP IRES-dependent translation (thus leading to reduced
expression of XIAP and hence increasing apoptosis) can be used for
treating cancer. The methods can also be used for the identification of
agents that upregulate XIAP translation and hence inhibit apoptosis,
which can be used to treat autoimmune diseases, degenerative diseases or
immunorejection. Such agents may, for example, be used to inhibit
apoptosis of neurons in conditions such as Alzheimer's disease; islet
cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
infarction. They can also be used to enhance the survival of cell or
organ transplants. XIAP IRES elements can also be incorporated into
expression constructs which encode XIAP or other IAPs (inhibitor of
apoptosis proteins, e.g., XIAP; AAY81440). Such constructs may be used in

CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents the RNA sequence of the wild-type human XIAP IRES
CC polypyrimidine tract which, along with mutant polypyrimidine tracts
CC (AAA06947-A06954), was used in an exemplification of the present
CC invention to determine whether the polypyrimidine tract is important for
CC XIAP IRES function
XX
SQ Sequence 12 BP; 0 A; 2 C; 1 G; 0 T; 9 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 734 AGAAACAGACACA 745
Db 12 AAAAAAGAGACACA 1
RESULT 422
ABH75798
ID ABH75798 standard; DNA; 12 BP.
XX AC ABH75798;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 275791 for detecting SNP TSC0004001.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 275791; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABQ0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAAC 745
:|||||
Db 13 RAAACACAA 3

RESULT 419
AAA06941/c
ID AAA06941 standard; DNA; 12 BP.
XX
AC AAA06941;
DT 03-JUL-2000 (first entry)
XX
DE Human XIAP IRES polypyrimidine tract.
XX
KW X-linked inhibitor of apoptosis protein; XIAP; IRES;
KW internal ribosome entry site; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy; polypyrimidine tract; ds.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB001415.
XX
PR 24-JUL-1998; 98US-00121979.
PR 14-JUN-1999; 99US-00332319.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
DR WPI; 2000-338644/29.
XX
PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer.
XX
PS Disclosure; Page 31; 87pp; English.

CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining the
CC amount of translation from the XIAP IRES reporter cistron exposed to the
CC compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation that increases XIAP IRES-
CC dependent (cap independent) translation. XIAP protein plays a critical
CC role in the regulation of apoptosis by suppressing activation of
CC downstream caspase-3 and caspase-7. Compounds identified by the method
CC which decrease XIAP IRES-dependent translation (thus leading to reduced
CC expression of XIAP and hence increasing apoptosis) can be used for
CC treating cancer. The methods can also be used for the identification of
CC agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease; islet
CC cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP: AY81440). Such constructs may be used in
CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents the polypyrimidine tract of human XIAP IRES, which is
CC necessary for IRES-dependent translation of XIAP
XX
Sequence 12 BP; 0 A; 2 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAACAGAAC 745
:|||||
Db 12 AAAAGAGAAC 1

RESULT 420
AAA06942
ID AAA06942 standard; DNA; 12 BP.
XX
AC AAA06942;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human XIAP IRES polypyrimidine tract antisense oligonucleotide.
XX
KW X-linked inhibitor of apoptosis protein; XIAP; IRES;
KW internal ribosome entry site; human; cap-independent translation;
KW drug screening; cancer; autoimmune disease; degenerative disease;
KW immunorejection; gene therapy; polypyrimidine tract; antisense; ss.
XX
OS Homo sapiens.
XX
PN WO200005366-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-IB001415.
XX
PR 24-JUL-1998; 98US-00121979.
PR 14-JUN-1999; 99US-00332319.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Korneluk RG, Holcik M, Liston P;
DR WPI; 2000-338644/29.
XX
PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer.
XX
PS Disclosure; Page 31; 87pp; English.

CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining the
CC amount of translation from the XIAP IRES reporter cistron exposed to the
CC compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation that increases XIAP IRES-
CC dependent (cap independent) translation. XIAP protein plays a critical
CC role in the regulation of apoptosis by suppressing activation of
CC downstream caspase-3 and caspase-7. Compounds identified by the method
CC which decrease XIAP IRES-dependent translation (thus leading to reduced
CC expression of XIAP and hence increasing apoptosis) can be used for
CC treating cancer. The methods can also be used for the identification of
CC agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease; islet
CC cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP: AY81440). Such constructs may be used in
CC gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents the polypyrimidine tract of human XIAP IRES, which is
CC necessary for IRES-dependent translation of XIAP
XX
Sequence 12 BP; 0 A; 2 C; 1 G; 9 T; 0 U; 0 Other;

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 68284; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 1 G; 5 T; 0 U; 1 Other;
SQ
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 731 AGGAGAAAC 739
Db 11 AGGAGAAAC 3
RESULT 417
ABH65495/C
ID ABH65495 standard; DNA; 13 BP.
XX
XX AC ABH65495;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 265472 for detecting SNP TSC0064332.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 265472; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 1 Other;
SQ
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 734 AGAAACAGAAC 744
Db 11 AGAAACAGAA 1
RESULT 418
ABF34136/C
ID ABF34136 standard; DNA; 13 BP.
XX
XX AC ABF34136;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 134133 for detecting SNP TSC0033441.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 134133; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;
SQ
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


```
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 1 Other;

Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAAACA 745
Db 1 RAACATAACA 11

RESULT 412
ABH65494
ID ABH65494 standard; DNA; 13 BP.
XX AC ABH65494;
XX DT 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 265471 for detecting SNP TSC0064332.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 265471; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
```

```
SQ Sequence 13 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACAGAAAC 744
Db 3 AGAAGAGAAAY 13

RESULT 413
ABC68266
ID ABC68266 standard; DNA; 13 BP.
XX AC ABC68266;
XX DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 68283 for detecting SNP TSC0017813.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 68283; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 5 A; 1 C; 5 G; 1 T; 0 U; 1 Other;

Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
Db 3 AGGAGAAAC 11

RESULT 414
ABF34137
```


CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 13 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 1 Other;
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
:|||||

Db 1 RACACACACC 11

RESULT 407
ABF24041
ID ABF24041 standard; DNA; 13 BP.
AC ABF24041;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 124038 for detecting SNP TSC0031015.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 124038; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 13 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 1 Other;
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAACAGAACCA 745
:|||||

Db 1 RACACGACCA 11

RESULT 408
ABC80016/c
ID ABC80016 standard; DNA; 13 BP.
XX
AC ABC80016;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 90033 for detecting SNP TSC0020318.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 80033; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 13 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 1 Other;
Query Match 40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
:|||||

Db 13 RACACACACC 3

RESULT 409
ABF81152/c
ID ABF81152 standard; DNA; 13 BP.
XX
AC ABF81152;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 191149 for detecting SNP TSC0004966.
XX

PD 22-MAY-2003.
XX
XX 19-MAR-2002; 2002US-00100957.
XX
XX 27-FEB-1997; 97US-00810983.
XX
XX 27-FEB-1998; 98US-00034271.
XX
XX 26-FEB-1999; 99US-0122152P.
XX
XX 08-MAR-1999; 99US-0123399P.
XX
XX 12-JUL-1999; 99US-00352171.
XX
XX 31-AUG-1999; 99US-0151797P.
XX
XX 17-SEP-1999; 99US-00398965.
XX
XX 29-OCT-1999; 99US-00430656.
XX
XX 01-DEC-1999; 99US-0168408P.
XX
XX 25-FEB-2000; 2000US-00513783.
XX
XX (CELL-) CELLOMICS INC.
XX
XX Giuliano K, Kapur R;
XX
XX WPI; 2003-786988/74.
XX
XX P-PSDB; ADC18388.
XX
XX Cell based toxin characterization method for e.g. in drug discovery
XX paradigm, involves treating cells possessing luminescent reporter
XX molecules with fluorescence based molecules reagents to detect presence
XX of toxins.
XX
XX Example 10; SEQ ID NO 75; 98pp; English.
XX
XX The invention relates to characterising cell based toxins, where the cell
XX possessing luminescent reporter molecules (biosensors) are provided on a
XX microchip, and are treated with fluorescence based molecular reagents.
XX The cells are photographed with fluorescence optics, and the optical
XX information is converted into digital data. The presence of the toxin in
XX a reagent, is detected using the digital data, based on changes in the
XX localisation, distribution structure of identifier, detector and
XX classifier in each cell. Also included are a computer readable storage
XX medium storing a cell based toxin characterisation program, and a kit for
XX detecting a biological cell based toxin that affect particular biological
XX functions and for preparing molecular biochemical arrays for new drug
XX discovery paradigm. It is also used in automated DNA sequencing, PCR
XX application, positional cloning, hybridisation arrays and bioinformatics
XX using cell based scanning and screening system. The method improves the
XX target validation and candidate optimisation by combining many cell
XX screening formats with fluorescence based molecular reagents, thereby
XX resulting in increased quantity and speed of data collection, shortened
XX cycle times and faster evaluation of promising drug candidates. The
XX method also provides increased throughput while decreasing the volumes of
XX reagent and test compounds required in each assay. The biosensor
XX comprises a signal component (fluorescent protein (fused e.g. MAP4,
XX tethering it to microtubules) or detectable signal (epitope or affinity
XX tag)), a protease recognition site (e.g. for a caspase protein) and a
XX target domain (localising the biosensor to a particular cellular
XX compartment). The present sequence encodes a protease recognition site
XX for a biosensor of the invention.
XX
XX Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query March 40.9%; Score 9; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 734 AGAACACAGA 742
XX
XX DB 3 AGAACACAGA 11
XX
XX RESULT 403
XX ABF34134/C
XX ID ABF34134 standard; DNA; 13 BP.
XX
XX AC ABF34134;

XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 134131 for detecting SNP TSC0033441.
XX
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 134131; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ASC00010
XX -ABG99989, ABF0010-ABF99989, ABH0010-ABH99989 and AB10010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 1 Other;
XX
XX Query Match 40.9%; Score 9; DB 1; Length 13;
XX Best Local Similarity 81.8%; Pred. No. 4.7e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 735 GAACACAGACA 745
XX
XX DB 13 RAACACATAACA 3
XX
XX RESULT 404
XX ABF34135
XX ID ABF34135 standard; DNA; 13 BP.
XX
XX AC ABF34135;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 134132 for detecting SNP TSC0033441.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX

XX PF 07-SEP-2001; 2001WO-EP010366.
 XX PI
 XX PR 07-SEP-2000; 2000US-00657479.
 XX PA (AXAR-) AXARON BIOSCIENCE AG.
 XX PI Schneider A, Hiemisch H, Rossner M, Klugmann M, Naim J,
 XX PI Eisenhardt G, Kuner R, Lanahan A, Worley P, Spielvogel D, Scheek S;
 XX DR WPI; 2002-292287/33.
 XX PT Diagnosis of neurodegenerative disease comprises detecting level of M30-
 XX PT family proteins.
 XX PS Example 11; Page 47; 130pp; German.
 XX CC The present invention relates to a method of diagnosing neurodegenerative
 CC diseases, comprising determining the concentration of a protein in a body
 CC sample, where the protein may be M30 or a variant thereof, M31, M32 or
 CC M33. The method is used to diagnose neurodegenerative diseases.
 CC Particularly stroke but also e.g. fragile X syndrome, Huntington's,
 CC Parkinson's and Alzheimer's diseases, multiple sclerosis etc. Also
 CC overexpression of M31 can be used for diagnosis of carcinoma and sarcoma,
 CC especially ovarian cancer. The proteins can be used to identify specific
 CC ligands, potentially useful for treating neurodegeneration, immune-system
 CC disorders (e.g. autoimmune diseases, allergy, viral infection, leukaemia,
 CC inflammation etc.), carcinoma and sarcoma. Inhibitors of the interaction
 CC between the proteins and the protein kinase IRAK-1 can be used to treat
 CC neurodegeneration. The present sequence is a fragment of the M33 gene
 XX SQ Sequence 12 BP; 1 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 734 AGAARACAGA 742
 DB 10 AGAARACAGA 2
 RESULT 401
 ADC18373
 ID ADC18373 standard; DNA; 12 BP.
 AC ADC18373;
 XX 18-DEC-2003 (first entry)
 XX Protease recognition site for caspase-3 DNA.
 XX ds; cell based toxin; luminescent reporter molecule; biosensor;
 XX microchip; drug discovery; MAP4; epitope; affinity tag;
 XX protease recognition site; caspase; target domain.
 XX Unidentified.
 XX US2003096322-A1.
 XX 22-MAY-2003.
 XX 19-MAR-2002; 2002US-00100957.
 XX 27-FEB-1997; 97US-00810983.
 XX 27-FEB-1998; 98US-00031271.
 XX 26-FEB-1999; 99US-0122152P.
 XX 08-MAR-1999; 99US-0123399P.
 XX 12-JUL-1999; 99US-00352171.
 XX 31-AUG-1999; 99US-0151797P.
 XX 17-SEP-1999; 99US-00398965.
 XX 29-OCT-1999; 99US-00430856.
 XX 01-DEC-1999; 99US-0168408P.

PR 25-FEB-2000; 2000US-00513783.
 XX (CELL-) CELLOMICS INC.
 XX PI Giuliano K, Kapur R;
 XX DR WPI; 2003-786988/74.
 XX DR P-PSDB; ADC18374.
 XX PT Cell based toxin characterization method for e.g. in drug discovery
 XX PT paradigm, involves treating cells possessing luminescent reporter
 XX PT molecules with fluorescence based molecules reagents to detect presence
 XX of toxins.
 XX PS Example 10; SEQ ID NO 61; 98pp; English.
 XX CC The invention relates to characterising cell based toxins, where the cell
 CC possessing luminescent reporter molecules (biosensors) are provided on a
 CC microchip, and are treated with fluorescence based molecular reagents.
 CC The cells are photographed with fluorescence optics, and the optical
 CC information is converted into digital data. The presence of the toxin in
 CC a reagent, is detected using the digital data, based on changes in the
 CC localisation, distribution structure of identifier, detector and
 CC classifier in each cell. Also included are a computer readable storage
 CC medium storing a cell based toxin characterisation program, and a kit for
 CC cell based toxin detection. The method is used for characterising or
 CC detecting a biological cell based toxin that affect particular biological
 CC functions and for preparing molecular biochemical arrays for new drug
 CC discovery paradigm. It is also used in automated DNA sequencing, PCR
 CC application, positional cloning, hybridisation arrays and bioinformatics
 CC using cell based scanning and screening system. The method improves the
 CC target validation and candidate optimisation by combining many cell
 CC screening formats with fluorescence based molecular reagents, thereby
 CC resulting in increased quantity and speed of data collection, shortened
 CC cycle times and faster evaluation of promising drug candidates. The
 CC method also provides increased throughput while decreasing the volumes of
 CC reagent and test compounds required in each assay. The biosensor
 CC comprises a signal component (fluorescent protein (fused e.g. MAP4,
 CC tethering it to microtubules) or detectable signal (epitope or affinity
 CC tag)), a protease recognition site (e.g. for a caspase protein) and a
 CC target domain (localising the biosensor to a particular cellular
 CC compartment). The present sequence encodes a protease recognition site
 CC for a biosensor of the invention.
 XX SQ Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 734 AGAARACAGA 742
 DB 3 AGAARACAGA 11
 RESULT 402
 ADC18387
 ID ADC18387 standard; DNA; 12 BP.
 AC ADC18387;
 XX 18-DEC-2003 (first entry)
 XX Protease recognition site for procaspase-8 DNA.
 XX ds; cell based toxin; luminescent reporter molecule; biosensor;
 XX microchip; drug discovery; MAP4; epitope; affinity tag;
 XX protease recognition site; caspase; target domain.
 XX Unidentified.
 XX US2003096322-A1.
 XX

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PR 31-AUG-1999; 99US-0151797P.
PR 17-SEP-1999; 99US-00398965.
PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
XX
PA (GIUL/) GIULIANO K.
PA (KAPU/) KAPUR R.
XX
PI Giuliano K, Kapur R;
XX
DR WPI; 2002-634730/68.
DR P-PSDB; ABG94459.
XX
XX Automated cell-based toxin detection, classification, and/or
PT identification by treating cells involves use of three classes of
PT luminescent reporter molecules such as detectors, classifiers or
PT identifiers.
XX
PS Example 10; Fig 29B; 214pp; English.
XX
CC The invention describes methods of automated detection, classification
CC and identification comprising treating cells containing luminescent
CC reporter molecules (I) in array of locations with a test substance, where
CC (I) are detectors, classifiers or identifiers, imaging cells in each
CC location to obtain luminescent signals and converting optical information
CC into digital data to interpret presence of toxins in the test substance.
CC The method are useful for detection of toxins chosen from proteases, ADP-
CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
CC Three classes of cell-based luminescent reporter molecules such as
CC detectors, classifiers and identifiers are described and serve as
CC reporters of toxic threat agents. The first two levels of
CC characterisation ensure a rapid readout of toxin class without
CC sacrificing the ability to detect many new mutant toxins or dissect
CC several complex mixtures of known toxins. This sequence encodes a
CC protease biosensor recognition site used in the cell-based screening
CC system
XX
SQ Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 734 AGAAACAGA 742
DB 3 AGAAACAGA 11
|||||
RESULT 399
ABS71499
ID ABS71499 standard; DNA; 12 BP.
XX
AC ABS71499;
XX
DT 27-NOV-2002 (first entry)
XX
DE DNA encoding protease biosensor recognition site #5.
XX
KW Detection; classification; identification; toxin detection; protease;
KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
KW toxic threat agent; ds.
XX
OS Synthetic.
XX
XX US6416959-B1.
XX
XX 09-JUL-2002.
XX
XX 25-FEB-2000; 2000US-00513783.
XX
XX 27-FEB-1997; 97US-00810983.
XX
XX 27-FEB-1998; 98US-00031271.
XX
XX 26-FEB-1999; 99US-0122152P.
PR
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PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
PR 31-AUG-1999; 99US-0151797P.
PR 17-SEP-1999; 99US-00398965.
PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
XX
XX (GIUL/) GIULIANO K.
XX (KAPU/) KAPUR R.
XX
PI Giuliano K, Kapur R;
XX
DR WPI; 2002-634730/68.
DR P-PSDB; ABG94452.
XX
XX Automated cell-based toxin detection, classification, and/or
PT identification by treating cells involves use of three classes of
PT luminescent reporter molecules such as detectors, classifiers or
PT identifiers.
XX
PS Example 10; Fig 29B; 214pp; English.
XX
CC The invention describes methods of automated detection, classification
CC and identification comprising treating cells containing luminescent
CC reporter molecules (I) in array of locations with a test substance, where
CC (I) are detectors, classifiers or identifiers, imaging cells in each
CC location to obtain luminescent signals and converting optical information
CC into digital data to interpret presence of toxins in the test substance.
CC The method are useful for detection of toxins chosen from proteases, ADP-
CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
CC Three classes of cell-based luminescent reporter molecules such as
CC detectors, classifiers and identifiers are described and serve as
CC reporters of toxic threat agents. The first two levels of
CC characterisation ensure a rapid readout of toxin class without
CC sacrificing the ability to detect many new mutant toxins or dissect
CC several complex mixtures of known toxins. This sequence encodes a
CC protease biosensor recognition site used in the cell-based screening
CC system
XX
SQ Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 734 AGAAACAGA 742
DB 3 AGAAACAGA 11
|||||
RESULT 400
AAL46301/C
ID AAL46301 standard; DNA; 12 BP.
XX
AC AAL46301;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human M33 protein coding sequence intron 1 fragment.
XX
KW Neurodegenerative disease; M30; M31; M32; M33; stroke;
KW fragile X syndrome; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; multiple sclerosis; ovarian cancer;
KW neurodegeneration; immune disorder; autoimmune disease; allergy;
KW infection; leukaemia; inflammation; neuroprotective; cerebroprotective;
KW immunosuppressive; cytostatic; nootropic; antiparkinsonian; antiallergic;
KW virucide; antiinflammatory; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200221138-A2.
XX
XX 14-MAR-2002.
XX
XX
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PR 30-OCT-1998; 98US-0106308P.
 PR 26-MAY-1999; 99US-0136078P.
 PA (CELL-) CELLOMICS INC.
 PI Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;
 XX WPI; 2000-365644/31.
 DR P-PSDB; AAY79592.
 XX Recombinant nucleic acid encoding a protease biosensor useful for
 PT fluorescence based cell and molecular biochemical assays for drug
 PT discovery comprising three operably linked nucleic acid sequences.
 XX Claim 6; Fig 29B; 218pp; English.

CC The present sequence is that of DNA encoding the substrate recognition
 CC sequence (see AAY79592) of procaspase-3. The DNA is used in a claimed
 CC recombinant nucleic acid encoding a protease biosensor. The nucleic acid
 CC (see AA227627-43) comprises: (1) a sequence (see AAA27568-76) encoding at
 CC least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-611)
 CC that encodes at least 1 protease recognition site, such as the present
 CC sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1
 CC reactant target sequence. An expression vector, a genetically engineered
 CC host cell and a recombinant protease biosensor are also claimed. A
 CC claimed method for identifying compounds that modify protease activity in
 CC a cell involves contacting a host cell that possesses the recombinant
 CC protease biosensor with a test compound, and determining the recombinant
 CC biosensor distribution in the host cell, where changes in the
 CC distribution of the protease biosensor are correlated with modification
 CC of protease activity by the test compound. Claimed kits for identifying
 CC compounds that modify protease activity in a host cell include the
 CC recombinant nucleic acid, or the recombinant protease biosensor, or the
 CC vector, or the host cell. The protease biosensor is useful in high
 CC content screens to detect in vivo activation of enzymatic activity, and
 CC to identify specific activity based on cleavage of a known recognition
 CC motif

XX Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 734 AGAARACAGA 742
 DB |||||

3 AGAARACAGA 11

RESULT 397
 AAA27588
 ID AAA27588 standard; DNA; 12 BP.
 XX AC AAA27588;
 XX 29-AUG-2000 (first entry)

XX DNA encoding procaspase-8 substrate recognition sequence.
 XX Protease; biosensor; caspase-8; substrate recognition sequence;
 KW cell screening; assay; analysis; drug discovery; ss.

XX Unidentified.
 XX WO200026408-A2.
 XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025431.
 XX 30-OCT-1998; 98US-0106308P.
 PR 26-MAY-1999; 99US-0136078P.
 PR

PA (CELL-) CELLOMICS INC.
 XX Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;
 XX WPI; 2000-365644/31.
 DR P-PSDB; AAY79599.
 XX Recombinant nucleic acid encoding a protease biosensor useful for
 PT fluorescence based cell and molecular biochemical assays for drug
 PT discovery comprising three operably linked nucleic acid sequences.
 XX Claim 6; Fig 29B; 218pp; English.

CC The present sequence is that of DNA encoding the substrate recognition
 CC sequence (see AAY79599) of procaspase-8. The DNA is used in a claimed
 CC recombinant nucleic acid encoding a protease biosensor. The nucleic acid
 CC (see AA227627-43) comprises: (1) a sequence (see AAA27568-76) encoding at
 CC least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-611)
 CC that encodes at least 1 protease recognition site, such as the present
 CC sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1
 CC reactant target sequence. An expression vector, a genetically engineered
 CC host cell and a recombinant protease biosensor are also claimed. A
 CC claimed method for identifying compounds that modify protease activity in
 CC a cell involves contacting a host cell that possesses the recombinant
 CC protease biosensor with a test compound, and determining the recombinant
 CC biosensor distribution in the host cell, where changes in the
 CC distribution of the protease biosensor are correlated with modification
 CC of protease activity by the test compound. Claimed kits for identifying
 CC compounds that modify protease activity in a host cell include the
 CC recombinant nucleic acid, or the recombinant protease biosensor, or the
 CC vector, or the host cell. The protease biosensor is useful in high
 CC content screens to detect in vivo activation of enzymatic activity, and
 CC to identify specific activity based on cleavage of a known recognition
 CC motif

SQ Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 734 AGAARACAGA 742
 DB |||||

3 AGAARACAGA 11

RESULT 398
 ABS71506
 ID ABS71506 standard; DNA; 12 BP.

XX AC ABS71506;

XX 27-NOV-2002 (first entry)
 XX DNA encoding protease biosensor recognition site #12.

XX Detection; classification; identification; toxin detection; protease;
 KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
 XX toxic threat agent; ds.
 XX Synthetic.

XX US6416959-B1.
 XX 09-JUL-2002.

XX 25-FEB-2000; 2000US-00513783.
 XX 27-FEB-1997; 97US-00810983.
 PR 27-FEB-1998; 98US-00031271.
 PR 26-FEB-1998; 98US-0122152P.
 PR 08-MAR-1999; 99US-0123399P.
 PR 12-JUL-1999; 99US-00352171.
 PR

CC region of the cell. Once acted on by the protease of interest, the
CC fluorescent protein is cleaved from the localisation sequence, and is
CC free to migrate to other locations within the cell. The presence of a
CC second localisation signal attached to the fluorescent protein enables
CC the fluorescent protein to be directed to a different cellular
CC compartment after cleavage of the protease recognition sequence. The
CC change in distribution of the fluorescent protein can be detected using
CC imaging methods with a high degree of spatial resolution. The methods and
CC biosensors of the invention can be used to investigate a wide range of
CC cellular activities and to screen compounds which modulate these
CC activities. Biosensors containing a recognition site for caspase, for
CC example, may be used for the screening of compounds which modulate
CC apoptosis, while biosensors containing other protease recognition sites
CC may be used for the detection of proteolytic toxins (such as anthrax
CC lethal factor). The method provides improved target validation and
CC candidate compound optimisation by combining many cell screening formats
CC with fluorescence-based molecular reagents and computer-based feature
CC extraction, data analysis and automation, resulting in increased quantity
CC and speed of data collection and faster evaluation of drug candidates.
CC Sequences AAA93377-A93411 and AAA93440 represent protease recognition
CC sites (AAB22886-B22920, AAB22935) which may be used as components of
CC biosensor fusion proteins of the invention
SQ Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAACACAGA 742
Db 3 AGAACACAGA 11
|||||
3 AGAACACAGA 11

RESULT 395
AAA93381
ID AAA93381 standard; DNA; 12 BP.
AC AAA93381;
XX
DT 10-JAN-2001 (first entry)
XX
DE DNA encoding procaspase-3 substrate recognition sequence, SEQ ID NO:61.
XX
KW Biotector protein; fusion protein; recognition site;
KW cellular targeting sequence; cellular localisation; fluorescent protein;
KW protease activity detection; toxin detection; cellular stress detection;
KW drug discovery; cell based screening; protease recognition site;
KW cleavage site; ds.
XX
OS Unidentified.
XX
PN WO200050872-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004794.
XX
PR 26-FEB-1999; 9SUS-0122152P.
PR 08-MAR-1999; 9SUS-0123399P.
PR 12-JUL-1999; 9SUS-00352171.
XX
XX (CELL-) CELLOMICS INC.
PA Giuliano KA, Kapur R;
XX
XX WPI; 2000-594086/56.
DR P-FSDB; AAB22890.
XX
XX Automated cell-based characterization of toxin by contacting cells
PT containing luminescent reporter molecules with test substance and
PT analyzing optically.
PT
XX

PS Example 11; Fig 29B; 336pp; English.
XX
CC The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreporter
CC molecules which, when acted on by a compound of interest, cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreporter proteins can be used to detect protease
CC activity. Such protease bioreporter fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreporter protein is localised to a particular
CC region of the cell. Once acted on by the protease of interest, the
CC fluorescent protein is cleaved from the localisation sequence, and is
CC free to migrate to other locations within the cell. The presence of a
CC second localisation signal attached to the fluorescent protein enables
CC the fluorescent protein to be directed to a different cellular
CC compartment after cleavage of the protease recognition sequence. The
CC change in distribution of the fluorescent protein can be detected using
CC imaging methods with a high degree of spatial resolution. The methods and
CC biosensors of the invention can be used to investigate a wide range of
CC cellular activities and to screen compounds which modulate these
CC activities. Biosensors containing a recognition site for caspase, for
CC example, may be used for the screening of compounds which modulate
CC apoptosis, while biosensors containing other protease recognition sites
CC may be used for the detection of proteolytic toxins (such as anthrax
CC lethal factor). The method provides improved target validation and
CC candidate compound optimisation by combining many cell screening formats
CC with fluorescence-based molecular reagents and computer-based feature
CC extraction, data analysis and automation, resulting in increased quantity
CC and speed of data collection and faster evaluation of drug candidates.
CC Sequences AAA93377-A93411 and AAA93440 represent protease recognition
CC sites (AAB22886-B22920, AAB22935) which may be used as components of
CC biosensor fusion proteins of the invention
XX
SQ Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAACACAGA 742
Db 3 AGAACACAGA 11
|||||
3 AGAACACAGA 11

RESULT 396
AA27581
ID AA27581 standard; DNA; 12 BP.
XX
AC AA27581;
XX
DT 29-AUG-2000 (first entry)
XX
DE DNA encoding procaspase-3 substrate recognition sequence.
XX
KW Protease; biosensor; caspase-3; substrate recognition sequence;
KW cell screening; assay; analysis; drug discovery; ss.
XX
OS Unidentified.
XX
PN WO200026408-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025431.
XX

CC diseases. The human ESR-alpha gene is located on chromosome 6. ABA98969
CC to ABA98972 represent ESR-alpha gene single nucleotide polymorphism (SNP)
CC containing oligonucleotides, which are used in an example from the
CC present invention
XX
SQ Sequence 11 BP; 7 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 736 AACAGAAC 744
Db 2 AACAGAAC 10
RESULT 393
ABZ95855/C
ID ABZ95855 standard; DNA; 11 BP.
XX
AC ABZ95855;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human prostaglandin D synthase antisense fragment no.1715.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
KW antiallergic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11097; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, anti-allergic, antiallergic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC

CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAA 737
Db 11 CCAGGAGAA 3
RESULT 394
AAA93388
ID AAA93388 standard; DNA; 12 BP.
XX
AC AAA93388;
XX
DT 10-JAN-2001 (first entry)
XX
DE DNA encoding procaspase-8 substrate recognition sequence, SEQ ID NO:75.
XX
KW Bioreactor protein; fusion protein; recognition site;
KW cellular targeting sequence; cellular localisation; fluorescent protein;
KW protease activity detection; toxin detection; cellular stress detection;
KW drug discovery; cell based screening; protease recognition site;
KW cleavage site; ds.
XX
OS Unidentified.
XX
FN WO2000050872-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004794.
XX
PR 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
XX
PA (CELL-) CELLOMICS INC.
XX
PI Giuliano KA, Kapur R;
XX
DR WPI; 2000-594086/56.
DR P-PSDB; AAB22897.
XX
PT Automated cell-based characterization of toxin by contacting cells
PT containing luminescent reporter molecules with test substance and
PT analyzing optically.
XX
PS Example 11; Fig 29B; 336pp; English.
XX
CC The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreactor
CC molecules which, when acted on by a compound of interest cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreactor proteins can be used to detect protease
CC activity. Such protease bioreactor fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreactor protein is localised to a particular
CC

XX SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 739 CAGAACACC 747
 - - - - -
 3 CAGAACACC 11
 Db
 RESULT 391
 ABA89897
 ID ABA89897 standard; DNA; 11 BP.
 XX AC ABA89897;
 XX DT 11-FEB-2002 (first entry)
 XX DE ESR-alpha gene Liverpool clinical tissue sample SNP oligo #29.
 XX KW Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
 KW synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
 KW cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
 KW cardiovascular disease; oestrogen receptor; SNP;
 KW single nucleotide polymorphism; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT variation replace(6,G)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX WO200162969-A2.
 XX PD 30-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US005358.
 XX PR 22-FEB-2000; 2000US-0183756P.
 XX PR 20-OCT-2000; 2000US-00692414.
 XX PR 24-JAN-2001; 2001US-00768184.
 XX PA (PEXE) PE CORP NY.
 XX PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;
 XX WPI; 2002-041152/05.
 XX PT Novel variant of estrogen receptor alpha polypeptide useful for
 PT determining the biological activity of a protein for high throughput
 PT screening and for raising antibodies that elicit an immune response in
 PT host.
 XX Claim 17; Fig 2a sheet 2; 333pp; English.
 XX The present invention describes an isolated peptide (I) consisting of an
 CC amino acid sequence selected from: (a) the amino acid sequence of a
 CC variant of the estrogen receptor alpha (ESR-alpha) protein in AAG68251;
 CC or (b) a fragment comprising at least 10 contiguous amino acids of the
 CC protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and
 CC vasotropic activities, and can be used in gene therapy and vaccine
 CC production. (I) is useful for identifying an agent that binds to (I), by
 CC contacting (I) with an agent and assaying the contacted mixture to
 CC determine whether a complex is formed with the agent bound to the
 CC peptide. A polynucleotide (II), encoding (I), is useful in the
 CC development of diagnostics and therapies for diseases and disorders
 CC mediated/modulated by an estrogen receptor (ER). (II) is also useful in
 CC gene therapy for treating cancer, osteoporosis and cardiovascular
 CC diseases. The human ESR-alpha gene is located on chromosome 6. ABA89897
 CC to ABA89972 represent ESR-alpha gene single nucleotide polymorphism (SNP)

CC containing oligonucleotides, which are used in an example from the
 CC present invention
 XX SQ Sequence 11 BP; 7 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 736 AAACAGAAC 744
 - - - - -
 2 AAACAGAAC 10
 Db
 RESULT 392
 ABA89949
 ID ABA89949 standard; DNA; 11 BP.
 XX AC ABA89949;
 XX DT 11-FEB-2002 (first entry)
 XX DE ESR-alpha gene Coriell Diversity panel oligo #29.
 XX KW Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2;
 KW synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic;
 KW cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis;
 KW cardiovascular disease; oestrogen receptor; SNP;
 KW single nucleotide polymorphism; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT variation replace(6,G)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX WO200162969-A2.
 XX PD 30-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US005358.
 XX PR 22-FEB-2000; 2000US-0183756P.
 XX PR 20-OCT-2000; 2000US-00692414.
 XX PR 24-JAN-2001; 2001US-00768184.
 XX PA (PEXE) PE CORP NY.
 XX PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;
 XX WPI; 2002-041152/05.
 XX PT Novel variant of estrogen receptor alpha polypeptide useful for
 PT determining the biological activity of a protein for high throughput
 PT screening and for raising antibodies that elicit an immune response in
 PT host.
 XX Claim 17; Fig 2b sheet 2; 333pp; English.
 XX The present invention describes an isolated peptide (I) consisting of an
 CC amino acid sequence selected from: (a) the amino acid sequence of a
 CC variant of the estrogen receptor alpha (ESR-alpha) protein in AAG68251;
 CC or (b) a fragment comprising at least 10 contiguous amino acids of the
 CC protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and
 CC vasotropic activities, and can be used in gene therapy and vaccine
 CC production. (I) is useful for identifying an agent that binds to (I), by
 CC contacting (I) with an agent and assaying the contacted mixture to
 CC determine whether a complex is formed with the agent bound to the
 CC peptide. A polynucleotide (II), encoding (I), is useful in the
 CC development of diagnostics and therapies for diseases and disorders
 CC mediated/modulated by an estrogen receptor (ER). (II) is also useful in
 CC gene therapy for treating cancer, osteoporosis and cardiovascular

XX	CC	XX	The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
XX	CC	XX	Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 U; 0 Other;
XX	CC	XX	Query Match 40.9%; Score 9; DB 1; Length 11;
XX	CC	XX	Best Local Similarity 100.0%; Pred.No. 4.4e-02;
XX	CC	XX	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	Db	738 ACAGAACAC 746	
		9 ACAGAACAC 1	
RESULT 390			
ABV67302			
ID	ABV67302	standard; cDNA; 11 BP.	
XX	AC	ABV67302;	
XX	DT	21-OCT-2002 (first entry)	
XX	DE	Human skin EST 5088.	
XX	XX	Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200253774-A2.	
XX	PN	11-JUL-2002.	
XX	PD		
XX	XX	20-DEC-2001; 2001WO-EP015179.	
PF	PF		
XX	XX	03-JAN-2001; 2001DE-01000127.	
PR	XX	(HENK) HENKEL KGAA.	
XX	PA		
PI	PI	Petersohn D, Contadt M, Hofmann K;	
XX	XX		
XX	DR	WPI; 2002-590638/63.	
XX	XX		
PT	PT	In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.	
PT	PT		
PS	PS	Disclosure; Page 165; 1345pp; German.	
XX	XX		
CC	CC	The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention	

XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PD 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 85; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC promote skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 Db 3 CCAGGAGAA 11
 RESULT 388
 ABV64098/c
 ID ABV64098 standard; cDNA; 11 BP.
 XX
 AC ABV64098;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 1894.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX

XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PD 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 85; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC promote skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 Db 3 CCAGGAGAA 11
 RESULT 388
 ABV64098/c
 ID ABV64098 standard; cDNA; 11 BP.
 XX
 AC ABV64098;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 1894.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX

PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 310; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 729 CCAGGAGAA 737
DB 3 CCAGGAGAA 11
|||||||
RESULT 384
ABV62393/c
ID ABV62393 standard; cDNA; 11 BP.
XX
AC ABV62393;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 179.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 31; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 736 AAACAGAAC 744
DB 9 AAACAGAAC 1
|||||||
RESULT 385
ABV69814/c
ID ABV69814 standard; cDNA; 11 BP.
XX
AC ABV69814;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7600.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 240; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 736 AAACAGAAC 744

XX PF 24-MAR-2000; 2000WO-US008020.
XX XX
XX PF 06-APR-1999; 99US-0127958P.
XX XX
XX (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX PA
XX NYCE JW;
XX PI
XX WPI; 2000-679539/66.
XX DR
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
XX PT adenosine receptors during metabolism, useful e.g. for treating cancers
XX PT and respiratory obstructions.
XX XX
XX Claim 14; Page 141; 1592pp; English.
XX PS
XX The present invention describes low adenosine (A) content antisense
XX CC oligonucleotides and compositions (I) comprising them. In the antisense
XX CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX CC The antisense oligonucleotides and (I) can be used to down-regulate the
XX CC expression and/or activity of target polypeptides associated with
XX CC lung/respiratory disorders and malignancies, such as stimulating and
XX CC activating peptide factors and transmitters, transcription factors,
XX CC immunoglobulins and antibodies, antibody receptors, cytokines and
XX CC chemokines, endogenously produced specific and non-specific enzymes,
XX CC binding proteins, adhesion molecules and their receptors, cytokine and
XX CC chemokine receptors, adenosine receptors, bradykinin receptors, central
XX CC nervous system (CNS) and peripheral nervous and non-nervous system
XX CC receptors, CNS and peripheral nervous and non-nervous system peptide
XX CC transmitters, defensins, growth factors, vasoactive peptides and
XX CC receptors, binding proteins and malignancy associated proteins. The
XX CC antisense oligonucleotides may be used in this way to treat disorders
XX CC including respiratory obstruction (especially pulmonary obstruction
XX CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
XX CC surfactant hypoproduction which are associated with a disease or
XX CC condition selected from pulmonary vasoconstriction, inflammation,
XX CC allergies, asthma, impaired respiration, respiratory distress syndrome
XX CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX CC fragments and antisense oligonucleotides used in the exemplification of
XX CC the present invention
XX SQ
XX Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 40.9%; Score 9; DB 1; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 729 CCAGGAGAA 737
XX Db |||||
XX 11 CCAGGAGAA 3
XX
XX RESULT 382
XX ABQ86412
XX ID ABQ86412 standard; cDNA; 11 BP.
XX AC
XX ABQ86412;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 167.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX

PN WO200253773-A2.
XX 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-528865/56.
XX DR Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 44; 325pp; German.
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX SQ
XX Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 40.9%; Score 9; DB 1; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+02;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 729 CCAGGAGAA 737
XX Db |||||
XX 3 CCAGGAGAA 11
XX
XX RESULT 383
XX ABV71807
XX ID ABV71807 standard; cDNA; 11 BP.
XX AC ABV71807;
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 9593.
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antisborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX
XX WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX XX

PI Nyce JW;
 XX DR WPI; 1999-229400/19.
 XX PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.
 XX PS Disclosure; Page 45; 120pp; English.
 XX CC The specification describes antisense oligonucleotides (AA52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes. Gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AA55272-74. These multiple target oligonucleotides
 CC (specifically AA55180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impaired respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 Db 11 CCAGGAGAA 3
 RESULT 380
 ID AAA34039/c
 AC AAA34039 standard; DNA; 11 BP.
 AC AAA34039;
 DT 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1728.
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 OS Homo sapiens.
 PN WO200009525-A2.
 XX 24-FEB-2000.
 XX 03-AUG-1999; 99WO-US017712.
 XX 03-AUG-1998; 98US-0095212P.
 PA (UYEC-) UNIV EAST CAROLINA.
 PI Nyce JW;

XX DR WPI; 2000-205971/18.
 XX PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX PS Disclosure; Page 479; 1343pp; English.
 XX CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 729 CCAGGAGAA 737
 Db 11 CCAGGAGAA 3
 RESULT 381
 ID AAF20161/c
 AC AAF20161 standard; DNA; 11 BP.
 AC AAF20161;
 DT 14-MAR-2001 (first entry)
 DE Human prostaglandin D synthase polynucleotide fragment #1728.
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 OS Homo sapiens.
 XX WO200062736-A2.
 XX 26-OCT-2000.

XX 13-DEC-2001.
 XX
 XX
 PF 06-JUN-2001; 2001WO-US018321.
 XX
 XX
 PR 06-JUN-2000; 2000US-0209564P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 XX
 PI Kliem SE, Koshy B, Tanguay DA;
 XX
 XX WPI; 2002-097928/13.
 DR
 XX
 XX New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
 PT useful in expressing PCDH2 protein for screening candidate drugs to treat
 PT diseases related to PCDH2 activity.
 XX
 XX Claim 18; Page 14; 127pp; English.
 PS
 XX The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
 CC comprising determining which of the haplotypes given in the specification
 CC defines one or both copies of the individual's PCDH2 gene. The
 CC polymorphisms are within a 30244 base pair sequence (ABA05413), fully
 CC defined in the specification. The polymorphic variants are useful in
 CC studying the expression and function of PCDH2, in expressing PCDH2
 CC protein for use in screening for candidate drugs to treat diseases such
 CC as cancer, related to PCDH2 activity, in studying the effect of the
 CC variation on the biological activity of PCDH2 and the binding affinity of
 CC candidate drugs targeting PCDH2. The haplotyping methods are useful in
 CC validating PCDH2 as a candidate target for treating a specific condition
 CC or disease predicted to be associated with PCDH2 activity or in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease associated with PCDH2 activity. The present sequence
 CC is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
 CC the invention
 XX
 XX Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 735 GAAACAGAA 743
 |||||
 Db 10 GAAACAGAA 2
 RESULT 378
 AAL39543
 ID AAL39543 standard; DNA; 10 BP.
 XX
 AC AAL39543;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE CCBP2 detecting ASO primer SEQ ID No 70.
 XX
 XX Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
 KW polymorphic gene variant; single nucleotide polymorphism; human; primer;
 KW PCR; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200232926-A2.
 FN
 XX
 PD 25-APR-2002.
 XX
 XX 12-OCT-2001; 2001WO-US042685.
 PF
 XX
 XX 12-OCT-2000; 2000US-0239638P.
 PR
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX

PI Armstrong B, Kazemi A, Koshy B;
 XX
 XX WPI; 2002-435524/46.
 DR
 XX
 XX New genetic variants having polymorphisms in the chemokine binding
 PT protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
 PT treating disorders affected by expression or function of the CCBP2
 PT isogene.
 XX
 XX Claim 15; Page 14; 84pp; English.
 PS
 XX The invention relates to an isolated polynucleotide comprising genes and
 CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic
 CC variants of the CCBP2 gene are useful in studying the expression and
 CC function of CCBP2, and in expressing CCBP2 proteins for use in screening
 CC candidate drugs for treating diseases associated with CCBP2 activity.
 CC Polynucleotides comprising a polymorphic gene variant or fragment may be
 CC used for therapeutic purposes, where a patient could benefit from
 CC expression or increased expression of a particular CCBP2 protein isoform,
 CC or an expression vector encoding the isoform may be administered to the
 CC patient. Haplotype information is useful in improving the efficiency and
 CC output of several steps in drug discovery and development process,
 CC including target validation, identifying lead compounds, and early phase
 CC clinical trials. The polynucleotides of the invention can be used to
 CC treat disorders related to the CCBP2 gene by gene therapy. This
 CC polynucleotide sequence represents a preferred ASO primer for detecting
 CC CCBP2 gene polymorphisms relating to the invention
 XX
 XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 731 AGGAGAAAC 739
 |||||
 Db 2 AGGAGAAAC 10
 RESULT 379
 AAX54592/c
 ID AAX54592 standard; DNA; 11 BP.
 XX
 AC AAX54592;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Prostaglandin D synthase antisense oligonucleotide fragment.
 XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9913886-A1.
 FN
 XX
 PD 25-MAR-1999.
 XX
 XX 17-SEP-1998; 98WO-US019419.
 PF
 XX
 XX 17-SEP-1997; 97US-0059160P.
 PR
 XX 09-JUN-1998; 98US-00093972.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX

ID ABK81376 standard; DNA; 10 BP.
 AC ABK81376;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human FOS gene allele-specific oligonucleotide PCR primer #19.
 XX
 KW Human; v-fos PBJ murine osteosarcoma viral oncogene homologue; FOS; PCR;
 KW cytostatic; gene therapy; single nucleotide polymorphism; haplotyping;
 KW haplotype pair; developmental bone disorder; cancer; tumour; ss; primer;
 KW chromosome 14q21-q31.
 XX
 OS Homo sapiens.
 XX
 PN WO200232931-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 19-OCT-2001; 2001WO-US046142.
 XX
 PR 19-OCT-2000; 2000US-0241620P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AE, Klem SE, Koshy B, Lee HH;
 XX
 DR WPI; 2002-435529/46.
 XX
 PT Novel genetic variants of V-Fos PBJ Murine Osteosarcoma Viral Oncogene
 PT Homolog (FOS) isogenes, useful for improving efficiency and reliability
 PT in drug development for treating developmental bone disorders.
 XX
 PS Claim 17; Page 15; 73pp; English.
 XX
 CC The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human v-fos PBJ murine osteosarcoma viral oncogene homologue
 CC (FOS) polypeptide. A method for haplotyping the FOS gene in an individual
 CC comprises identifying the nucleotide at one or more polymorphic sites and
 CC determining whether one of the copies of the gene is defined by one of
 CC the FOS haplotypes given in the specification or whether both copies are
 CC defined by a haplotype pair. This method is useful in genotyping whereby
 CC all possible haplotype pairs can be assigned to specific genotypes. An
 CC association between a trait and a haplotype or haplotype pair of the FOS
 CC gene can be identified by comparing the frequency of the haplotype or
 CC haplotype pair in a population exhibiting the trait with the frequency of
 CC the haplotype or haplotype pair in a reference population, where a higher
 CC haplotype frequency in the trait population indicates the trait is
 CC associated with the haplotype or haplotype pair. FOS and its
 CC corresponding DNA are used for studying the expression and function of
 CC FOS, for use in screening for candidate drugs to treat diseases related
 CC to FOS activity, such as developmental bone disorders and tumours. The
 CC sequences are also useful for studying the effect of variation on the
 CC biological activity of FOS as well as on the binding affinity of
 CC candidate drugs targeting FOS. Sequences ABK81376-ABK81377 represent
 CC allele-specific oligonucleotide PCR primers used for detecting FOS gene
 CC polymorphisms
 XX
 SQ Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 732 GGAGAAACA 740
 |||||
 Db 1 GGAGAAACA 9
 RESULT 376
 ABV78423/C
 ID ABV78423 standard; cDNA; 10 BP.
 XX

AC ABV78423;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human Th1 cell preferentially expressed gene SAGE tag, SEQ ID NO:134.
 XX
 KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
 KW activated T cell; T lymphocyte; immune response; expression pattern;
 KW preferential expression; immune disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN JF2002186482-A.
 XX
 PD 02-JUL-2002.
 XX
 PF 19-DEC-2000; 2000JP-00385816.
 XX
 PR 19-DEC-2000; 2000JP-00385816.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-594261/54.
 XX
 PT Human activated Th1 and Th2 cell expression gene group, useful for the
 PT diagnosis and treatment of Th1 and Th2-related diseases.
 XX
 PS Claim 19; Page 10; 60pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
 CC inhibitors of the expression of groups of genes that are expressed in
 CC either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78350-ABV78560 are SAGE tags
 CC representing 171 genes which are more highly expressed in Th1 cells
 CC compared with Th2 cells
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 740 AGAACACCG 748
 |||||
 Db 10 AGAACACCG 2
 RESULT 377
 AB199152/C
 ID AB199152 standard; DNA; 10 BP.
 XX
 AC AB199152;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human PCDH2 ASO PCR primer SEQ ID NO 109.
 XX
 KW Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
 KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
 KW allele-specific oligonucleotide; ASO; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200194361-A2.

CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is a primer used to detect
CC CSF1R gene polymorphisms by primer extension, described in the method of
CC the invention
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAAC 739
DB 2 AGGAGAAAC 10
|||||

RESULT 373
ABL99040/c
ID ABL99040 standard; cDNA; 10 BP.
XX
AC ABL99040;
XX
DT 25-JUN-2002 (first entry)
XX
DE Mouse neuronal regeneration related SAGE EST 35.
XX
KW Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
KW learning disorder; serial analysis of gene expression; SAGE;
KW gene expression; hippocampus; expressed sequence tag; EST; ss.
XX
OS Mus sp.
XX
PN DE10048893-A1.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2000; 2000DE-01048893.
XX
PR 02-OCT-2000; 2000DE-01048893.
XX
PA (LION-) LION BIOSCIENCE AG.
XX
DR WPI; 2002-341428/38.
XX
PT New nucleic acids involved in neuronal regeneration, useful in screening
PT for modulators of regeneration or synaptic efficiency, and potential
PT therapeutic agents.
XX
PS Example 6; Page 9; 38pp; German.
XX
CC The invention relates to nucleic acids (ABL98957-ABL99004) involved in
CC regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)
CC used to screen for compounds and potential therapeutic agents that
CC modulate nerve cell regeneration and/or synaptic efficiency. They may
CC also be used for treatment or diagnosis of defective or pathological
CC memory and learning conditions. The present sequence is that of an EST
CC isolated from serial analysis of gene expression (SAGE) experiments
CC comparing gene expression in the hippocampus of GFAP/L1 transgenic mice
CC versus a wildtype control. The resultant EST were used to isolate the
CC nucleic acids of the invention
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 739 CAGAACACC 747
DB 9 CAGAACACC 1
|||||

RESULT 374
ABK96032
ID ABK96032 standard; DNA; 10 BP.
XX
AC ABK96032;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human LIPE gene polymorphism detection oligonucleotide primer #7.
XX
KW Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
KW polymorphism; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200240502-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-US043518.
XX
PR 16-NOV-2000; 2000US-02493302P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;
XX
DR WPI; 2002-519369/55.
XX
PT Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPE activity, e.g. obesity and male sterility.
XX
PS Claim 17; Page 16; 142pp; English.
XX
CC The present invention relates to a new polynucleotide comprising a
CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
CC isogenes. The invention is useful in screening for drugs targeting LIPE
CC isogenes that are useful for treating obesity and male sterility. The
CC methods of the invention are useful for improving the efficiency and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with LIPE activity. The polynucleotide
CC is useful in studying the expression and function of LIPE, and in
CC expressing LIPE protein for use in screening for candidate drugs to treat
CC diseases related to LIPE activity. It is also useful in studying the
CC effect of the variation on the biological activity of LIPE as well as on
CC the binding affinity of candidate drugs targeting LIPE for the treatment
CC of obesity and male sterility. The invention is useful for studying the
CC expression of LIPE isogenes in vivo, for in vivo screening and testing of
CC drugs targeted against LIPE protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating obesity and male sterility
CC in a biological system. The present nucleic acid sequence represents one
CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
CC used in the invention to detect polymorphisms in the human LIPE gene
XX
SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGA 736
DB 1 GCCAGGAGA 9
|||||

RESULT 375
ABK81376

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
 SQ Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 731 AGGAGAAAC 739
 DB 2 AGGAGAAAC 10
 |||||

RESULT 371
 AAS19577
 ID AAS19577 standard; DNA; 10 BP.
 AC AAS19577;
 XX 26-MAR-2002 (first entry)
 XX Primer-extension oligonucleotide #8 to detect human MPL polymorphisms.
 DE Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34;
 KW myeloproliferative leukaemia virus oncogene; haplotyping; genotyping;
 KW congenital amegakaryocytic thrombocytopaenia; CAMT; primer; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200179232-A2.
 FN 25-OCT-2001.
 PD 16-APR-2001; 2001WO-US012301.
 PF 14-APR-2000; 2000US-0197839P.
 PR (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Choi JY, Koshy B, Stephens JC;
 PI WPI; 2002-055251/07.

XX Nucleotide polymorphisms in the human myeloproliferative leukemia virus
 PT oncogene (MPL) gene, useful for studying the function of and expressing
 PT MPL protein for use in screening drugs for treating diseases related to
 PT MPL activity.
 XX Claim 17; Page 15; 85pp; English.
 CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL)
 CC gene located on chromosome 1p34, and methods for haplotyping and/or
 CC genotyping the MPL gene. The methods of the invention make use of allele-

CC specific oligonucleotides (ASOs) as probes and primers and/or primer-
 CC extension oligonucleotides for detecting MPL gene polymorphisms. The
 CC polynucleotides and screened compounds are useful for the treatment of
 CC diseases associated with MPL activity, such as congenital amegakaryocytic
 CC thrombocytopaenia (CAMT). AAS19570-AAS19607 represent primer-extension
 CC oligonucleotides for detecting human MPL gene polymorphisms

SQ Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 40.9%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 732 GGAGAAACA 740
 DB 2 GGAGAAACA 10
 |||||

RESULT 372
 AAS98810
 ID AAS98810 standard; DNA; 10 BP.
 AC AAS98810;
 XX 26-MAR-2002 (first entry)
 XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #176.
 DE Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytostatic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; primer;
 KW primer extension; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200179225-A2.
 FN 25-OCT-2001.
 PD 12-APR-2001; 2001WO-US012044.
 PF 12-APR-2000; 2000US-0196411P.
 PR (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Choi JY, Koshy B;
 PI WPI; 2002-075058/10.

XX Novel polymorphic variants of colony stimulating factor 1 receptor useful
 PT in studying expression and function of the protein, useful for screening
 PT candidate drugs to treat diseases e.g. inflammatory disorders.
 XX Claim 17; Page 17; 164pp; English.
 CC The invention describes a novel isolated polynucleotide (I) comprising a
 CC sequence which is a polymorphic variant (PV) of a reference sequence for
 CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
 CC polypeptide are useful for improving the discovery and development of
 CC drugs for treating diseases associated with CSF1R activity, e.g.,
 CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
 CC and the haplotypes can be used to validate CSF1R as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
 CC be used in developing diagnostic tests and therapeutic treatments. (I) is
 CC useful in studying the expression and function of CSF1R, and in
 CC expressing CSF1R protein for use in screening for candidate drugs to
 CC treat diseases related to CSF1R activity and in studying the effect of
 CC the variation on the biological activity of CSF1R as well as on the
 CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A transgenic animal is useful in studying expression of the

CC (transient receptor potential) family protein; (iii) is connected with
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving 15p15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MTR1 is involved in
CC regulation of intracellular calcium ion levels, which are essential for
CC cellular responses to hormones and/or growth factors; also in apoptosis
CC and cell growth, death and differentiation, and in urogenital diseases,
CC including polycystic kidney disease. (I) and related ribozymes, antisense
CC RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases
CC associated with altered expression of the MTR1 gene or activity of its
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC used for diagnosis of such diseases. (I) can also be used for recombinant
CC production of MTR1 proteins (II) (used for analysis, characterization and
CC therapy), as tissue or chromosomal markers, for identifying genetic
CC diseases and related sequences, as primers for genetic fingerprinting, as
CC source of oligonucleotides for biochips, and to raise anti-protein or
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC competitive assays for (II), as tissue markers; for identifying
CC interacting proteins and in screening for (ant)agonists. This sequence
CC represents human MTR1 gene intron9/exon10 junction region described in
CC the method of the invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 CCAGGAGAA 737
Db 2 CCAGGAGAA 10
|||||
AAAF70411/C
ID AAF70411 standard; DNA; 10 BP.
XX AAF70411;
AC AAF70411;
XX 20-APR-2001 (first entry)
XX Human DRD2 polymorphism detection oligonucleotide primer SEQ ID NO:154.

XX Human, dopamine receptor D2; DRD2; polymorphism; allele specific;
KW drug target isogene; detection; single nucleotide polymorphism; SNP;
KW genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; MD;
KW probe; PCR primer; ss.
XX Homo sapiens.
OS
XX WO200105832-A1.
PN 25-JAN-2001.
XX 19-JUL-2000; 2000WO-US019644.
PF 19-JUL-1999; 99US-0144493P.
PR (GENA-) GENAISSANCE PHARM INC.
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI WPI; 2001-091967/10.
XX
XX Polynucleotides comprising single nucleotide polymorphisms in the human
PT dopamine receptor D2, useful for detecting mutations associated with,
PT e.g. schizophrenia, Parkinson's and myoclonus dystonia.
XX
XX Disclosure; Page 24; 135pp; English.
PS
XX The present invention describes polynucleotides comprising single
CC nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).

CC The polynucleotides may be used in assays to detect and characterise
CC polymorphisms in DRD2 that affect its expression and activity and are
CC involved in disorders such as schizophrenia, Parkinson's and myoclonus
CC dystonia (MD). This information would be useful for studying the
CC biological function of DRD2 as well as in identifying drugs targeting
CC this protein for the treatment of disorders related to its abnormal
CC expression or function. Polymorphisms in the DRD2 gene affect the
CC expression of active and functional polypeptides. Therefore it is
CC advantageous to detect polymorphisms in the DRD2 gene and how those
CC polymorphisms are combined in different copies of the gene. AAF70261 to
CC AAF70308 represent human DRD2 allele specific oligonucleotide probes, and
CC AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide
CC primers which are used in the detection of DRD2 polymorphisms. AAF70405
CC to AAF70452 represent oligonucleotide primers for the detection of human
CC DRD2 polymorphisms which are given in the exemplification of the present
CC invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2
CC gene which are used in examples from the present invention
XX
SQ Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAACACAGAA 743
Db 10 GAACACAGAA 2
|||||
AAAF42486
ID AAF42486 standard; DNA; 10 BP.
XX AAF42486;
AC AAF42486;
XX 23-MAR-2001 (first entry)
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10625.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
PN 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
PF 16-JUN-1999; 99US-00335032.
PR (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 329; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

XX Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACACA 742
Db 2 AGAAACACA 10

RESULT 367
AAZ86656
ID AAZ86656 standard; DNA; 10 BP.

XX AAZ86656;

AC AAZ86656;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #5890.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B.L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

XX Claim 1; Page 213; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), all-based particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

XX Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 ACAGAACAC 746
Db 2 ACAGAACAC 10

RESULT 368

AAH20544

ID AAH20544 standard; DNA; 10 BP.

XX AAH20544;

AC AAH20544;

DT 09-AUG-2001 (first entry)

DE Human MTR1 intron9/exon10 junction.

XX MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW cell growth; cell death; cell differentiation; urogenital disease;
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW rhabdomyosarcoma; ds.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Intron

FT 1..5

FT /*tag= a

FT /number= 9

FT 6..10

FT /*tag= b

FT /number= 10

XX WO200132693-A2.

XX 10-MAY-2001.

XX 06-NOV-2000; 2000WO-DE003876.

XX 04-NOV-1999; 99DE-01053167.

XX (UYGU-) UNIV GUTENBERG JOHANNES.

XX Prawitt D, Pelletier J, Zabel B;

XX WPI; 2001-316417/33.

XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies.
XX Example 2; Fig 2; 46pp; German.
XX This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP

CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
 Db 14 GCAGAAAGAGGACA 1

RESULT 364
 ABZ96451/c
 ID ABZ96451 standard; DNA; 14 BP.

XX AC ABZ96451;

XX DT 17-OCT-2003 (first entry)

XX DE Human nucleic acid sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antischismatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX XX 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX XX (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPT; 2003-229219/22.

XX FT Pharmaceutical composition for treating ailments associated with impaired
 FT respiration, has oligo(s) antisense to specific gene(s) or its
 FT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 FT ubiquinone.

XX PS Disclosure; SEQ ID NO 11693; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antischismatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
 Db 14 GCAGAAAGAGGACA 1

RESULT 365

AAZ79493/c

ID AAZ79493 standard; DNA; 10 BP.

XX AC AAZ79493;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:1921.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX XX 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.

XX PR 19-JUN-1998; 98US-0089844P.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089878P.

XX PR 19-JUN-1998; 98US-0089911P.

XX PR 19-JUN-1998; 98US-0089922P.

XX PR 19-JUN-1998; 98US-0089933P.

XX PR 19-JUN-1998; 98US-0089944P.

XX PR 19-JUN-1998; 98US-0089977P.

XX PR 19-JUN-1998; 98US-0089999P.

XX PR 19-JUN-1998; 98US-0090000P.

XX PR 19-JUN-1998; 98US-0090035P.

XX PR 19-JUN-1998; 98US-0090036P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PR 19-JUN-1998; 98US-0090042P.

XX PR 19-JUN-1998; 98US-0090043P.

XX PR 19-JUN-1998; 98US-0090044P.

XX PR 19-JUN-1998; 98US-0090045P.

XX PR 19-JUN-1998; 98US-0090047P.

XX PR 19-JUN-1998; 98US-0090048P.

XX PR 19-JUN-1998; 98US-0090072P.

XX PR 19-JUN-1998; 98US-0090076P.

XX PR 19-JUN-1998; 98US-0090077P.

XX PR 19-JUN-1998; 98US-0090078P.

XX PR 19-JUN-1998; 98US-0090079P.

XX PR 19-JUN-1998; 98US-0090080P.

XX PR 08-DEC-1998; 98US-0111715P.

Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
Db 14 GCAGAAAGAGGACA 1

RESULT 362
AAF21460/C
ID AAF21460 standard; DNA; 14 BP.
XX AC AAF21460;
XX DT 14-MAR-2001 (first entry)
XX DE Human multiple target antisense (MTA) oligonucleotide #3027.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX KW human; airway disorder; bronchoconstriction; lung inflammation;
XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX KW respiratory obstruction; pulmonary obstruction; impeded respiration;
XX KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX KW cancer; ss.
XX OS Homo sapiens.
XX XX
XX XX WO200062736-A2.
XX PN 26-OCT-2000.
XX PD 24-MAR-2000; 2000WO-US008020.
XX PF 06-APR-1999; 99US-0127958P.
XX PR (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX XX
XX PI Nyce JW;
XX XX
XX XX WPI; 2000-679539/66.
XX DR
XX PT Low adenosine (A) content antisense oligonucleotides which do not trigger
XX PT adenosine receptors during metabolism, useful e.g. for treating cancers
XX PT and respiratory obstructions.
XX PS Disclosure; Page 296; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or

CC surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention
XX
XX Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;
SQ Query Match 41.8%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 745
Db 14 GCAGAAAGAGGACA 1

RESULT 363
AB297154/C
ID AB297154 standard; DNA; 14 BP.
XX AC AB297154;
XX DT 17-OCT-2003 (first entry)
XX DE Human MTA oligonucleotide.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX XX
XX XX WO200285308-A2.
XX PN 31-OCT-2002.
XX PD 23-APR-2002; 2002WO-US013135.
XX PF 24-APR-2001; 2001US-0286137P.
XX PR (EPIG-) EPIGENESIS PHARM INC.
XX PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX XX
XX XX WPI; 2003-229219/22.
XX DR
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12396; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also

KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 XX W09950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US006507.
 XX 27-MAR-1998; 98US-0079678P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 XX of an mRNA encoding an angiogenic factors.
 XX Claim 56; Page 136; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with RNA
 XX cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 XX and AAA19155 to AAA19222 represent their corresponding target sequences;
 XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 XX AAA21596 to AAA21688 represent their corresponding target sequences;
 XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 XX AAA23422 represent their corresponding target sequences. The ribozymes of
 XX the invention are used for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding angiogenic factor, especially ARNT,
 XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 XX especially used to treat cancer, diabetic retinopathy, age related
 XX macular degeneration (ARMD), inflammation, and arthritis, as well as
 XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
 XX integrin subunit alpha-6, or integrin subunit beta-3
 XX Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 SQ Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAAC 744
 Db 14 AGAGGAAACAGCAC 1
 RESULT 359
 AAX55188/c
 ID AAX55188 standard; DNA; 14 BP.
 AC AAX55188;
 XX 05-JUL-1999 (first entry)
 XX Multiple antisense oligonucleotide 9.
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW

KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX Synthetic.
 XX W09913886-A1.
 XX 25-MAR-1999.
 XX 17-SEP-1998; 98WO-US019419.
 XX 17-SEP-1997; 97US-0059160P.
 XX 09-JUN-1998; 98US-00093972.
 XX (UYEC-) UNIV EAST CAROLINA.
 XX Nyce JW;
 XX WPI; 1999-229400/19.
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction.
 XX Disclosure; Page 73; 120pp; English.
 XX The specification describes antisense oligonucleotides (AAX52869-X55271)
 XX directed against at least 2 mRNAs selected from target genes, coding and
 XX non-coding regions of RNAs corresponding to target genes, gene initiation
 XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 XX end and the juxta-section between coding and non-coding regions and all
 XX segments of RNAs encoding proteins associated with one or more diseases,
 XX conditions or mixtures. The antisense oligonucleotides may be derived
 XX from sequences AAX55272-74. These multiple target oligonucleotides
 XX (specifically AAX55180-271) can be used for the antisense treatment of
 XX diseases and conditions. Typical diseases and conditions are those
 XX associated with impaired respiration and inflammation, including lung
 XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 XX acute asthma, allergies, asthma, impeded respiration, respiratory
 XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
 XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 XX well as all types of cancers which may metastasize or have metastasized
 XX to the lungs, including breast and prostate cancer
 XX Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;
 SQ Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 732 GGAGAAACAGAAC 745
 Db 14 GCAGAAAGAGGACA 1
 RESULT 360
 AAA34635/c
 ID AAA34635 standard; DNA; 14 BP.
 AC AAA34635;
 XX 28-JUL-2000 (first entry)
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2324.
 DE

KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; antisense oligonucleotide; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2003006470-A1.
 XX 23-JAN-2003.
 XX 10-JUL-2002; 2002WO-US021664.
 XX 10-JUL-2001; 2001US-0303820P.
 XX (OLIG-) OLIGOS ETC INC.
 XX Dale RMK, Arrow A, Thompson T;
 XX WPI; 2003-221709/21.
 XX Composition with a modified oligonucleotide useful for treating a patient
 PT with a pathological disorder such as abnormal appetite, hypertension,
 PT eczema, anxiety, stress, and cancer.
 XX Claim 17; Page 6; 173pp; English.
 XX The present invention describes a composition (I) suitable for
 CC administration in a mammal, which comprises a modified oligonucleotide
 CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
 CC modified oligonucleotide is complementary to a region of a gene
 CC associated with a pathological disorder. Also described: (1) a
 CC nutritional supplement comprising (II); and (2) a cosmetic composition
 CC comprising (II), where the modified oligonucleotide is complementary to a
 CC region of a gene associated with a skin disorder. (I) and (II) can have
 CC hypotensive, antilipemic, vasotropic, dermatological, antidepressant,
 CC tranquiliser, antiinflammatory, antitumor, laxative, antimigraine,
 CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
 CC vulnary, antiarthritic, antipsoriatic, antimicrobial, cytostatic and
 CC litholytic activities. (I) can be used for treating a patient with a
 CC pathological disorder selected from abnormal appetite, hypertension,
 CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
 CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
 CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
 CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
 CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
 CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
 CC inflammation, heart burn, infection, psoriasis, prostatic,
 CC melanoma, and malignant nasal polyps. The nutritional supplement is
 CC useful for supplementing the diet of an individual, and the cosmetic
 CC composition is useful for improving the appearance of the skin in an
 CC individual with a skin disorder. ACF63279 to ACF63410 represent
 CC nucleotide sequence given in the exemplification of the present invention
 XX
 XX Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 727 TGCAGGAGGAA 737
 DB |||||
 3 TGTCTCAGGAGAA 13
 RESULT 357
 AAQ78386
 ID AAQ78386 standard; DNA; 14 BP.
 XX
 AC AAQ78386;
 XX
 DT 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)
 XX Antisense oligonucleotide hybridising to TGF-beta gene.
 DE
 XX
 KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX Synthetic.
 OS
 XX WO9425588-A2.
 XX 10-NOV-1994.
 XX 29-APR-1994; 94WO-EP001362.
 XX 30-APR-1993; 93EP-00107089.
 XX 13-MAY-1993; 93EP-00107849.
 XX (BT0G-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 XX Bogdahn U;
 XX WPI; 1994-358266/44.
 XX New transforming growth factor beta antisense oligonucleotide(s) - for
 PT treating immunosuppression, tumours, etc.
 XX Claim 6; Page 34; 74pp; English.
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 14 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 41.8%; Score 9.2; DB 1; Length 14;
 Best Local Similarity 78.6%; Pred. No. 4.5e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 730 CAGGAGAAACAGAA 743
 DB |||||
 1 CATGAGAGACGGA 14
 RESULT 358
 AAA19155/C
 ID AAA19155 standard; RNA; 14 BP.
 XX
 AC AAA19155;
 XX
 XX 19-JUN-2000 (first entry)
 XX Human TIE-2 target site SEQ ID NO:2381.
 DE
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW

XX 23-APR-2002; 2002WO-US013135.
 XX PF
 XX 24-APR-2001; 2001US-0286137P.
 XX PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX PI Miller S, Tang L, Shahabuddin S;
 XX PT
 XX WPI; 2003-229219/22.
 XX DR
 XX Pharmaceutical composition for treating ailments associated with impaired
 XX PT respiration, has oligo(s) antisense to specific gene(s) or its
 XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 XX PT ubiquinone.
 XX PS
 XX Disclosure; SEQ ID NO 11128; 872pp; English.
 XX CC
 XX The invention relates to a novel pharmaceutical composition, which has a
 XX CC first active agent comprising an oligonucleotide antisense to the
 XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 XX CC junctions of genes encoding a polypeptide associated with lung and/or
 XX CC nasal airway dysfunction and a second active agent comprising an
 XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
 XX CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,
 XX CC immunosuppressive, and cytostatic activity. The composition may have a
 XX CC use in antisense gene therapy. The composition is useful for treating or
 XX CC preventing a respiratory, lung or malignant disease or condition, also
 XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
 XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
 XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
 XX CC Note: The sequence data for this patent is not represented in the printed
 XX CC specification, but was obtained in electronic format directly from WIPO
 XX CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ
 XX Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAACAC 741
 Db 11 AGGAGAACAC 1
 RESULT 355
 ABZ95313/c
 ID ABZ95313 standard; DNA; 14 BP.
 XX AC
 XX ABZ95313;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human IL-6 receptor fragment no.1177.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX WO200285308-A2.
 XX FN
 XX 31-OCT-2002.
 PD

XX 23-APR-2002; 2002WO-US013135.
 XX PF
 XX 24-APR-2001; 2001US-0286137P.
 XX PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX PI Miller S, Tang L, Shahabuddin S;
 XX PT
 XX WPI; 2003-229219/22.
 XX DR
 XX Pharmaceutical composition for treating ailments associated with impaired
 XX PT respiration, has oligo(s) antisense to specific gene(s) or its
 XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 XX PT ubiquinone.
 XX PS
 XX Disclosure; SEQ ID NO 10555; 872pp; English.
 XX CC
 XX The invention relates to a novel pharmaceutical composition, which has a
 XX CC first active agent comprising an oligonucleotide antisense to the
 XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 XX CC junctions of genes encoding a polypeptide associated with lung and/or
 XX CC nasal airway dysfunction and a second active agent comprising an
 XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
 XX CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,
 XX CC immunosuppressive, and cytostatic activity. The composition may have a
 XX CC use in antisense gene therapy. The composition is useful for treating or
 XX CC preventing a respiratory, lung or malignant disease or condition, also
 XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
 XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
 XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
 XX CC Note: The sequence data for this patent is not represented in the printed
 XX CC specification, but was obtained in electronic format directly from WIPO
 XX CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ
 XX Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 728 GCCAGAGAGAA 738
 Db 12 GCCAGAGAGAA 2
 RESULT 356
 ACF63279
 ID ACF63279 standard; DNA; 14 BP.
 XX AC
 XX ACF63279;
 XX DT 09-OCT-2003 (first entry)
 XX DE Human phosphodiesterase 4 antisense oligonucleotide SEQ ID NO:1.
 XX KW Human; pharmacological; hypotensive; antilipemic; vasotropic; laxative;
 KW dermatological; antidepressant; tranquilizer; antiinflammatory; eczema;
 KW antiulcer; antimitigaine; neuroprotective; antiparkinsonian; analgesic;
 KW gynaecological; virucide; vulvar; antiarthritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple lateral sclerosis; trauma;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; chronic
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;

PN EP1174514-A1.
XX 23-JAN-2002.
XX
XX 20-JUL-2000; 2000EP-00115626.
XX
XX 20-JUL-2000; 2000EP-00115626.
XX
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Hobom G, Menke A, Meyer-Rogge S;
XX
XX WPI; 2002-156694/21.
XX
XX Recombinant influenza virus for transfer and expression of foreign genes
PT and RNA molecules into cells and for preventing, treating influenza, has
PT bisclstronic viral RNAs coding for two genes in tandem arrangement.
XX
XX Disclosure; Page 15; 39pp; English.
XX
XX The invention describes a recombinant influenza virus (I), stable in the
XX absence of any helper virus, that has a viral RNA segment being a
XX bisclstronic RNA molecule coding for two genes in tandem arrangement
XX (tandem RNA segment, TRS). (I) is useful for expression of incorporated
XX foreign gene(s) and RNA molecules in cells. (II), preferably a recombinant
XX influenza A virus is useful for: preventing and/or treating influenza,
XX and for preparing a medicament for vaccination purposes; somatic gene
XX therapy, and as immunogen for inducing antibodies; as an expression
XX vector for producing proteins or glycoproteins; preparing agents for
XX somatic gene therapy; immunotherapy, preferably autologous immunotherapy;
XX transfer and expression of foreign genes and RNA molecules into cells
XX infected by such viruses, where the RNA molecules to be expressed include
XX antisense or double-stranded sequences relative to the target cell
XX cellular mRNA molecules, and/or the agent is suitable for sequence-
XX specific gene silencing, preferably by antisense RNA or RNA interference
XX mechanisms. (I) gives high-yield expression for foreign genes. This
XX sequence represents a 3' conserved region mutant of influenza C virus
XX that is incorporated into the mutant influenza C construct, described in
XX the method of the invention
XX
SQ Sequence 14 BP; 1 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 14 AGTAGAAACAG 4
RESULT 353
ABZ95299/c
ID ABZ95299 standard; DNA; 14 BP.
XX
XX ABZ95299;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human IL-6 receptor fragment no.1163.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antialsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
PD

XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
XX Disclosure; SEQ ID NO 10541; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiqunone. A composition of the invention
XX has antiinflammatory, antiallergic, antialsthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiqunone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAA 738
DB 14 GCCAGGAGACA 4
RESULT 354
ABZ95886/c
ID ABZ95886 standard; DNA; 14 BP.
XX
XX ABZ95886;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human monocyte activating factor antisense fragment no.1746.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antialsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
PD

KW virus-associated antigen; VAA; recombinant influenza virus; vaccine;
KW viral infection; immune; influenza C virus; ss.
XX Influenza virus.
XX
XX
XX Bp1201760-A1.
XX
XX 02-MAY-2002.
XX
XX 30-OCT-2000; 2000EP-00123687.
XX
XX 30-OCT-2000; 2000EP-00123687.
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann R;
XX WPI; 2002-418777/45.
XX
XX Expressing tumor or viral associated antigens by dendritic cells, used
XX for treating tumors or viral infections, comprises using recombinant
XX influenza virus containing nucleic acid encoding the antigens.
XX
XX Disclosure; Page 16; 33pp; English.
XX
XX The invention relates to a method for the expression of tumour associated
XX antigens (TAA) or virus-associated antigens (VAA) by dendritic cells
XX comprising: preparing a recombinant influenza virus containing a
XX nucleotide sequence coding for the TAA or VAA; and infecting dendritic
XX cells with the recombinant virus. The method is used for expressing TAA
XX or VAA in dendritic cells. The cells are used for preparing a medicament
XX for treating tumors or viral infections. A vaccine can be created by
XX using dendritic cells presenting tumour antigens to induce an immune
XX response. This polynucleotide sequence represents an RNA region of a
XX modified influenza C virus of the invention
XX
XX Sequence 14 BP; 1 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 14;
XX Best Local Similarity 90.9%; Pred. No. 4.2e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 731 AGGAGAAACAG 741
DB 14 AGTAAACAG 4
XX
XX
XX
XX
XX
XX 07-NOV-2002 (first entry)
XX
XX Influenza C virus general structure oligonucleotide SEQ ID NO:19.
XX
XX Influenza virus; transcription; replication; RNA polymerase; vaccine;
XX gene therapy; cytosolic; anti-HIV; hepatotropic; antiinflammatory;
XX immunomodulator; virucide; infectious disease; ss.
XX
XX Influenza virus.
XX Synthetic.
XX
XX WO200264757-A2.
XX
XX 22-AUG-2002.
XX
XX 07-FEB-2002; 2002WO-EP001257.
XX
XX 09-FEB-2001; 2001EP-00103060.
XX (ARTE-) ARTEMIS PHARM GMBH.
XX

XX Hobom G, Menke A;
XX WPI; 2002-657594/70.
XX
XX New human influenza virus comprising an RNA-sequence encoding a modified
XX RNA-polymerase, useful for preparing agents for therapeutic and
XX prophylactic vaccination, or treating a growing tumor or a chronic
XX infectious disease.
XX
XX Disclosure; Page 16; 172pp; English.
XX
XX The present invention describes a human influenza virus (I) comprising an
XX RNA-sequence encoding a modified RNA-polymerase that differs from the
XX wild-type RNA-polymerase of the human influenza virus in that at least 1
XX of the amino acid residues distinguishing the wild-type RNA-polymerase of
XX the human influenza virus from FV Bratistava RNA-polymerase has been
XX replaced with the corresponding amino acid residue(s) as present in FV
XX Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV,
XX hepatotropic, antiinflammatory and immunomodulator activities and can be
XX used in gene therapy and vaccines. The influenza virus is useful for
XX preparing agents for: (a) gene transfer into cells, preferably into
XX mammalian cells, particularly into human cells, by viral infection; (b)
XX gene transfer into antigen-presenting cells, and the use of the obtained
XX product for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo
XX vaccination, including therapeutic and prophylactic vaccination; (c)
XX eliciting an immune response, including the induction of a T-cell
XX response; (d) treating a growing tumour or a chronic infectious disease;
XX (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer
XX and expression of foreign genes into cells infected by such viruses; or
XX (g) transfer and expression of RNA molecules into cells infected by such
XX viruses, preferably the RNA molecules to be expressed are antisense
XX sequences or double-strand sequences relative to the target cellular mRNA
XX molecules, and/or the agent is suitable for sequence-specific gene
XX silencing, preferably by antisense RNA or RNA interference mechanisms
XX such as ribozyme cleavages of target RNAs. The recombinant viruses can be
XX made for use in vaccines against HIV, hepatitis B or C virus, herpes
XX viruses or papilloma viruses. The present sequence represents an
XX influenza virus general structure related oligonucleotide, given in the
XX exemplification of the present invention
XX
XX Sequence 14 BP; 1 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 14;
XX Best Local Similarity 90.9%; Pred. No. 4.2e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 731 AGGAGAAACAG 741
DB 14 AGTAAACAG 4
XX
XX
XX
XX
XX
XX 08-MAY-2002 (first entry)
XX
XX Influenza C, 3' conserved region mutant.
XX
XX Influenza C; tandem RNA segment; TRS; gene expression; influenza;
XX vaccine; somatic gene therapy; expression vector; immunotherapy;
XX autologous immunotherapy; gene silencing; ss; mutant.
XX
XX Influenza virus.
XX
XX Key Location/Qualifiers
XX misc_feature 2..14
XX /*tag= a
XX /note= "Specifically claimed in claim 11"
XX

```

XX AC AAA65226;
XX DT 19-DEC-2000 (first entry)
XX DE Modified end-blocked acid-resistant oligonucleotide #1.
XX KW End-blocked acid-resistant oligonucleotide; infection;
XX KW inflammatory disease; cancer; antibacterial application;
XX KW phosphorothioate linkage; primer; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..14
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Optional phosphorothioate backbone"
XX PN WO200040592-A1.
XX PD 13-JUL-2000.
XX PF 16-DEC-1999; 99WO-US030266.
XX PR 30-DEC-1998; 98US-00223498.
XX PR 19-JUL-1999; 99US-00356069.
XX PA (OLIG-) OLIGOS ETC INC.
XX PI Dale RMK, Gatton SL, Arrow A;
XX DR WPI; 2000-465945/40.
XX PT Modified nucleic acid polymer used for treating inflammation, cancer,
XX PT bacterial, viral and fungal infections and in disinfectants has a
XX PT blocking chemical modification at the end of the polymer.
XX PS Example 2; Page 32; 56pp; English.
XX CC The present sequence is an oligonucleotide which was used to demonstrate
XX CC the invention. The invention concerns end-blocked acid resistant
XX CC oligonucleotides which are also resistant to nuclease degradation and are
XX CC capable of binding specifically in an antisense manner. This means that
XX CC they are useful in the treatment and prevention of infections,
XX CC inflammatory diseases and cancer, as well as having non-therapeutic
XX CC applications in cosmetics, for example in skin tanning products. In
XX CC addition, they can be used in antibacterial applications such as
XX CC sterilisation of surgical instruments, and in antibacterial lotions and
XX CC soaps. A number of different versions of this sequence were produced,
XX CC including an unblocked 2'-O-methyl RNA, a 2'-O-methyl RNA with 3' and 5',
XX CC buranol blocked ends, a 3'-O-methyl phosphodiester, a 2'-O-propargyl and
XX CC a 2'-O-methyl phosphodiester. These were all used to show that the
XX CC modified sequence is less susceptible to degradation than the natural
XX CC sequence
XX SQ Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 727 TGCCAGGAGAA 737
Db 3 TGTCAGGAGAA 13

RESULT 349
AAA57799
ID AAA57799 standard; DNA; 14 BP.
XX AC AAA57799;
XX CC Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell;

```

```

DT 20-OCT-2000 (first entry)
XX Antisense oligonucleotide for the human PDE4D gene.
XX DE Antisense oligonucleotide; phosphodiesterase 4; PDE4; cystic fibrosis;
XX KW acid resistant polymer; nuclease resistance; depression; thrombosis;
XX KW pulmonary hypertension; glaucoma; multiple sclerosis; gastric lesion;
XX KW atopic dermatitis; asthma; allergy; ss.
XX OS Homo sapiens.
XX PN WO200040714-A2.
XX PD 13-JUL-2000.
XX PF 15-DEC-1999; 99WO-US029976.
XX PR 30-DEC-1998; 98US-00223586.
XX PR 29-JUL-1999; 99US-00364626.
XX PA (OLIG-) OLIGOS ETC INC.
XX PI Dale RMK, Arrow A, Thompson T;
XX DR WPI; 2000-465980/40.
XX PT New acid resistant polymer complementary to phosphodiesterase 4 for
XX PT treating depression, thrombosis, cystic fibrosis, gastric lesions,
XX PT pulmonary hypertension, glaucoma, multiple sclerosis, atopic dermatitis
XX PT and asthma.
XX PS Claim 7; Page 17; 48pp; English.
XX CC The present sequence represents an antisense oligonucleotide, directed
XX CC against the phosphodiesterase 4D (PDE4D) gene. The oligonucleotide is
XX CC used to construct the polymer of the invention. The specification
XX CC describes an acid resistant polymer which is complementary to PDE4, and
XX CC comprises a nucleic acid with a backbone structure that is modified from
XX CC that of a naturally occurring nucleotide polymer and a blocking chemical
XX CC modification at or near one end of the nucleic acid. The acid resistant
XX CC polymer is characterized by a pH stability of an hour at pH 0.01 to 10
XX CC and a nuclease resistance of twice that of naturally occurring nucleic
XX CC acids which have the same number of nucleotides. The polymers are used to
XX CC inhibit the expression of genes encoding PDE4. They are useful as
XX CC analytical tools in the study of individual PDE isoforms and can treat
XX CC depression, thrombosis, cystic fibrosis, gastric lesions, pulmonary
XX CC hypertension, glaucoma, multiple sclerosis, atopic dermatitis, asthma,
XX CC and other allergic disorders. Other illnesses in which an increase of
XX CC cyclic AMP or decrease in phosphodiesterase levels is useful, can also be
XX CC treated
XX SQ Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 727 TGCCAGGAGAA 737
Db 3 TGTCAGGAGAA 13

RESULT 350
AAL37793/C
ID AAL37793 standard; RNA; 14 BP.
XX AC AAL37793;
XX OS 05-AUG-2002 (first entry)
XX DT RNA region of modified influenza C virus #2.
XX DE Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell;
XX KW

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PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 XX Nyce JW;
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 209; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adenosine molecules and their receptors, cytokine and
 CC chemokine receptors, adhesion molecules and their receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, defensins, growth factors, vasoactive peptides and
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, CNS and peripheral nervous and non-nervous system
 CC receptors, defensins, growth factors, vasoactive peptides and
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 728 GCCAGGAGAAA 738
 |||||
 Db 12 GCCAGGAGAAA 2
 RESULT 347
 AAF19605/C
 ID AAF19605 standard; DNA; 14 BP.
 XX
 AC AAF19605;
 XX
 XX 14-MAR-2001 (first entry)
 DT
 XX Human IL6 receptor polynucleotide fragment #1172.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 XX cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX Nyce JW;
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 209; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adenosine molecules and their receptors, cytokine and
 CC chemokine receptors, adhesion molecules and their receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, defensins, growth factors, vasoactive peptides and
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, CNS and peripheral nervous and non-nervous system
 CC receptors, defensins, growth factors, vasoactive peptides and
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 728 GCCAGGAGAAA 738
 |||||
 Db 14 GCCAGGAGACA 4
 RESULT 348
 AAF65226
 ID AAF65226 standard; DNA; 14 BP.

CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytosolic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3213 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738

Db 12 GCCAGGGGAAA 2

RESULT 345

AAF20192/C
 ID AAF20192 standard; DNA; 14 BP.

AC AAF20192;

XX 14-MAR-2001 (first entry)

DE Human endothelial monocyte activating factor DNA fragment #1759.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 human; airway disorder; bronchoconstriction; lung inflammation;
 surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 respiratory obstruction; pulmonary obstruction; impeded respiration;
 surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger

PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

XX Claim 14; Page 207; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;

Best Local Similarity 90.9%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGCAGAACACAG 741

Db 11 AGCAGAACACAG 1

RESULT 346

AAF19619/C
 ID AAF19619 standard; DNA; 14 BP.

XX AAF19619;

XX 14-MAR-2001 (first entry)

DE Human IL6 receptor polynucleotide fragment #1186.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 human; airway disorder; bronchoconstriction; lung inflammation;
 surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 respiratory obstruction; pulmonary obstruction; impeded respiration;
 surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAGAA 738
 DB 14 GCCAGGAGAGACA 4
 AC
 AC
 AC
 XX 28-JUL-2000 (first entry)
 DT Human adenosine receptor related polynucleotide SEQ ID NO:1759.
 DE
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 FN
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US017712.
 PF
 XX 03-AUG-1998; 98US-0095212P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 483; 1343pp; English.
 XX
 XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation.
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing the
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX SQ Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
 DB 11 AGGAGAAACAG 1
 AC
 AC
 AC
 XX 28-JUL-2000 (first entry)
 DT Low adenosine antisense oligonucleotide SEQ ID NO:1186.
 DE
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 FN
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US017712.
 PF
 XX 03-AUG-1998; 98US-0095212P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Claim 18; Page 413; 1343pp; English.
 XX
 XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 728 GCCAGGAGAAA 738
 Db 14 GCCAGGAGACA 4

RESULT 341
 AAX54623/C
 ID AAX54623 standard; DNA; 14 BP.

XX
 AC AAX54623;

XX
 DT 05-JUL-1999 (first entry)

XX Endothelial mocyte activating factor antisense oligonucleotide.

XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impaired respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

XX Synthetic.

XX WO9913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US019419.

XX 17-SEP-1997; 97US-0059160P.

XX 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.

XX Disclosure; Page 47; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the junction between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX5272-74. These multiple target oligonucleotides
 CC (specifically AAX5180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impaired respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.

CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer

XX Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;

Best Local Similarity 90.9%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAG 741
 Db 11 AGGAGGACAG 1

RESULT 342
 AAX33483/C

ID AAX33483 standard; DNA; 14 BP.

XX
 AC AAX33483;

XX 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1172.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.

XX Claim 18; Page 411; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the

XX Query Match 42.7%; Score 9.4; DB 1; Length 14;
SQ Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 14 GCCAGGAGACA 4

RESULT 339
AAAX54053/C
ID AAX54053 standard; DNA; 14 BP.
XX AC AAX54053;
XX DT 05-JUL-1999 (first entry)
XX DE Human IL-6 receptor antisense oligonucleotide fragment.
XX KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX OS Synthetic.
XX WO9913886-A1.
XX PN 25-MAR-1999.
XX PD 17-SEP-1998; 98WO-US019419.
XX PF 17-SEP-1997; 97US-0059160P.
XX PR 09-JUN-1998; 98US-00093972.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX FI Nyce JW;
XX WPI; 1999-229400/19.
XX DR New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX PS Disclosure; Page 50; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAX55272-74. These multiple target oligonucleotides
XX (specifically AAX55180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer

XX Query Match 42.7%; Score 9.4; DB 1; Length 14;
SQ Best Local Similarity 90.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738
DB 12 GCCAGGAGAAA 2

RESULT 340
AAAX54039/C
ID AAX54039 standard; DNA; 14 BP.
XX AC AAX54039;
XX DT 05-JUL-1999 (first entry)
XX DE Human IL-6 receptor antisense oligonucleotide fragment.
XX KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX OS Synthetic.
XX WO9913886-A1.
XX PN 25-MAR-1999.
XX PD 17-SEP-1998; 98WO-US019419.
XX PF 17-SEP-1997; 97US-0059160P.
XX PR 09-JUN-1998; 98US-00093972.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX FI Nyce JW;
XX WPI; 1999-229400/19.
XX DR New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX PS Disclosure; Page 50; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAX55272-74. These multiple target oligonucleotides
XX (specifically AAX55180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer

CC The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, INOS,
 CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the ribozyme or the polynucleotide. Also described is a method
 CC for decreasing the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (I) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
 CC exemplification of the present invention

XX Sequence 13 BP; 1 A; 3 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741

DB 11 AGCAGAAACAG 1

RESULT 337
 AAT76263/C
 ID AAT76263 standard; DNA; 14 BP.

AC AAT76263;

DT 15-SEP-1997 (first entry)

XX Human IL6 receptor antisense oligonucleotide.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 XX chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
 XX Synthetic.

XX WO9640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009306.

XX 07-JUN-1995; 95US-00474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW, Metzger WJ;

XX WPI; 1997-051871/05.

XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligonucleotide to airway epithelium of
 PT subject.

PS Example 5; Page 32; 71pp; English.

XX A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for the human IL6 receptor. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-
 CC reactive airways

XX Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 14;
 Best Local Similarity 90.9%; Pred. No. 4.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAA 738

DB 12 GCCAGGAGAAA 2

RESULT 338

AAT76249/C

ID AAT76249 standard; DNA; 14 BP.

XX AAT76249;

XX 15-SEP-1997 (first entry)

XX Human IL6 receptor antisense oligonucleotide.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 XX chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
 XX Synthetic.

XX WO9640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009306.

XX 07-JUN-1995; 95US-00474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW, Metzger WJ;

XX WPI; 1997-051871/05.

XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligonucleotide to airway epithelium of
 PT subject.

XX Example 5; Page 32; 71pp; English.

XX A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for the human IL6 receptor. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-
 CC reactive airways

XX Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-1B000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 175624; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 735 GAACAGAACACC 747
Db 1 RAACAAACACC 13
RESULT 335
ABF56510/c
ID ABF56510 standard; DNA; 13 BP.
XX
XX AC ABF56510;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 156507 for detecting SNP TSC0039462.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-1B000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX PA

XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 156507; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 0 A; 1 C; 6 G; 5 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 735 GAACAGAACACC 747
Db 13 RAACCGAACCCC 1
RESULT 336
ABZ72819/c
ID ABZ72819 standard; RNA; 13 BP.
XX
XX AC ABZ72819;
XX
XX DT 09-APR-2003 (first entry)
XX
XX DE Rod opsin hammerhead ribozyme target oligonucleotide SEQ ID NO:59.
XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX Homo sapiens.
XX
XX PN WC200288320-A2.
XX
XX PD 07-NOV-2002.
XX
XX PF 01-MAY-2002; 2002WO-US013679.
XX
XX PR 01-MAY-2001; 2001US-00847601.
XX (UYFL) UNIV FLORIDA.
XX
XX PI Lewin AS, Shaw LC, Grant MB;
XX WPI; 2003-111880/10.
XX
XX PT A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.
XX Claim 1; Page 72; 115pp; English.
XX

CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACACAGAACAC 746

Db 3 AACACAGAACAC 13

RESULT 332

ABF50801

ID ABF50801 standard; DNA; 13 BP.

AC ABF50801;

XX

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 150798 for detecting SNP TSC0038055.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 150798; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;

Best Local Similarity 90.9%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACACAGAACAC 747

Db 1 AACACAGAACAC 11

RESULT 333

ABH48837

ID ABH48837 standard; DNA; 13 BP.

XX

AC ABH48837;

XX

DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 248814 for detecting SNP TSC0060796.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 248814; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;

Best Local Similarity 90.9%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACACAGAACAC 746

Db 3 AACACAGAACAC 13

RESULT 334

ABF75627

ID ABF75627 standard; DNA; 13 BP.

XX

AC ABF75627;

XX

DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 175624 for detecting SNP TSC0043631.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 250884; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 736 AAACGAGAACAC 746
Db |||||
2 AAACGAGAACAC 12
RESULT 325
ABC71283
ID ABC71283 standard; DNA; 13 BP.
XX
XX ABC71283;
AC
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 71300 for detecting SNP TSC0018470.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 71300; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 1 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 736 AAACGAGAACAC 748
Db |||||
1 AAAACGAGAACAC 13
RESULT 326
ABC72903
ID ABC72903 standard; DNA; 13 BP.
XX
XX ABC72903;
AC
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 72920 for detecting SNP TSC0018823.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 72920; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 733 GAGAAACAGAAC 745
Db 13 RACAAACACACAC 1
RESULT 320
ABC82726/c
ID ABC82726 standard; DNA; 13 BP.
AC ABC82726;
XX
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 82743 for detecting SNP TSC0020863.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 82743; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACAGAACAC 746
Db 12 AACACAGAACAC 2
RESULT 321
ABC83626/c
ID ABC83626 standard; DNA; 13 BP.
XX
AC ABC83626;
XX
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 83643 for detecting SNP TSC0021064.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 83643; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACAGAACAC 746
Db 12 AACACAGAACAC 2
RESULT 322
ABF56386

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 214794; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AACACGAAACAC 746
XX |||||
XX 3 AACACGAAACAC 13
XX
XX Db
XX
XX RESULT 318
XX ABC72271
XX ID ABC72271 standard; DNA; 13 BP.
XX AC ABC72271;
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 72288 for detecting SNP TSC0018670.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX

XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 72288; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AACACGAAACAC 746
XX |||||
XX 3 AACACGAAACAC 13
XX
XX Db
XX
XX RESULT 319
XX ABC72902/c
XX ID ABC72902 standard; DNA; 13 BP.
XX AC ABC72902;
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 72919 for detecting SNP TSC0018823.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 72919; 29pp + Sequence Listing; German.
XX

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AACAGAACAC 746
||||| |||||
Db 3 AACATAACAC 13

RESULT 315
ABCI1965/c
ID ABCI1965 standard; DNA; 13 BP.
XX AC ABCI1965;
XX 20-FEB-2002 (first entry)
DT XX
DE XX
DE Oligonucleotide SEQ ID NO 11972 for detecting SNP TSC0002869.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 11972; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABCI00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 731 AGGAGAACAG 741
||||| |||||

Db 11 AGGAGAAAGAG 1

RESULT 316
ABH14816/c
ID ABH14816 standard; DNA; 13 BP.
XX AC ABH14816;
XX 22-FEB-2002 (first entry)
DT XX
DE XX
DE Oligonucleotide SEQ ID NO 214793 for detecting SNP TSC0052269.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 214793; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 1 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AACAGAACAC 746
||||| |||||
Db 11 AACCGAACAC 1

RESULT 317
ABH14817
ID ABH14817 standard; DNA; 13 BP.
XX AC ABH14817;
XX 22-FEB-2002 (first entry)
DT XX
DE XX
DE Oligonucleotide SEQ ID NO 214794 for detecting SNP TSC0052269.

	Best Local Similarity	90.9%;	Pred. No. 4.1e+02;	Matches	10; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
QY	735	GAACAGAACCA	745						
DB	2	GAACAGAACCA	12						
RESULT 310									
ABCS6821									
ID	ABCS6821	standard; DNA; 13 BP.							
XX	XX								
AC	ABC56821;								
XX	XX								
DT	21-FEB-2002	(first entry)							
XX	XX								
DE	Oligonucleotide SEQ ID NO 56838	for detecting SNP TSC0015389.							
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;								
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;								
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.								
XX	XX								
OS	Homo sapiens.								
XX	WO200177384-A2.								
PN	18-OCT-2001.								
XX	XX								
PF	06-APR-2001; 2001WO-IB000713.								
XX	07-APR-2000; 2000DE-01019173.								
PR	(EPIG-) EPIGENOMICS AG.								
XX	Olek A, Piepenbrock C, Berlin K;								
PA	WPI; 2001-657177/75.								
PI	Set of oligonucleotides, useful for diagnosis and cell typing, is								
PT	designed to detect single-nucleotide polymorphisms and cytosine								
PT	methylation status.								
XX	Claim 1; SEQ ID NO 56838; 29pp + Sequence Listing; German.								
PS	This invention describes novel oligonucleotide primers or peptide nucleic								
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)								
CC	and cytosine methylation status in chemically pretreated genomic DNA. The								
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a								
CC	range of diseases including immune system, gastrointestinal, respiratory,								
CC	central nervous system, cardiovascular and metabolic disorders. The								
CC	oligomers are also used for detecting cell type differentiation. ABC00010								
CC	ABH99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073								
CC	represent the oligomers described in the invention. NOTE: The sequence								
CC	data for this patent did not form part of the printed specification, but								
CC	was obtained in electronic format from WIPO at								
CC	fnp.wipo.int/pub/published_pct_sequences								
XX	Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;								
SQ	Query Match	42.7%; Score 9.4; DB 1; Length 13;							
	Best Local Similarity	90.9%; Pred. No. 4.1e+02;							
	Matches	10; Conservative	0; Mismatches	1; Indels	0; Gaps	0; Gaps	0;		
QY	736	AACAGAACAC	746						
DB	2	AACCGAACAC	12						
RESULT 311									
ABH9989/c									
ID	ABH19618	standard; DNA; 13 BP.							
XX	XX								
AC	ABH19618;								

PI Olek A, Piepenbrock C, Berlin K;
 DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 180988; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 7 A; 3 C; 1 G; 1 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. NO. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 735 GAACAGAACCA 745
 DB 3 GAACATAACA 13
 RESULT 308
 ID ABF66158 standard; DNA; 13 BP.
 AC ABF66158;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 166155 for detecting SNP TSC0041649.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 166155; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 7 A; 3 C; 1 G; 1 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. NO. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 735 GAACAGAACCA 745
 DB 3 GAACATAACA 13
 RESULT 309
 ID ABC67297 standard; DNA; 13 BP.
 AC ABC67297;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 67314 for detecting SNP TSC0017613.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 67314; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. NO. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 735 GAACAGAACCA 747
 DB 13 RAAACAAACACC 1
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

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RESULT 305
ABC66043/c
ID ABC66043 standard; DNA; 13 BP.
XX
XX
AC ABC66043;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 66060 for detecting SNP TSC0017378.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 66060; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 5 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 733 GAGAAACAGAA 743
XX ||||| |||||
XX 11 GAGAAACAGAA 1
XX
RESULT 306
ABF30261
ID ABF30261 standard; DNA; 13 BP.
XX
XX
AC ABF30261;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 130258 for detecting SNP TSC0032538.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

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XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 130258; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 736 AAACAGAACAC 746
XX ||||| |||||
XX 2 AAACATAACAC 12
XX
RESULT 307
ABF80901
ID ABF80901 standard; DNA; 13 BP.
XX
XX
AC ABF80901;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 180898 for detecting SNP TSC0044758.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
```

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PS Claim 1; SEQ ID NO 57798; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 736 AAACGACAC 746
DB 2 AAACGACAC 12
|||||
RESULT 303
ABF66156/c
ID ABF66156 standard; DNA; 13 BP.
XX
AC ABF66156;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 166153 for detecting SNP TSC0041649.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 166153; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
XX
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 733 GAGAAACAGAA 743
DB 1 GAGAAACGAA 11
|||||

```

```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 1 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 735 GAAACAGAACAC 747
DB 13 RAAATAACAC 1
|||||

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```

RESULT 304
ABC73158
ID ABC73158 standard; DNA; 13 BP.
XX
AC ABC73158;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 73175 for detecting SNP TSC0018861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 73175; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
XX
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 733 GAGAAACAGAA 743
DB 1 GAGAAACGAA 11
|||||

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```
DE XX Oligonucleotide SEQ ID NO 16265 for detecting SNP TSC0041660.
XX XX
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX (EPIC-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT PT designed to detect single-nucleotide polymorphisms and cytosine
PT PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 16265; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC CC range of diseases including immune system, gastrointestinal, respiratory,
CC CC central nervous system, cardiovascular and metabolic disorders. The
CC CC oligomers are also used for detecting cell type differentiation. ABC00010
CC CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC CC represent the oligomers described in the invention. NOTE: The sequence
CC CC data for this patent did not form part of the printed specification, but
CC CC was obtained in electronic format from WIPO at
CC CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
XX XX
XX XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX XX
Oy 735 GAACAGAACACC 747
Db 13 RAACCGAAAC 1
:|||||
:|||||

RESULT 301
ABH50906/C
ID ABH50906 standard; DNA; 13 BP.
XX XX
XX AC ABH50906;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 250883 for detecting SNP TSC0061240.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX (EPIC-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT PT designed to detect single-nucleotide polymorphisms and cytosine
PT PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 16265; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC CC range of diseases including immune system, gastrointestinal, respiratory,
CC CC central nervous system, cardiovascular and metabolic disorders. The
CC CC oligomers are also used for detecting cell type differentiation. ABC00010
CC CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC CC represent the oligomers described in the invention. NOTE: The sequence
CC CC data for this patent did not form part of the printed specification, but
CC CC was obtained in electronic format from WIPO at
CC CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
XX XX
XX XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX XX
Oy 735 GAACAGAACACC 747
Db 13 RAACCGAAAC 1
:|||||
:|||||

RESULT 302
ABC57781
ID ABC57781 standard; DNA; 13 BP.
XX XX
XX AC ABC57781;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 57798 for detecting SNP TSC0015564.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX (EPIC-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT PT designed to detect single-nucleotide polymorphisms and cytosine
PT PT methylation status.
XX XX
```

CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 GAAACAGAACACC 746
 DB 11 AAAAAAACACC 1

RESULT 298
 ABF74448/c
 ID ABF74448 standard; DNA; 13 BP.

XX AC ABF74448;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 174445 for detecting SNP TSC0043390.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.

XX FN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 174445; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 1 C; 4 G; 6 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACC 747
 DB 13 RAAATCGAACACC 1

RESULT 299

ABF66159
 ID ABF66159 standard; DNA; 13 BP.

XX AC ABF66159;
 XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 166156 for detecting SNP TSC0041649.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX FN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 166156; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACACC 747
 DB 1 RAAACAAACACC 13

RESULT 300

ABF66268/c
 ID ABF66268 standard; DNA; 13 BP.

XX AC ABF66268;

XX DT 22-FEB-2002 (first entry)

PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 6059; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 GAGAAACAGAA 743
DB 3 GAGAAACAGAA 13
RESULT 296
ABF25407/C
ID ABF25407 standard; DNA; 13 BP.
XX
AC ABF25407;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 125404 for detecting SNP TSC0031343.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 125404; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 11 AGGAGAAACAG 1
RESULT 297
ABF74292/C
ID ABF74292 standard; DNA; 13 BP.
XX
AC ABF74292;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 174289 for detecting SNP TSC0043357.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
XX PF
XX 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 174289; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 5 C; 0 G; 7 T; 0 U; 0 Other;
SQ

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 736 AAACAGAACACG 748
Db 13 RAAACACACACG 1

RESULT 293
ABC51769
ID ABC51769 standard; DNA; 13 BP.

AC ABC51769;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 51786 for detecting SNP TSC0014434.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 51786; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 733 GAGAAACAGAAC 745
Db 1 RAAACACACACG 13

RESULT 294

ID ABC83627 standard; DNA; 13 BP.

XX ABC83627;
AC 21-FEB-2002 (first entry)
DT Oligonucleotide SEQ ID NO 83644 for detecting SNP TSC0021064.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 83644; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 736 AAACAGAACAC 746
Db 2 AAACGACAC 12

RESULT 295
ABC66042
ID ABC66042 standard; DNA; 13 BP.
XX ABC66042;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 66059 for detecting SNP TSC0017378.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 223068; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AAACAGAACAC 746
 Db 1 AAACAGAACAC 11
 RESULT 291
 ABF75626/C
 ID ABF75626 standard; DNA; 13 BP.
 AC ABF75626;
 XX
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 175623 for detecting SNP TSC0043631.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WC200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 175623; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 735 GAAACAGAACACC 747
 Db 13 GAAACAGAACACC 1
 RESULT 292
 ABC71282/C
 ID ABC71282 standard; DNA; 13 BP.
 AC ABC71282;
 XX
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 71299 for detecting SNP TSC0018470.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 71299; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;

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RESULT 288
ABC10581/C
ID ABC10581 standard; DNA; 13 BP.
AC ABC10581;
XX
XX
DT 20-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 10572 for detecting SNP TSC0002662.
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 10572; 29pp + Sequence Listing; German.
XX
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 4 C; 0 G; 9 T; 0 U; 0 Other;
XX
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 733 GAGAAACAGAA 743
DB 11 GAGAAAAAGAA 1
XX
XX
RESULT 289
ABF96836/C
ID ABF96836 standard; DNA; 13 BP.
AC ABF96836;
XX
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 196833 for detecting SNP TSC0048453.
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

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KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX
DR WPI; 2001-657177/75.
XX
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 196833; 29pp + Sequence Listing; German.
XX
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
XX
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 735 GAACAGACACC 747
DB 13 RAACACAAACC 1
XX
XX
RESULT 290
ABH23091
ID ABH23091 standard; DNA; 13 BP.
XX
XX
AC ABH23091;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 223068 for detecting SNP TSC0054311.
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX

```

PT methylation status.
XX Claim 1; SEQ ID NO 124392; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 733 GAGAACAGACACA 745
Db 1 RAACACATAACA 13
RESULT 286
ABF80900/C
ID ABF80900 standard; DNA; 13 BP.
XX AC ABF80900;
XX 22-FEB-2002 (first entry)
DT Oligonucleotide SEQ ID NO 180897 for detecting SNP TSC0044758.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
PD 06-APR-2001; 2001WO-IB000713.
PF 07-APR-2000; 2000DE-01019173.
PR (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 180897; 29pp + Sequence Listing; German.
PS This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 733 GAGAACAGACACA 745
Db 1 RAACACATAACA 13
RESULT 287
ABC57783
ID ABC57783 standard; DNA; 13 BP.
XX AC ABC57783;
XX 21-FEB-2002 (first entry)
DT Oligonucleotide SEQ ID NO 57800 for detecting SNP TSC0015564.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
PD 06-APR-2001; 2001WO-IB000713.
PF 07-APR-2000; 2000DE-01019173.
PR (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 57800; 29pp + Sequence Listing; German.
PS This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AAACAGACAC 746
Db 2 AAACCGACAC 12

ID	ABF56387/C	ABF56387 standard; DNA; 13 BP.
XX	AC	XX
XX	AC	ABF56387;
XX	XX	XX
XX	DI	21-FEB-2002 (first entry)
XX	DE	Oligonucleotide SEQ ID NO 156384 for detecting SNP TSC0039445.
XX	DE	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	OS	Homc sapiens.
XX	PN	WO200177384-A2.
XX	PN	18-OCT-2001.
XX	PD	XX
XX	PF	06-APR-2001; 2001WO-IB000713.
XX	PR	07-APR-2000; 2000DE-01019173.
XX	PA	(EPIG-) EPIGENOMICS AG.
XX	PA	Olek A, Piepenbrock C, Berlin K;
PI	PI	WPI; 2001-657177/75.
XX	DR	Set of oligonucleotides, useful for diagnosis and cell typing, is
XX	PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	PT	methylation status.
XX	PS	Claim 1; SEQ ID NO 156384; 29pp + Sequence Listing; German.
XX	PS	This invention describes novel oligonucleotide primers or peptide nucleic
CC	CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	CC	central nervous system, cardiovascular and metabolic disorders. The
CC	CC	oligomers are also used for detecting cell type differentiation. ASC000010
CC	CC	-ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH2073
CC	CC	represent the oligomers described in the invention. NOTE: The sequence
CC	CC	data for this patent did not form part of the printed specification, but
CC	CC	was obtained in electronic format from WIPO at
CC	CC	ftp.wipo.int/pub/published_pst_sequences
XX	XX	Sequence 13 BP; 0 A; 3 C; 0 G; 10 T; 0 U; 0 Other;
XX	XX	Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX	XX	Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX	XX	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	733	GAGAACACAGAA 743
DB	12	GAGAAAAAGAA 2
RESULT 278		
ABH15112/C		
ID	ABH15112 standard; DNA; 13 BP.	
XX	AC	ABH15112;
XX	AC	XX
XX	DT	22-FEB-2002 (first entry)
XX	DE	Oligonucleotide SEQ ID NO 215089 for detecting SNP TSC0052336.
XX	DE	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.

```

PR 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 11971; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 3 AGGAGAAAGG 13
RESULT 274
ABF24377
ID ABF24377 standard; DNA; 13 BP.
XX AC ABF24377;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 124374 for detecting SNP TSC0031092.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 124374; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 3 AGGAGAAAGG 13
RESULT 275
ABF74449
ID ABF74449 standard; DNA; 13 BP.
XX AC ABF74449;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 174446 for detecting SNP TSC0043390.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 174446; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

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Db      13 RAAAAACAAACA 1
      : ||||| |||
RESULT 271
ABCS7782/c
ID ABC57782 standard; DNA; 13 BP.
XX
AC ABC57782;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 57799 for detecting SNP TSC0015564.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 57799; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 736 AAACAGACAC 746
      ||||| |||||
Db 12 AAACCGAACAC 2
      ||||| |||||
RESULT 272
ABCS8201
ID ABC58201 standard; DNA; 13 BP.
XX
AC ABC58201;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 58218 for detecting SNP TSC0015626.

```

```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 58218; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 733 GAGAAACAGAAC 745
      .||| ||||| |||||
Db 1 RACAAACAAACA 13
      .||| ||||| |||||
RESULT 273
ABCI1964
ID ABCI1964 standard; DNA; 13 BP.
XX
AC ABCI1964;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 11971 for detecting SNP TSC0002869.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 130257; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746

Db 12 AAACATAACAC 2

RESULT 269

ABC72270/c

ID ABC72270 standard; DNA; 13 BP.

XX ABC72270;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 72287 for detecting SNP TSC0018670.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 72287; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746

Db 11 AAACAAAACAC 1

RESULT 270

ABC51768/c

ID ABC51768 standard; DNA; 13 BP.

XX ABC51768;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 51785 for detecting SNP TSC0014434.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 51785; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745

AC ABC37748;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 37765 for detecting SNP TSC0011740.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 37765; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 1 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 735 GAACAGAACACC 747
XX :|||||
XX 13 RAAACCGAACAC 1
XX
XX RESULT 267
XX ABF24394/C
XX ID ABF24394 standard; DNA; 13 BP.
XX
XX AC ABF24394;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 124391 for detecting SNP TSC0031094.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX

XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 124391; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 733 GAGAACAGAAC 745
XX :|||||
XX 13 RAAACACATAC 1
XX
XX RESULT 268
XX ABF30260/C
XX ID ABF30260 standard; DNA; 13 BP.
XX
XX AC ABF30260;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 130257 for detecting SNP TSC0032538.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 747
 Db 13 RAACATATAAC 1

RESULT 264

ABC82727
 ID ABC82727 standard; DNA; 13 BP.

XX AC ABC82727;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 82744 for detecting SNP TSC0020863.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 82744; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
 Db 2 AAACAGAACAC 12

RESULT 265

ABC58200/c
 ID ABC58200 standard; DNA; 13 BP.

XX AC ABC58200;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 58217 for detecting SNP TSC0015626.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 58217; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 76.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAAC 745
 Db 13 RACAAACAAACA 1

RESULT 266

ABC37748/c
 ID ABC37748 standard; DNA; 13 BP.

XX


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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 83642; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 7 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AAACGAGAACAC 746
XX Db 2 AAACGAGAACAC 12
XX
XX RESULT 262
XX ABC37749
XX ID ABC37749 standard; DNA; 13 BP.
XX AC ABC37749;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 37766 for detecting SNP TSC0011740.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA
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XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 37766; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 735 GAAACAGAACAC 747
XX Db 1 AAACCGAACAC 13
XX
XX RESULT 263
XX ABF75624/C
XX ID ABF75624 standard; DNA; 13 BP.
XX AC ABF75624;
XX XX 22-FEB-2002 (first entry)
XX DT Oligonucleotide SEQ ID NO 175621 for detecting SNP TSC0043631.
XX DE SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 175621; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACGAGACAC 746

Db 12 AAACGAGACAC 2

RESULT 259

ABF30258/c
ID ABF30258 standard; DNA; 13 BP.

XX AC ABF30258;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 130255 for detecting SNP TSC0032538.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

XX MPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 130255; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACGAGACAC 746

Db 12 AAACGAGACAC 2

RESULT 260

ABF96837
ID ABF96837 standard; DNA; 13 BP.

XX AC ABF96837;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 196834 for detecting SNP TSC0048453.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS WO200177384-A2.

PN 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX MPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 196834; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 747

Db 1 RAAACACAAAC 13

RESULT 261

ABC83625
ID ABC83625 standard; DNA; 13 BP.

XX AC ABC83625;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 83642 for detecting SNP TSC0021064.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

QY 735 GAACAGACACC 747
 Db 1 RAACCGAACCC 13
 RESULT 254
 ABH15113
 ID ABH15113 standard; DNA; 13 BP.
 XX
 AC ABH15113;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 215090 for detecting SNP TSC0052336.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 215090; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACAGACACC 746
 Db 1 AACACACAC 11
 RESULT 255
 ABH48836/C
 ID ABH48836 standard; DNA; 13 BP.
 XX
 AC ABH48836;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 73176 for detecting SNP TSC0018861.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 215090; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 DE Oligonucleotide SEQ ID NO 248813 for detecting SNP TSC0060796.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 248813; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 736 AACAGACACC 746
 Db 11 AACACACAC 1
 RESULT 256
 ABC73159/C
 ID ABC73159 standard; DNA; 13 BP.
 XX
 AC ABC73159;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 73176 for detecting SNP TSC0018861.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 248813; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 4.1e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 174290; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACAGAACAC 746
DB 3 AACAAACAC 13
RESULT 252
ABF50800/C
ID ABF50800 standard; DNA; 13 BP.
XX AC ABF50800;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 150797 for detecting SNP TSC0038055.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 150797; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 737 AACAGAACAC 747
DB 13 AACAAACAC 3
RESULT 253
ABF56511
ID ABF56511 standard; DNA; 13 BP.
XX AC ABF56511;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 156508 for detecting SNP TSC0039462.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 156508; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 5 A; 6 C; 1 G; 0 T; 0 U; 1 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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ID ABC83624 standard; DNA; 13 BP.
XX AC ABC83624;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 83641 for detecting SNP TSC0021064.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 83641; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 0 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 736 AACAGAACAC 746
XX Db 12 AACCGAACAC 2
XX RESULT 250
XX ABC10580
XX ID ABC10580 standard; DNA; 13 BP.
XX AC ABC10580;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 10571 for detecting SNP TSC0002662.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

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XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 10571; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 733 GAGAACAGAA 743
XX Db 3 GAGAAAGAGAA 13
XX RESULT 251
XX ABF74293
XX ID ABF74293 standard; DNA; 13 BP.
XX AC ABF74293;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 174290 for detecting SNP TSC0043357.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;

```

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db 3 AGGAGAAACAG 13
RESULT 247
ABH23090/C
ID ABH23090 standard; DNA; 13 BP.
XX
AC ABH23090;
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 223067 for detecting SNP TSC0054311.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 223067; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACAGAACAC 746
Db 13 AACAGAACAC 3
RESULT 248
ABH54889
ID ABH54889 standard; DNA; 13 BP.
XX
AC ABH54889;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 254866 for detecting SNP TSC0062123.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 254866; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 738 ACAGAACACG 748
Db 1 ACAGAACACG 11
RESULT 249
ABC83624/c

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 27537; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Mismatches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AACACAGAACAC 746
XX ||||| |||||
XX 11 AACATATACAC 1
XX
XX RESULT 245
XX ABC82729
XX ID ABC82729 standard; DNA; 13 BP.
XX AC
XX ABC82729;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 82746 for detecting SNP TSC0020863.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 125403; 29pp + Sequence Listing; German.

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 82746; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Mismatches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AACACAGAACAC 746
XX ||||| |||||
XX 2 AACATATACAC 12
XX
XX RESULT 246
XX ABP25406
XX ID ABP25406 standard; DNA; 13 BP.
XX AC
XX ABP25406;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 125403 for detecting SNP TSC0031343.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 125403; 29pp + Sequence Listing; German.


```
OS Synthetic.
XX Key
XX modified_base 5 Location/Qualifiers
XX
XX /*tag= a
XX /note= "Thiol-substituted nucleoside derivative, 5-(3-
XX thiopropyn-1-yl)-2'-deoxyurine, optionally disulphide
XX bonded to the nucleoside derivative at position 5 of
XX another strand of the same sequence"
XX
XX modified_base 6
XX /*tag= b
XX /note= "Thiol-substituted nucleoside derivative, 5-(3-
XX thiopropyn-1-yl)-2'-deoxyurine, optionally disulphide
XX bonded to the nucleoside derivative at position 6 of
XX another strand of the same sequence"
XX
XX modified_base 7
XX /*tag= c
XX /note= "Thiol-substituted nucleoside derivative, 5-(3-
XX thiopropyn-1-yl)-2'-deoxyurine, optionally disulphide
XX bonded to the nucleoside derivative at position 7 of
XX another strand of the same sequence"
XX
XX WO9714708-A1.
XX
XX 24-APR-1997.
XX
XX 29-MAR-1996; 96WO-US004525.
XX
XX 04-OCT-1995; 95US-0004778P.
XX
XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
XX Koal ET;
XX
XX WPI; 1997-245044/22.
XX
XX New C-5 thiol-substituted nucleoside derivatives - whose presence in
XX PT oligonucleotide(s) allows formation of covalent cross-links between non-
XX complementary DNA domains.
XX
XX Example 11; Page 101; 122pp; English.
XX
XX The present sequence represents a bridged oligonucleotide derivative. The
XX invention relates to C-5 thiol-substituted nucleoside derivatives which
XX can be incorporated into an RNA or DNA strand during synthesis of
XX oligonucleotides. These compounds can be in the form of cross-linked
XX linear, cross-linked hairpin or bridged circular oligonucleotides. The
XX oligonucleotides may be used for detection and isolation of target
XX nucleic acids, or for targeting drugs to specific cell types (e.g. for
XX treatment of Alzheimer's disease, beta-thalassemia, osteogenesis
XX imperfecta, arthritis, sickle cell anaemia or viral infections). The
XX presence of the nucleoside derivatives in a linear oligonucleotide allows
XX the formation of covalent crosslinks between non-complementary DNA
XX domains
XX
XX SQ Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 83.3%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 732 GGAGAAACAGAA 743
XX
XX Db 13 GAAGAAANAGAA 2
XX
XX RESULT 243
XX AAF61477/C
XX ID AAF61477 standard; RNA; 13 BP.
XX
XX AC AAF61477;
XX
XX DT 18-JUN-2001 (first entry)
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```
XX Wildtype influenza virus C promoter-UP variant 1104 RNA fragment 2.
DE
XX Major histocompatibility complex restricted antigen; antitumor vaccine;
XX MHC-restricted antigen; T cell-restricted antigen;
KW antigen identification; promoter; ss.
KW Influenza virus.
OS Influenza virus.
XX DE19962508-A1.
XX
XX 29-MAR-2001.
XX
XX 23-DEC-1999; 99DE-01062508.
XX
XX 21-SEP-1999; 99DE-01045171.
XX
XX 26-OCT-1999; 99DE-01051543.
XX
XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Mautner J, Bornkamm GW, Nimmerjahn F, Hobom G;
XX
XX WPI; 2001-246290/26.
XX
XX Identifying major histocompatibility complex-restricted antigens, useful
XX potentially in antitumor vaccines, by forming DNA bank in virus and
XX testing for T cell stimulation.
XX
XX Disclosure; Col 5; 10pp; German.
XX
XX This invention describes a novel method for identifying major
XX histocompatibility complex (MHC)-restricted antigens. A gene or cDNA bank
XX is constructed from the cells or organism under test, then incorporated
XX into a retroviral genome or, as additional RNA, into a modified influenza
XX virus that has increased transcription, replication and/or expression
XX rate, relative to the wild type, so as to produce viral particles (VP).
XX VP are used to infect immortalized autologous cells that express MHC
XX Class I and/or II molecules on the surface, so that proteins encoded by
XX the gene bank inserts are expressed and their cleavage products exposed
XX on the cell surface. These cells are co-cultured with T cells which are
XX stimulated if the autologous cells express a T cell-restricted antigen.
XX Clones that express antigens are isolated and the antigens sequenced. The
XX products of the invention can be used for identifying antigens for
XX possible use in antitumor vaccines, but may also identify autoantigens or
XX microbial antigens. The method does not require knowledge of the
XX restricted MHC molecule, allows unlimited proliferation of target cells
XX and can identify, simultaneously, both Class I and II antigens. The
XX lymphoblastic cells lines used as target cells ensure efficient gene
XX transfer, with high level expression of the inserted gene, providing high
XX sensitivity and simple detection
XX
XX SQ Sequence 13 BP; 1 A; 5 C; 1 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 13;
XX Best Local Similarity 90.9%; Pred. No. 4.1e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 731 AGGAGAAACAG 741
XX
XX Db 13 AGTAGAAACAG 3
XX
XX RESULT 244
XX ABC27520/C
XX ID ABC27520 standard; DNA; 13 BP.
XX
XX AC ABC27520;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 27537 for detecting SNP TSC0007662.
XX
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PD 22-MAY-2003.
 XX
 XX 19-MAR-2002; 2002US-00100957.
 XX
 XX 27-FEB-1997; 97US-00810983.
 PR 27-FEB-1998; 98US-00031271.
 PR 26-FEB-1999; 99US-0122152P.
 PR 08-MAR-1999; 99US-0123399P.
 PR 12-JUL-1999; 99US-00352171.
 PR 31-AUG-1999; 99US-0151797P.
 PR 17-SEP-1999; 99US-00398965.
 PR 29-OCT-1999; 99US-00430656.
 PR 01-DEC-1999; 99US-0168408P.
 PR 25-FEB-2000; 2000US-00513783.
 XX
 PA (CELL-) CELLOMICS INC.
 PI Giuliano K, Kapur R;
 XX
 XX WPI: 2003-786988/74.
 DR P-PSDB; ADC18386.
 XX
 PT Cell based toxin characterization method for e.g. in drug discovery
 PT paradigm, involves treating cells possessing luminescent reporter
 PT molecules with fluorescence based molecules reagents to detect presence
 PT of toxins.
 XX
 XX Example 10; SEQ ID NO 73; 98pp; English.
 PS
 CC The invention relates to characterising cell based toxins, where the cell
 CC possessing luminescent reporter molecules (biosensors) are provided on a
 CC microchip, and are treated with fluorescence based molecular reagents.
 CC The cells are photographed with fluorescence optics, and the optical
 CC information is converted into digital data. The presence of the toxin in
 CC a reagent, is detected using the digital data, based on changes in the
 CC localisation, distribution structure of identifier, detector and
 CC classifier in each cell. Also included are a computer readable storage
 CC medium storing a cell based toxin characterisation program, and a kit for
 CC cell based toxin detection. The method is used for characterising or
 CC detecting a biological cell based toxin that affect particular biological
 CC functions and for preparing molecular biochemical arrays for new drug
 CC discovery paradigm. It is also used in automated DNA sequencing, PCR
 CC application, positional cloning, hybridisation arrays and bioinformatics
 CC using cell based scanning and screening system. The method improves the
 CC target validation and candidate optimisation by combining many cell
 CC screening formats with fluorescence based molecular reagents, thereby
 CC resulting in increased quantity and speed of data collection, shortened
 CC cycle times and faster evaluation of promising drug candidates. The
 CC method also provides increased throughput while decreasing the volumes of
 CC reagent and test compounds required in each assay. The biosensor
 CC comprises a signal component (fluorescent protein (fused e.g. MAP4,
 CC tethering it to microtubules) or detectable signal (epitope or affinity
 CC tag)), a protease recognition site (e.g. for a caspase protein) and a
 CC target domain (localising the biosensor to a particular cellular
 CC compartment). The present sequence encodes a protease recognition site
 CC for a biosensor of the invention.
 XX
 XX Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;
 Qy 732 GGAGAAACAGCA 742
 Db 1 GTAGAAACAGCA 11
 RESULT 241
 AAV06771/c
 ID AAV06771 standard; DNA; 13 BP.
 XX
 AC AAV06771;

XX
 DT 02-JUN-1998 (first entry)
 XX
 DE Oligonucleotide containing a thiol-substituted nucleoside derivative.
 XX
 KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
 KW circular; bridged; hairpin; detection; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_difference 6 /tag= a
 FT /note= "thiopropynyldeoxyuridine or unmodified thymidine"
 XX
 FN WO9714708-A1.
 XX
 XX 24-APR-1997.
 PD
 XX 29-MAR-1996; 96WO-US004525.
 PF
 XX 04-OCT-1995; 95US-0004778P.
 PR
 XX (RESE) RESEARCH CORP TECHNOLOGIES INC.
 PA
 XX Kool ET;
 PI
 XX WPI: 1997-245044/22.
 DR
 XX New C-5 thiol-substituted nucleoside derivatives - whose presence in
 PT oligo:nucleotide(s) allows formation of covalent cross-links between non-
 PT complementary DNA domains.
 PT
 XX Example 5; Page 82; 122pp; English.
 PS
 XX This sequence represents an oligonucleotide containing a thiol-
 CC substituted nucleoside derivative or an unmodified oligonucleotide. The
 CC invention relates to a C-5 thiol-substituted nucleoside derivatives which
 CC can be incorporated into an RNA or DNA strand during synthesis of
 CC oligonucleotides. These compounds can be in the form of cross-linked
 CC linear, cross-linked hairpin or bridged circular oligonucleotides. The
 CC oligonucleotides may be used for detection and isolation of target
 CC nucleic acids, or for targeting drugs to specific cell types (e.g. for
 CC treatment of Alzheimer's disease, beta-thalassemia, osteogenesis
 CC imperfecta, arthritis, sickle cell anaemia or viral infections). The
 CC presence of the nucleoside derivatives in a linear oligonucleotide allows
 CC the formation of covalent crosslinks between non-complementary DNA
 CC domains
 XX
 SQ Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
 Query Match 42.7%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;
 Qy 732 GGAGAAACAGCA 743
 Db 13 GAAGAAANAGAA 2
 RESULT 242
 AAV06762/c
 ID AAV06762 standard; DNA; 13 BP.
 XX
 AC AAV06762;
 XX
 DT 02-JUN-1998 (first entry)
 DE Bridged oligonucleotide derivative.
 XX
 KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
 KW circular; bridged; hairpin; detection; ss.
 XX

XX WPI; 2002-657594/70.
XX
XX
XX New human influenza virus comprising an RNA-sequence encoding a modified
PT RNA-polymerase, useful for preparing agents for therapeutic and
PT prophylactic vaccination, or treating a growing tumor or a chronic
PT infectious disease.
XX
XX Claim 10; Page 50; 172pp; English.
XX
XX The present invention describes a human influenza virus (I) comprising an
CC RNA-sequence encoding a modified RNA-polymerase that differs from the
CC wild-type RNA-polymerase of the human influenza virus in that at least 1
CC of the amino acid residues distinguishing the wild-type RNA-polymerase of
CC the human influenza virus from FV Bratistava RNA-polymerase has been
CC replaced with the corresponding amino acid residue(s) as present in FV
CC Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV,
CC hepatotropic, antiinflammatory and immunomodulator activities and can be
CC used in gene therapy and vaccines. The influenza virus is useful for
CC preparing agents for: (a) gene transfer into cells, preferably into
CC mammalian cells, particularly into human cells, by viral infection; (b)
CC gene transfer into antigen-presenting cells, and the use of the obtained
CC product for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo
CC vaccination, including therapeutic and prophylactic vaccination; (c)
CC eliciting an immune response, including the induction of a T-cell
CC response; (d) treating a growing tumor or a chronic infectious disease;
CC (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer
CC and expression of foreign genes into cells infected by such viruses; or
CC (g) transfer and expression of RNA molecules into cells infected by such
CC viruses, preferably the RNA molecules to be expressed are antisense
CC sequences or double-strand sequences relative to the target cellular
CC molecules, and/or the agent is suitable for sequence-specific gene
CC silencing, preferably by antisense RNA or RNA interference mechanisms
CC such as ribozyme cleavages of target RNAs. The recombinant viruses can be
CC made for use in vaccines against HIV, hepatitis B or C virus, herpes
CC viruses or papilloma viruses. The present sequence represents a modified
CC 3' conserved region of an influenza virus, given in the exemplification
XX of the present invention
SQ Sequence 12 BP; 1 A; 4 C; 1 G; 0 T; 6 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAACACG 741
Db 12 AGTAGAACACG 2
RESULT 239
ABQ75464/C
ID ABQ75464 standard; RNA; 12 BP.
XX AC ABQ75464;
XX
XX 07-NOV-2002 (first entry)
XX
XX Modified influenza virus A 3' conserved region SEQ ID NO:6.
DE
XX Influenza virus; transcription; replication; RNA polymerase; vaccine;
KW gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory;
KW immunomodulator; virucide; infectious disease; ss.
XX
XX Influenza virus.
OS Synthetic.
XX
XX WO2000264757-A2.
FN
XX 22-AUG-2002.
PD
XX 07-FEB-2002; 2002WO-EP001257.
PF
XX

PR 09-FEB-2001; 2001EP-00103060.
XX
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
XX Hobom G, Menke A;
XX
XX WPI; 2002-657594/70.
DR
XX
XX New human influenza virus comprising an RNA-sequence encoding a modified
PT RNA-polymerase, useful for preparing agents for therapeutic and
PT prophylactic vaccination, or treating a growing tumor or a chronic
PT infectious disease.
XX
XX Disclosure; Page 16; 172pp; English.
PS
XX The present invention describes a human influenza virus (I) comprising an
CC RNA-sequence encoding a modified RNA-polymerase that differs from the
CC wild-type RNA-polymerase of the human influenza virus in that at least 1
CC of the amino acid residues distinguishing the wild-type RNA-polymerase of
CC the human influenza virus from FV Bratislava RNA-polymerase has been
CC replaced with the corresponding amino acid residue(s) as present in FV
CC Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV,
CC hepatotropic, antiinflammatory and immunomodulator activities and can be
CC used in gene therapy and vaccines. The influenza virus is useful for
CC preparing agents for: (a) gene transfer into cells, preferably into
CC mammalian cells, particularly into human cells, by viral infection; (b)
CC gene transfer into antigen-presenting cells, and the use of the obtained
CC product for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo
CC vaccination, including therapeutic and prophylactic vaccination; (c)
CC eliciting an immune response, including the induction of a T-cell
CC response; (d) treating a growing tumor or a chronic infectious disease;
CC (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer
CC and expression of foreign genes into cells infected by such viruses; or
CC (g) transfer and expression of RNA molecules into cells infected by such
CC viruses, preferably the RNA molecules to be expressed are antisense
CC sequences or double-strand sequences relative to the target cellular
CC molecules, and/or the agent is suitable for sequence-specific gene
CC silencing, preferably by antisense RNA or RNA interference mechanisms
CC such as ribozyme cleavages of target RNAs. The recombinant viruses can be
CC made for use in vaccines against HIV, hepatitis B or C virus, herpes
CC viruses or papilloma viruses. The present sequence represents a modified
CC 3' conserved region of an influenza virus, given in the exemplification
XX of the present invention
SQ Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAACACG 741
Db 12 AGGAGAACACG 2
RESULT 240
ADC18385
ID ADC18385 standard; DNA; 12 BP.
XX AC ADC18385;
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Protease recognition site for caspase-8 DNA.
DE
XX ds; cell based toxin; luminescent reporter molecule; biosensor;
KW microchip; drug discovery; MAP4; epitope; affinity tag;
KW protease recognition site; caspase; target domain.
XX
XX Unidentified.
OS
XX US2003096322-A1.
PN
XX

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XX PN EP1201760-A1.
XX PD 02-MAY-2002.
XX PF 30-OCT-2000; 2000EP-00123687.
XX PR 30-OCT-2000; 2000EP-00123687.
XX PA (ARTE-) ARTEMIS PHARM GMBH.
XX PI Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann R;
XX DR WPI; 2002-418777/45.
XX PS Expressing tumor or viral associated antigens by dendritic cells, used
XX PT for treating tumors or viral infections, comprises using recombinant
XX PT influenza virus containing nucleic acid encoding the antigens.
XX PS Claim 7; Page 19; 33pp; English.
XX CC The invention relates to a method for the expression of tumour associated
XX CC antigens (TAA) or virus-associated antigens (VAA) by dendritic cells
XX CC comprising: preparing a recombinant influenza virus containing a
XX CC nucleotide sequence coding for the TAA or VAA; and infecting dendritic
XX CC cells with the recombinant virus. The method is used for expressing TAA
XX CC or VAA in dendritic cells. The cells are used for preparing a medicament
XX CC for treating tumours or viral infections. A vaccine can be created by
XX CC using dendritic cells presenting tumour antigens to induce an immune
XX CC response. This polynucleotide sequence represents a preferred 3'
XX CC conserved RNA influenza virus region of the invention
XX SQ Sequence 12 BP; 1 A; 4 C; 1 G; 0 T; 6 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
DB 12 AGTAGAACAG 2
RESULT 237
ABS71505
ID ABS71505 standard; DNA; 12 BP.
XX AC ABS71505;
XX DT 27-NOV-2002 (first entry)
XX DE DNA encoding protease biosensor recognition site #11.
XX KW Detection; classification; identification; toxin detection; protease;
XX KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
XX KW toxic threat agent; ds.
XX OS Synthetic.
XX PN US6416959-B1.
XX PD 09-JUL-2002.
XX PF 25-FEB-2000; 2000US-00513783.
XX PR 27-FEB-1997; 97US-00810983.
XX PR 27-FEB-1998; 98US-00031271.
XX PR 26-FEB-1999; 99US-0122152P.
XX PR 08-MAR-1999; 99US-0123395P.
XX PR 12-JUL-1999; 99US-00352171.
XX PR 31-AUG-1999; 99US-0151757P.
XX PR 17-SEP-1999; 99US-00398965.
XX PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
XX (GIUL/) GIULIANO K.
XX PA (KAPU/) KAPUR R.
XX PI Giuliano K, Kapur R;
XX DR WPI; 2002-634730/68.
XX DR P-PSDB; ABG94458.
XX PT Automated cell-based toxin detection, classification, and/or
XX PT identification by treating cells involves use of three classes of
XX PT luminescent reporter molecules such as detectors, classifiers or
XX PT identifiers.
XX Example 10; Fig 28B; 214pp; English.
XX CC The invention describes methods of automated detection, classification
XX CC and identification comprising treating cells containing luminescent
XX CC reporter molecules (l) in array of locations with a test substance, where
XX CC (l) are detectors, classifiers or identifiers, imaging cells in each
XX CC location to obtain luminescent signals and converting optical information
XX CC into digital data to interpret presence of toxins in the test substance.
XX CC The method are useful for detection of toxins chosen from proteases, ADP-
XX CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
XX CC Three classes of cell-based luminescent reporter molecules such as
XX CC detectors, classifiers and identifiers are described and serve as
XX CC reporters of toxic threat agents. The first two levels of
XX CC characterization ensure a rapid readout of toxin class without
XX CC sacrificing the ability to detect many new mutant toxins or dissect
XX CC several complex mixtures of known toxins. This sequence encodes a
XX CC protease biosensor recognition site used in the cell-based screening
XX CC system
XX SQ Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 732 GGAGAAACAGA 742
DB 1 GTAGAACAGA 11
RESULT 238
ABQ75463/C
ID ABQ75463 standard; RNA; 12 BP.
XX AC ABQ75463;
XX DT 07-NOV-2002 (first entry)
XX DE Modified influenza virus A 3' conserved region SEQ ID NO:5.
XX KW Influenza virus; transcription; replication; RNA polymerase; vaccine;
XX KW gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory;
XX KW immunomodulator; virucide; infectious disease; ss.
XX OS Influenza virus.
XX OS Synthetic.
XX PN WO200264757-A2.
XX PD 22-AUG-2002.
XX PF 07-FEB-2002; 2002WO-EP001257.
XX PR 09-FEB-2001; 2001EP-00103060.
XX PA (ARTE-) ARTEMIS PHARM GMBH.
XX PI Hobom G, Menke A;

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```
ABIS1887
XX ID ABIS1887 standard; DNA; 12 BP.
XX AC ABIS1887;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 351860 for detecting SNP TSC0047526.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 351860; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI02073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 736 AACACAGACAC 746
XX |||||
XX 2 AACACACAC 12
XX Db
XX RESULT 235
XX AAL37781/C
XX ID AAL37781 standard; RNA; 12 BP.
XX AC AAL37781;
XX DT 05-AUG-2002 (first entry)
XX DE 3'-terminal RNA influenza virus mutant G3C, USC, C8G.
XX CYTOSTATIC; antiviral; tumour associated antigen; TAA; dendritic cell;
XX virus-associated antigen; VAA; recombinant influenza virus; vaccine;
XX viral infection; immune; mutant; ss.
XX OS Influenza virus.
OS Influenza virus.
XX Key Location/Qualifiers
XX mutation 3
XX /*tag= a
XX /*note= "The wild-type nucleotide G has been replaced with
XX C"
XX mutation 5
XX /*tag= b
XX /*note= "The wild-type nucleotide U has been replaced with
XX C"
XX mutation 8
XX /*tag= c
XX /*note= "The wild-type nucleotide C has been replaced with
XX G"
XX EP1201760-A1.
XX PD 02-MAY-2002.
XX PF 30-OCT-2000; 2000EP-00123687.
XX PR 30-OCT-2000; 2000EP-00123687.
XX PA (ARTE-) ARTEMIS PHARM GMBH.
XX PI Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann R;
XX WPI; 2002-418777/45.
XX Expressing tumor or viral associated antigens by dendritic cells, used
XX for treating tumors or viral infections, comprises using recombinant
XX PT influenza virus containing nucleic acid encoding the antigens.
XX Disclosure; Page 6; 33pp; English.
XX The invention relates to a method for the expression of tumour associated
XX antigens (TAA) or virus-associated antigens (VAA) by dendritic cells
XX comprising: preparing a recombinant influenza virus containing a
XX nucleotide sequence coding for the TAA or VAA; and infecting dendritic
XX cells with the recombinant virus. The method is used for expressing TAA
XX or VAA in dendritic cells. The cells are used for preparing a medicament
XX for treating tumours or viral infections. A vaccine can be created by
XX using dendritic cells presenting tumour antigens to induce an immune
XX response. This polynucleotide sequence represents a preferred 3'-terminal
XX RNA region of an influenza virus mutant G3C, USC, C8G of the invention
XX Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 731 AGGAGAAACAG 741
XX |||||
XX 12 AGGAGAACCCAG 2
XX Db
XX RESULT 236
XX AAL37780/C
XX ID AAL37780 standard; RNA; 12 BP.
XX AC AAL37780;
XX DT 05-AUG-2002 (first entry)
XX DE Preferred 3' conserved RNA influenza virus region.
XX CYTOSTATIC; antiviral; tumour associated antigen; TAA; dendritic cell;
XX virus-associated antigen; VAA; recombinant influenza virus; vaccine;
XX viral infection; immune; ss.
XX OS Influenza virus.
```

```

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 AACATAACACC 11

RESULT 232
ABI23313/C
ID ABI23313 standard; DNA; 12 BP.
XX AC ABI23313;
XX AC ABI23313;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 323286 for detecting SNP TSC0031304.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 323286; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 AACATAACACC 11

RESULT 232
ABI23313/C
ID ABI23313 standard; DNA; 12 BP.
XX AC ABI23313;
XX AC ABI23313;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 323286 for detecting SNP TSC0031304.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 323286; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

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XX SQ Sequence 12 BP; 0 A; 6 C; 0 G; 6 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
Db 12 GGAGAAACAGA 2

RESULT 233
ABI48554/C
ID ABI48554 standard; DNA; 12 BP.
XX AC ABI48554;
XX AC ABI48554;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 348527 for detecting SNP TSC0045634.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 348527; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
      Query Match      42.7%; Score 9.4; DB 1; Length 12;
      Best Local Similarity 90.9%; Pred No. 4e+02;
      Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAAACAG 2

RESULT 234

```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 275098; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACGACAC 746
Db 11 AACACGACAC 1
RESULT 230
AB113566/c
ID AB113566 standard; DNA; 12 BP.
XX
XX AB113566;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 313539 for detecting SNP TSC0025831.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX

PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 313539; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 736 AACACGACAC 746
Db 12 AACACGACAC 2
RESULT 231
ABH96894
ID ABH96894 standard; DNA; 12 BP.
XX
XX ABH96894;
AC
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 296887 for detecting SNP TSC0017334.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 296887; 29pp + Sequence Listing; German.
PS

```

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACACC 747
Db 1 AACAAACAC 11

RESULT 227
ABH69260/C
ID ABH69260 standard; DNA; 12 BP.
XX
AC ABH69260;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 269237 for detecting SNP TSC0001673.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 269237; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGAACACC 746
Db 1 AACAAACAC 11

RESULT 227
ABH69260/C
ID ABH69260 standard; DNA; 12 BP.
XX
AC ABH69260;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 269237 for detecting SNP TSC0001673.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 269237; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 AACAGAACACC 745
Db 1 AACAAACAC 11

RESULT 229
ABH75111/C
ID ABH75111 standard; DNA; 12 BP.
XX
AC ABH75111;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 275098 for detecting SNP TSC0003783.

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Db 11 AACAAACAC 1
RESULT 228
ABH99600
ID ABH99600 standard; DNA; 12 BP.
XX
AC ABH99600;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 299593 for detecting SNP TSC0018645.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 299593; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 0 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACG 741
Db 1 AGGAGAACACG 11

RESULT 229
ABH75111/C
ID ABH75111 standard; DNA; 12 BP.
XX
AC ABH75111;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 275098 for detecting SNP TSC0003783.

```



```

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 2 AAACAGAACAC 12

RESULT 222
ABI24222
ID ABI24222 standard; DNA; 12 BP.
XX
AC ABI24222;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 324195 for detecting SNP TSC0031857.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 324195; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 GAGAAACAGAA 743
Db 2 GAGAAACAGAA 12

RESULT 223
ABI03119
ID ABI03119 standard; DNA; 12 BP.
XX
AC ABI03119;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 303092 for detecting SNP TSC0020318.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 303092; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match          42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACAC 746
Db 1 AAACAGAACAC 11

RESULT 224
ABH77763
ID ABH77763 standard; DNA; 12 BP.
XX
AC ABH77763;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 277756 for detecting SNP TSC0004835.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
WO200177384-A2.
XX

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```

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
PI acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX range of diseases including immune system, cardiovascular and metabolic disorders. The
DR oligonucleotides are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
PT data for this patent did not form part of the printed specification, but
PT methylation status.
XX ftp.wipo.int/pub/published_pct_sequences
XX Claim 1; SEQ ID NO 309289; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX range of diseases including immune system, cardiovascular and metabolic disorders. The
XX oligonucleotides are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 0 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AAACGAGAACAC 746
XX DB 11 AAACGAGAACAC 1
XX
XX RESULT 220
XX ABI66282
XX ID ABI66282 standard; DNA; 12 BP.
XX AC ABI66282;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 366255 for detecting SNP TSC0055626.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 366255 for detecting SNP TSC0055626.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 366255; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

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CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 736 AAACGAGAACAC 746
XX DB 2 AAACGAGAACAC 12
XX
XX RESULT 221
XX ABH95965
XX ID ABH95965 standard; DNA; 12 BP.
XX AC ABH95965;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 295958 for detecting SNP TSC0016826.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 295958; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

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RESULT 217
ABI59474
ID ABI59474 standard; DNA; 12 BP.
XX
AC ABI59474;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359447 for detecting SNP TSC0051611.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS
XX Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 359447; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 736 AAACAGAACAC 746
DB 1 AAACAAACAC 11

RESULT 218
ABH71042/c
ID ABH71042 standard; DNA; 12 BP.
XX
AC ABH71042;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 271019 for detecting SNP TSC002368.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 271019; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 736 AAACAGAACAC 746
DB 1 AAACAAACAC 1

RESULT 219
ABI09316/c
ID ABI09316 standard; DNA; 12 BP.
XX
AC ABI09316;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 309289 for detecting SNP TSC0023461.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.

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XX PS Claim 1; SEQ ID NO 36398; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 733 GAGAAACAGAA 743
Db 12 GAGAAAAGAA 2
|||||
|

RESULT 215
AB122641
ID AB122641 standard; DNA; 12 BP.
XX
AC AB122641;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322614 for detecting SNP TSC0030968.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 322614; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
```

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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 733 GAGAAACAGAA 743
Db 2 GAGAAAAGAA 12
|||||
|

RESULT 216
AB103293/C
ID AB103293 standard; DNA; 12 BP.
XX
AC AB103293;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 303266 for detecting SNP TSC0020413.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 303266; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 736 AACACAAACAC 746
Db 12 AACAAAAACAC 2
|||||
|
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XX DE Oligonucleotide primer SEQ ID NO 309520 for detecting SNP TSC0023558.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 309520; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 736 AAACAGAACAC 746
DB 1 AAACATACAC 11
|||||
RESULT 213
ABI45019
ID ABI45019 standard; DNA; 12 BP.
AC ABI45019;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 344992 for detecting SNP TSC0010376.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 309520; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 736 AAACAGAACAC 746
DB 1 AAACATACAC 11
|||||
RESULT 213
ABI45019
ID ABI45019 standard; DNA; 12 BP.
AC ABI45019;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 344992 for detecting SNP TSC0053822.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

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PF 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 344992; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 42.7%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 4e+02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 736 AAACAGAACAC 746
DB 2 AAACAAACAC 12
|||||
RESULT 214
ABI63425/C
ID ABI63425 standard; DNA; 12 BP.
XX AC ABI63425;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 363398 for detecting SNP TSC0053822.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

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CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AACAGACACAC 746
Db 2 AACAAACAC 12
|||||
RESULT 210
ABH94121/C
ID ABH94121 standard; DNA; 12 BP.
XX
XX
AC ABH94121;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 294114 for detecting SNP TSC0015962.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 294114; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAAATAG 2
|||||
RESULT 212
ABI09547
ID ABI09547 standard; DNA; 12 BP.
XX
XX
AC ABI09547;
XX
XX
DT 22-FEB-2002 (first entry)
```

```
QY 737 AACAGACACAC 747
Db 11 AACAAACACAC 1
|||||
RESULT 211
ABH70673/C
ID ABH70673 standard; DNA; 12 BP.
XX
XX
AC ABH70673;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 270650 for detecting SNP TSC0002216.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 270650; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAG 741
Db 12 AGGAGAAATAG 2
|||||
RESULT 212
ABI09547
ID ABI09547 standard; DNA; 12 BP.
XX
XX
AC ABI09547;
XX
XX
DT 22-FEB-2002 (first entry)
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SQ Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
  Query Match 42.7%; Score 9.4; DB 1; Length 12;
  Best Local Similarity 90.9%; Pred. No. 4e+02;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 731 AGGAGAAACAG 741
Db 2 AGGAGAAACGG 12

RESULT 205
AAH21574
ID AAH21574 standard; DNA; 12 BP.
XX AC AAH21574;
XX DT 10-AUG-2001 (first entry)
XX DE Human hypocretin receptor 2 (HCRTR2) splice acceptor site SEQ ID NO:36.
XX KW Human; narcolepsy; hypocretin receptor 2; orexin receptor 2; HCRTR2;
XX KW diagnosis; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200130991-A2.
XX PD 03-MAY-2001.
XX PF 22-AUG-2000; 2000WO-US023021.
XX PR 25-OCT-1999; 99US-00426290.
XX PA (DECO-) DECODE GENETICS EHF.
XX PI Olafsdottir BR, Gulcher J;
XX DR WPI; 2001-300504/31.
XX PT Gene for hypocretin (orexin) receptor 2 (HCRTR2) which is associated with
XX PT narcolepsy, useful in methods of diagnosis of narcolepsy and
XX PT pharmaceutical compositions for therapy.
XX PS Example 1; Page 26; 85pp; English.
XX CC The present invention describes the human hypocretin (orexin) receptor 2
XX CC (HCRTR2) gene (given in AAH21613), which is associated with narcolepsy.
XX CC Identification of the HCRTR2 nucleic acid molecule permits the diagnosis
XX CC of narcolepsy. A method from the present invention is provided for
XX CC treating narcolepsy by administering to the individual an isolated HCRTR2
XX CC nucleic acid in a therapeutically effective amount so that the cells
XX CC produce native HCRTR2 receptor. The diagnosis of narcolepsy has been
XX CC difficult to differentiate from other conditions such as chronic fatigue
XX CC syndrome or other sleep disorders but detection of HCRTR2 nucleic acid
XX CC makes it possible to accurately diagnose narcolepsy. AAH21541 to AAH21612
XX CC represent primers used in the identification of the narcolepsy gene in an
XX CC example from the present invention. AAH21613 represents the HCRTR2 gene
XX CC which encodes the HCRTR2 protein given in AAH98007
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 28468 for detecting SNP TSC0013526.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
OS ABH75383
ABH75383 standard; DNA; 12 BP.
ABH75383;
22-FEB-2002 (first entry)
Oligonucleotide primer SEQ ID NO 275374 for detecting SNP TSC0003875.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EFIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 275374; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABCF9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABIC0010-ABI92073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
  Query Match 42.7%; Score 9.4; DB 1; Length 12;
  Best Local Similarity 90.9%; Pred. No. 4e+02;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 733 GAGAAACAGAA 743
Db 1 GAGAAACAGAA 11

RESULT 207
ABH88475
ID ABH88475 standard; DNA; 12 BP.
XX AC ABH88475;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 28468 for detecting SNP TSC0013526.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

CC second localisation signal attached to the fluorescent protein enables
 CC the fluorescent protein to be directed to a different cellular
 CC compartment after cleavage of the protease recognition sequence. The
 CC change in distribution of the fluorescent protein can be detected using
 CC imaging methods with a high degree of spatial resolution. The methods and
 CC biosensors of the invention can be used to investigate a wide range of
 CC cellular activities and to screen compounds which modulate these
 CC activities. Biosensors containing a recognition site for caspase, for
 CC example, may be used for the screening of compounds which modulate
 CC apoptosis, while biosensors containing other protease recognition sites
 CC may be used for the detection of proteolytic toxins (such as anthrax
 CC lethal factor). The method provides improved target validation and
 CC candidate compound optimisation by combining many cell screening formats
 CC with fluorescence-based molecular reagents and computer-based feature
 CC extraction, data analysis and automation, resulting in increased quantity
 CC and speed of data collection and faster evaluation of drug candidates.
 CC Sequences AAA93377-A93411 and AAA93440 represent protease recognition
 CC sites (AAB22886-B22920, AAB22935) which may be used as components of
 CC biosensor fusion proteins of the invention

XX Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
 Db 1 GTAGAAACAGA 11

RESULT 203

AAA27587
 ID AAA27587 standard; DNA; 12 BP.

AC AAA27587;

XX 29-AUG-2000 (first entry)

XX DNA encoding caspase-8 substrate recognition sequence.

XX Protease; biosensor; caspase-8; substrate recognition sequence;
 XX cell screening; assay; analysis; drug discovery; ss.

XX Unidentified.

XX WO200026408-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025431.

XX 30-OCT-1998; 98US-0106308P.

XX 26-MAY-1999; 99US-0136078P.

XX (CELL-) CELLOMICS INC.

XX Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;

XX WPI; 2000-365644/31.

XX P-PSDB; AAY79598.

XX Recombinant nucleic acid encoding a protease biosensor useful for
 XX fluorescence based cell and molecular biochemical assays for drug
 XX discovery comprising three operably linked nucleic acid sequences.

XX Claim 6; Fig 29b; 218pp; English.

XX The present sequence is that of DNA encoding the substrate recognition
 XX sequence (see AAY79598) of caspase-8. The DNA is used in a claimed
 XX recombinant nucleic acid encoding a protease biosensor. The nucleic acid
 XX (see AAZ27627-43) comprises: (1) a sequence (see AAA27568-76) encoding at
 XX least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-611)

CC that encodes at least 1 protease recognition site, such as the present
 CC sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1
 CC reactant target sequence. An expression vector, a genetically engineered
 CC host cell and a recombinant protease biosensor are also claimed. A
 CC claimed method for identifying compounds that modify protease activity in
 CC a cell involves contacting a host cell that possesses the recombinant
 CC protease biosensor with a test compound, and determining the recombinant
 CC biosensor distribution in the host cell, where changes in the
 CC distribution of the protease biosensor are correlated with modification
 CC of protease activity by the test compound. Claimed kits for identifying
 CC compounds that modify protease activity in a host cell include the
 CC recombinant nucleic acid, or the recombinant protease biosensor, or the
 CC vector, or the host cell. The protease biosensor is useful in high
 CC content screens to detect in vivo activation of enzymatic activity, and
 CC to identify specific activity based on cleavage of a known recognition
 CC motif

XX Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 42.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 732 GGAGAAACAGA 742
 Db 1 GTAGAAACAGA 11

RESULT 204

AAC97936
 ID AAC97936 standard; DNA; 12 BP.

XX AAC97936;

XX 28-FEB-2001 (first entry)

XX Primer used to illustrate DNA amplification method SEQ ID 162.

XX Primer; amplification; selective; ss.

XX Synthetic.

XX JP2000270867-A.

XX 03-OCT-2000.

XX 19-MAR-1999; 99JP-00076844.

XX 19-MAR-1999; 99JP-00076844.

XX (SAOL) SANYO ELECTRIC CO LTD.
 XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.

XX WPI; 2001-011047/02.

XX Amplification of a DNA fragment and its apparatus.

XX Example 1; Page 11; 32pp; Japanese.

XX This invention relates to a method for amplifying a DNA fragment. The
 XX method comprises successive repetitions of heat-denaturing, annealing of
 XX a primer and an extending step using a DNA polymerase. The method makes
 XX use of a cDNA pool in which the primer is one primer or a pair of primer
 XX sets and has an amplification probability which allows it to amplify a
 XX DNA fragment from a limited number of the cDNAs among the DNA pool (where
 XX the limited number is in the range of 1 to 25). Also included in the
 XX invention are apparatus used for carrying out the method, a primer and a
 XX DNA polymerase and a kit used for amplifying a DNA fragment. The method
 XX can be used to amplify a limited number of cDNAs from a pool in which a
 XX wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
 XX represent primers used in an example illustrating the method of the
 XX invention

XX
PS Disclosure; Page 26; 32pp; Japanese.
XX
CC The specification describes a method for the determination of the
CC nucleotide sequence of a polynucleotide. The method comprises providing a
CC set of primers in which each primer has an extension region containing a
CC terminal nucleotide, a template arranging segment and at least one
CC complexity-decreasing nucleotide, forming a template containing primer-
CC combining sites and the polynucleotide in which the primer-combining
CC sites are complementary to at least one primer of the set, forming an
CC amplicon from the template by amplifying a double-stranded DNA formed
CC selectively by extending the primer from the set in which the extending
CC region forms a double-strand completely matched to primer-combining sites
CC of the template, identifying the terminal nucleotide of the extending
CC region of the primer by an identification of the amplicon, shifting the
CC primer-combining sites by one nucleotide to the direction of extension by
CC varying the primer-combining sites of the template, and repeating this
CC until the nucleotide sequence of the polynucleotide is determined. The
CC method can be used for DNA sequencing. The present sequence represents a
CC primer used to demonstrate the invention
XX
SQ Sequence 12 BP; 1 A; 5 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. NO. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAA 738
Db |||||
12 GCCAGGAGAGA 2
RESULT 201
AAZ41585
ID AAZ41585 standard; DNA; 12 BP.
XX
AC AAZ41585;
XX
DT 19-JAN-2000 (first entry)
XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #162.
XX
KW Microbe; detection; organic waste; arbitrarily primer PCR;
KW random amplified polymorphic DNA; amplification; PCR primer; ss.
OS Synthetic.
XX
PN JP11276176-A.
XX
PD 12-OCT-1999.
XX
PF 31-MAR-1998; 98JP-00087652.
XX
PR 31-MAR-1998; 98JP-00087652.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 1999-626940/54.
XX
PT Amplification of a DNA fragment - in order to establish the state of
PT existence of a microbe.
XX
PS Example; Page 9; 40pp; Japanese.
XX
CC A method has been developed for the amplification of a DNA fragment in
CC which amplification is carried out on the DNA fragments of a number of
CC different DNAs. The method comprises a PCR reaction repeatedly carrying
CC out a heat-denaturing step, a primer annealing step and a polymerase
CC extending step, to amplify the DNA fragments of a plural of different
CC DNAs. The method can detect the existence of a microbe in organic waste.
CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in

CC organic waste
XX Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
SQ Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. NO. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 731 AGGAGAAACAG 741
Db |||||
2 AGGAGAAACGG 12
RESULT 202
AAA93387
ID AAA93387 standard; DNA; 12 BP.
XX
AC AAA93387;
XX
DT 10-JAN-2001 (first entry)
XX
DE DNA encoding caspase-8 substrate recognition sequence, SEQ ID NO:73.
XX
KW Bioreactor protein; fusion protein; recognition site;
KW cellular targeting sequence; cellular localisation; fluorescent protein;
KW protease activity detection; toxin detection; cellular stress detection;
KW drug discovery; cell based screening; protease recognition site;
KW cleavage site; ds.
XX
OS Synthetic.
XX
PN WO200050872-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004794.
XX
PR 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
XX
PA (CELL-) CELLOMICS INC.
XX
PI Giuliano KA, Kapur R;
XX
DR WPI; 2000-594086/56.
DR P-PSDE; AAB22896.
XX
PT Automated cell-based characterization of toxin by contacting cells
PT containing luminescent reporter molecules with test substance and
PT analyzing optically.
XX
PS Example 11; Fig 29B; 336pp; English.
XX
CC The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreactor
CC molecules which, when acted on by a compound of interest, cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreactor proteins can be used to detect protease
CC activity. Such protease bioreactor fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreactor protein is localised to a particular
CC region of the cell. Once acted on by the protease of interest, the
CC fluorescent protein is cleaved from the localisation sequence, and is
CC free to migrate to other locations within the cell. The presence of a

XX The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86346-ABQ87680) of the invention
XX
XX SQ Sequence 11 BP; 1 A; 2 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAACAGAAC 744
DB 11 AGAACAGATC 1
RESULT 196
ID ABV66898 standard; cDNA; 11 BP.
XX
XX AC ABV66898;
XX
XX DT 21-OCT-2002 (first entry)
XX
XX DE Human skin EST 4684.
XX
XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253774-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX
XX PA (HENK) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-590638/63.
XX
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX
XX PS Disclosure; Page 154; 1345pp; German.
XX
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention

SQ Sequence 11 BP; 1 A; 2 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 734 AGAACAGAAC 744
DB 11 AGAACAGATC 1
RESULT 197
ID AAQ24029 standard; DNA; 12 BP.
XX
XX AC AAQ24029;
XX
XX DT 25-MAR-2003 (revised)
XX DT 21-SEP-1992 (first entry)
XX
XX DE Herpesvirus inhibiting antisense oligonucleotide.
XX
XX KW HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
KW Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
XX
XX OS Synthetic.
XX
XX PN WO9205284-A.
XX
XX PD 02-APR-1992.
XX
XX PF 18-SEP-1991; 91WO-US006646.
XX
XX PR 21-SEP-1990; 90US-00586185.
XX
XX PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX
XX PI Aurelian L, Tso P;
XX
XX DR WPI; 1992-132145/16.
XX
XX PT New anti-sense oligonucleotide(s) for inhibiting HSV - also used for
XX PT diagnosis and for inhibiting HIV activation by herpes virus.
XX
XX PS Claim 1; Page 38; 77pp; English.
XX
XX CC The sequence is that of an antisense oligonucleotide which can be used
XX CC for inhibiting growth or replication of herpesviruses. It corresponds to
XX CC an antisense sequence of a herpesvirus site, pref. in a gene that is
XX CC essential for synthesising nucleic acids e.g. the immediate early genes
XX CC or VMW65. It can be prepd. by solid phase triester or phosphor- amide
XX CC chemistry or by recombinant DNA techniques. It can be used for treating
XX CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
XX CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
XX CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
XX CC inhibition of herpesvirus growth or replication may indirectly forestall
XX CC the progression of events from HIV exposure to the clinical manifestation
XX CC of AIDS. It may also be useful in the detection, diagnosis and
XX CC manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
XX CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 12 BP; 0 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAA 738
DB 12 GCCAAGAGAAA 2

CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic bacteria or viruses for
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
 SQ

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACGAGACA 745
 Db 14 GAGAAACGAGAAAA 2

RESULT 194

ABX76569/C
 ID ABX76569 standard; DNA; 15 BP.

XX AC ABX76569;

XX 01-APR-2003 (first entry)

XX M. avium 23S rRNA mutated probe #6.

XX Probe; 23S rRNA; 16S rRNA; tuberculosis; MTC; MOTT; peptide nucleic acid;
 KW mycobacterium tuberculosis complex; precursor rRNA; rDNA; 5S rRNA; ss;
 KW mycobacterium other than tuberculosis; 23S-mediated macrolide resistance;
 KW mutant.

OS Mycobacterium avium.
 OS Synthetic.

XX Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "G is covalently linked to Lys (Rho) where Rho=
 Rhodamine, optional"
 FT modified_base 15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "C is amidated"

PN US2002137035-A1.

XX 26-SEP-2002.

XX 07-APR-2000; 2000US-00544934.

XX 07-APR-2000; 2000US-00544934.

XX (STEN/) STENDER H.

XX (LUND/) LUND K.

XX (MOLL/) MOLLERUP T A.

XX Stender H, Lund K, Mollerup TA;

XX WPI; 2003-174116/17.

XX Peptide nucleic acid probes for detecting target sequences of

PT Mycobacteria in samples, e.g., sputum, which are capable of hybridizing
 PT to a target sequence of mycobacterial rDNA, precursor rRNA or rRNA
 PT forming detectable hybrids.

XX Claim 22; Page 40; 74pp; English.

XX The invention relates to a peptide nucleic acid capable of hybridizing to
 CC a target sequence of mycobacterial rDNA, precursor rRNA or rRNA (5S, 16S
 CC or 23S) forming detectable hybrids. Also included are detecting a target
 CC sequence of mycobacteria in a sample comprising contacting rRNA or rDNA
 CC in the sample with peptide nucleic acid probes (hybridisation takes place
 CC between the probe and the rRNA or rDNA), observing or measuring any
 CC formed detectable hybrids and relating the observation or measurement to
 CC the presence of a target sequence of mycobacteria in the sample, and a
 CC kit for detecting a target sequence of mycobacteria in particular a
 CC target sequence of mycobacteria of M. tuberculosis complex (MTC). The
 CC probes are used for detecting a target sequence of MTC (and
 CC distinguishing them from mycobacterium other than tuberculosis, MOTT)
 CC present in a sample, e.g. sputum, laryngeal swabs, gastric lavage,
 CC bronchial washings, biopsies, aspirates, expectorates, body fluids,
 CC urine, tissue sections as well as food samples, soil, air and water
 CC samples and their cultures. The probe is able to penetrate the cell wall
 CC of the mycobacteria. It is able to hybridise to mycobacterial precursor
 CC rRNA and rRNA without harsh treatment of the mycobacterial cells,
 CC therefore avoiding a risk of interfering with the morphology of the
 CC cells. The present sequence is an M. avium mutated probe for 23S rRNA
 CC around positions 2568-2569, associated with 23S-mediated macrolide
 CC resistance

XX Sequence 15 BP; 0 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGA 742

Db 14 CAGGAGCAACAGA 2

RESULT 195

ABQ87464/C

ID ABQ87464 standard; CDNA; 11 BP.

XX AC ABQ87464;

XX 10-SEP-2002 (first entry)

XX Human skin stress/ageing related EST SEQ ID NO 1219.

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX Homo sapiens.

XX WO200253773-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015178.

XX 03-JAN-2001; 2001DE-01000121.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-528865/56.

XX Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.

XX Claim 8; Page 87; 325pp; German.

PS Claim 14; Page 14; 84pp; English.

CC The invention relates to an isolated polynucleotide comprising genes and

CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic

CC variants of the CCBP2 gene are useful in studying the expression and

CC function of CCBP2, and in expressing CCBP2 proteins for use in screening

CC candidate drugs for treating diseases associated with CCBP2 activity.

CC Polynucleotides comprising a polymorphic gene variant or fragment may be

CC used for therapeutic purposes, where a patient could benefit from

CC expression or increased expression of a particular CCBP2 protein isoform,

CC or an expression vector encoding the isoform may be administered to the

CC patient. Haplotype information is useful in improving the efficiency and

CC output of several steps in drug discovery and development process,

CC including target validation, identifying lead compounds, and early phase

CC clinical trials. The polynucleotides of the invention can be used to

CC treat disorders related to the CCBP2 gene by gene therapy. This

CC polynucleotide sequence represents a preferred ASO primer for detecting

CC CCBP2 gene polymorphisms relating to the invention

XX

SQ Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 1 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 727 TGCAGGAGAAAC 739

Db 1 TGCAGGAGAAAC 13

RESULT 192

ABV99157/C

ID ABV99157 standard; DNA; 15 BP.

XX

AC ABV99157;

XX

DT 17-JAN-2003 (first entry)

XX

DE Human CYP7A1 allele-specific oligonucleotide probe #7.

XX

KW Human; CYP7A1; hepatotropic; antilipaeamic; cholesterol disorder;

XX

KW cirrhosis; bile disorder; hypertriglyceridaemia; hypercholesterolaemia;

KW cytochrome P450, subfamily VIIA, polypeptide 1; probe; ss.

XX

OS Homo sapiens.

XX

XX WO200260915-A1.

PN

XX

PD 08-AUG-2002.

XX

PF 31-JAN-2001; 2001WO-US003164.

XX

PR 31-JAN-2001; 2001WO-US003164.

XX

XX (GENA-) GENAISSANCE PHARM INC.

PA

XX

PI Chew A, Denton RR, Nandabalan K, Stephens JC;

XX

DR WPI; 2002-713314/77.

XX

XX New cytochrome P450 subfamily VIIA (cholesterol 7 alphanomoxigenase)

PT polypeptide 1 gene variants, useful for studying the expression and

PT activity of CYP7A1 and screening drugs for treating disorders of

PT cholesterol and bile metabolism.

XX

PS Claim 16; Page 21; 84pp; English.

XX

CC The invention relates to a novel polymorphic variant of a sequence of

CC CYP7A1 protein or its fragment. The polypeptide has hepatotropic and

CC antilipemic activity. The polymorphic variants are useful in studying

CC the expression and function of CYP7A1, in expressing CYP7A1 protein for

CC use in screening candidate drugs to treat diseases related to CYP7A1

CC activity, in studying the effect of the variation on the biological

CC activity of CYP7A1, and the binding affinity of candidate drugs targeting

CC CYP7A1 for the treatment of disorders such as cholesterol and bile

CC disorders. Haplotyping methods are useful in validating CYP7A1 as a

CC candidate target for treating a specific condition or disease predicted

CC to be associated with CYP7A1 activity, or in the design of clinical

CC trials of candidate drugs for treating a specific condition or disease

CC associated with CYP7A1 activity, such as cirrhosis, familial

CC hypertriglyceridaemia and hypercholesterolaemia. Transgenic animals are

CC also useful for studying expression of the CYP7A1 isogenes in vivo, for

CC in vivo screening and testing of drugs targeted against CYP7A1 protein,

CC and for testing the efficacy of therapeutic agents and compounds related

CC to cholesterol and bile acid metabolism. The present sequence represents

CC an allele-specific oligonucleotide (ASO) probe, used in the invention to

XX detect CYP7A1 gene polymorphisms

SQ Sequence 15 BP; 1 A; 3 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

Db 14 AAGACAAACAGAA 2

RESULT 193

ABX98147/C

ID ABX98147 standard; DNA; 15 BP.

XX

AC ABX98147;

XX

DT 07-OCT-2002 (first entry)

XX

DE Triple helix forming associated oligonucleotide #30.

XX

KW Triple-helix formation; purine-rich target sequence; double-helix DNA;

KW Gene expression; regulatory sequence; pathogenic double-stranded DNA;

KW pathogenic bacteria; virus; replication; virulence; cancer;

KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

OS Synthetic.

XX

XX US6403302-B1.

PN

XX

PD 11-JUN-2002.

XX

PF 16-DEC-1993; 93US-00168920.

XX

PR 17-SEP-1992; 92US-00946976.

XX

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

PA

XX

PI Dervan PB, Beal PA;

XX

DR WPI; 2002-536030/57.

XX

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an

PT oligonucleotide which binds in parallel and antiparallel orientation,

PT respectively, for targeting sequences on alternate strands of DHNA to

PT control gene expression.

XX

PS Example 2; Fig 4B; 108pp; English.

XX

CC The present invention relates to methods and oligonucleotides for forming

CC a triple-helix comprising a double helical nucleic acid comprising first

CC and second substantially complementary strands, and an oligonucleotide

CC bound to a purine-rich target sequence within the double helical nucleic

CC acid, where the oligonucleotide binds in a parallel and antiparallel

CC orientation, respectively, to target sequences on alternate strands of

CC the double helical nucleic acid. The method has therapeutic applications,

CC where gene expression is controlled by selective triple-helix formation

CC within expression regulatory sequences of a target gene. The

```

OS Homo sapiens.
XX US6333152-B1.
PN
XX
PD 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
PF
XX
XX 20-MAY-1998; 98US-00081646.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
PI WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 53; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 15 BP; 1 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACA 740
DB 15 GCGACGAGAAACA 3
||| |||||
RESULT 190
ABX00872/c
ID ASX00872 standard; RNA; 15 BP.
XX
AC ABX00872;
XX
XX 23-DEC-2002 (first entry)
DT
XX
XX Hepatitis C virus substrate #654 for HCV hammerhead ribozyme #654.
DE
XX
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
XX Hepatitis C virus.
CS
XX US2002082225-A1.
PN
XX
XX 27-JUN-2002.
PD
XX
XX 23-MAR-1999; 99US-00274553.
PF
XX
XX 23-MAR-1999; 99US-00274553.
PR
XX
XX (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
XX

```

```

PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX Claim 1; Page 40; 80pp; English.
XX
XX The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psa/pdbEntry.html
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 732 GGAGAAACAGAAC 744
DB 13 GGTGAACAGTAC 1
||| |||||
RESULT 191
AAL39513
ID AAL39513 standard; DNA; 15 BP.
XX
AC AAL39513;
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX CCBP2 detecting ASO primer SEQ ID No 40.
DE
XX
XX Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
KW polymorphic gene variant; single nucleotide polymorphism; human; primer;
KW PCR; ss.
XX
XX Homo sapiens.
OS
XX WO200232926-A2.
PN
XX 25-APR-2002.
PD
XX
XX 12-OCT-2001; 2001WO-US042685.
PF
XX
XX 12-OCT-2000; 2000US-0239638P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Armstrong B, Kazemi A, Koshy B;
PI WPI; 2002-435524/46.
XX
XX New genetic variants having polymorphisms in the chemokine binding
PT protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
PT treating disorders affected by expression or function of the CCBP2
PT isogene.
XX

```


Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 3.8e+02;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAACAG 741
|||||:||||
15 TGCCAGGAGGTTTCAG 1

Db

RESULT 187
AABN80567/C
ID AEN80567 standard; DNA; 15 BP.
XX AC
XX AEN80567;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P450(cytochrome) oxidoreductase allele specific PCR primer #7.
XX
XX Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
KW single nucleotide polymorphism; flavoprotein; enzyme; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200226768-A2.
PN
XX
XX 04-APR-2002.
PD
XX
XX 01-OCT-2001; 2001WO-US030877.
XX
XX 29-SEP-2000; 2000US-0236449P.
PR
XX (GENA-) GENAISANCE PHARM INC.
PA
XX
XX Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;
PI WPI; 2002-394236/42.
XX
XX
DR
XX
XX New genetic variants comprising haplotypes of the P450 (cytochrome)
PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
PT screening protocols for compounds targeting POR.
XX
XX
PS Claim 14; Page 14; 141pp; English.
XX
CC The present invention provides the protein, gene and cDNA sequences of
CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
CC polymorphisms (SNPs) identified therein. The sequences can be used to
CC haplotype the POR gene of an individual, and to establish whether POR is
CC a suitable target for drugs to treat cancer and disorders associated with
CC impaired protein synthesis in cells. The present sequence is an allele
CC specific primer for the coding sequences of the invention
XX
XX Sequence 15 BP; 1 A; 3 C; 5 G; 5 T; 0 U; 1 Other;
SQ

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACCA 740
|||||:|||||
13 GCCTGCAGAACCA 1

Db

RESULT 188
AAD24257/c
ID AAD24257 standard; DNA; 15 BP.
XX AC
XX AAD24257;
XX
DT 07-MAR-2002 (first entry)
XX
DE Duplex forming PNA #1 targeted to Escherichia coli ribosomal RNA.

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 734 AGAACACAGACAC 746
 Db 2 AGCAACACAGACAC 14

RESULT 185
 AAF79911/c
 ID AAF79911 standard; DNA; 15 BP.

XX AAF79911;

XX 11-JUN-2001 (first entry)

XX Nucleotide sequence of a control peptide nucleic acid.

XX Peptide nucleic acid; PNA; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..14

FT /tag= a

FT /note= "N-acetyl(2-aminoethyl)glycine backbone"

FT modified_base 15

FT /tag= b

FT /note= "N-[acetyl(2-aminoethyl)]-C-lysine-glycine backbone"

XX US6190866-B1.

XX 20-FEB-2001.

XX 27-MAR-1998; 98US-00049190.

XX 16-SEP-1997; 97US-00932140.

XX (NIEL/) NIELSEN P E.

XX Nielsen PE, Good L;

XX WPI; 2001-256212/26.

XX Determining bacterial target gene function, involves preparing peptide
 PT nucleic acid (PNA) compounds complementary to bacterial nucleotide
 PT sequence, determining activity of PNA, contacting active PNA compounds
 PT and determining the effect.

XX Example 5; Col 13; 34pp; English.

XX The present sequence represents a control peptide nucleic acid (PNA),
 CC which used in the method of the invention. The specification describes a
 CC method for determining target gene function in bacteria. The method
 CC comprises providing a nucleotide sequence of the target gene from the
 CC bacteria, selecting and preparing PNAs with regions complementary to a
 CC part of the nucleotide sequence, in anti-parallel orientation,
 CC determining activity of PNA by selected assay to identify active PNA
 CC compounds, contacting the bacteria with the active PNA compounds, and
 CC determining effect of these on the bacteria. The method is useful for
 CC determining the function of target gene in a bacteria. The method is also
 CC useful in the design of antisense antibacterial drugs and gene function
 CC analysis in bacteria. The method is used for killing or inhibiting of

CC bacteria

XX SQ Sequence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 731 AGGAGAAACAGAA 743

Db 15 AGGAGAAAGCTA 3

RESULT 186

ABA99292/c

ID ABA99292 standard; DNA; 15 BP.

XX ABA99292;

XX 13-MAY-2002 (first entry)

XX Human ALDH5 allele-specific oligonucleotide SEQ ID No 12.

XX ALDH5; human; gene; polymorphism; haplotype; aldehyde dehydrogenase 5;
 KW binding affinity; drug targeting; alcoholism; alcohol-induced disorder;
 KW antialcoholic; ss.

XX Homo sapiens.

XX WO200192279-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US017253.

XX 26-MAY-2000; 2000US-0207508P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Finkel K, Kazemi A, Messer C, Sanchis A;

XX WPI; 2002-122054/16.

XX New genetic variants with polymorphisms in the aldehyde dehydrogenase 5
 PT (ALDH5) gene, useful for studying the function of ALDH5, and for
 PT expressing ALDH5 protein which is useful in screening drugs for treating
 PT ALDH5-related diseases.

XX Claim 17; Page 76; 96pp; English.

XX This invention describes a novel isolated genes and haplotypes of the
 CC human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites.
 CC The polymorphic ALDH5 variant is useful in studying the effect of the
 CC variation on the biological activity of ALDH5 and on the binding affinity
 CC of candidate drugs targeting ALDH5 for the treatment of alcoholism and
 CC alcohol-induced disorders. Polynucleotides comprising a polymorphic gene
 CC variant or fragment may be used for therapeutic purposes. ALDH5 protein
 CC isoforms may be used in assays to measure the binding affinities of one
 CC or more candidate drugs targeting the ALDH5 protein. ALDH5 proteins may
 CC be used to generate antibodies. Haplotyping method can be used by
 CC scientists to validate ALDH5 as a candidate target for treating a
 CC specific condition or disease predicted to be associated with ALDH5
 CC activity, and in the design of clinical trials of candidate drugs for
 CC treating a specific condition or disease predicted to be associated with
 CC ALDH5 activity. Information on polymorphisms on the ALDH5 gene can be
 CC applied for studying the biological function of ALDH5 as well as in
 CC identifying drugs targeting this protein for the treatment of disorders
 CC related to its abnormal expression or function. The products of the
 CC invention have antialcoholic activity. This sequence represents a human
 CC ALDH5 allele-specific oligonucleotide described in the disclosure of the
 CC invention

XX Sequence 15 BP; 3 A; 6 C; 3 G; 2 T; 0 U; 1 Other;

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744
 Db 3 GGAGAGCTGAAC 15
 ||||| |||||
 ||||| |||||

RESULT 183
 AAF50112/C
 ID AAF50112 standard; DNA; 15 BP.
 XX
 AC AAF50112;
 XX
 DT 30-MAR-2001 (first entry)
 DE IGF-I oligonucleotide #1072.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 67; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGAGAAACAGA 742
 Db 13 CAGAAAGTAACAGA 1
 ||||| |||||
 ||||| |||||

RESULT 184
 AAF53454
 ID AAF53454 standard; DNA; 15 BP.
 XX
 AC AAF53454;
 XX
 DT 30-MAR-2001 (first entry)
 DE IGF-I oligonucleotide #4414.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 89; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

PS Example 8; Page 93; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744

Db 1 GGAGAGCTGAC 13

RESULT 181

AAAF50109/c

ID AAF50109 standard; DNA; 15 BP.

AC AAF50109;

XX 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #1069.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

PS Example 8; Page 67; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743

Db 15 AGAAGTAACAGAA 3

RESULT 182

AAAF54011

ID AAF54011 standard; DNA; 15 BP.

AC AAF54011;

XX 30-MAR-2001 (first entry)

XX IGF-I oligonucleotide #4971.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 93; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an

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XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX XX WPI; 2001-041421/05.
XX DR
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 89; 20pp; English.
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 7 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGACAGAGAC 746
DB |||||
3 AGCAGACAGAC 15
RESULT 179
AAF54012
ID AAF54012 standard; DNA; 15 BP.
XX AC AAF54012;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4972.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX XX WPI; 2001-041421/05.
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering

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FT XX C-5"

PN XX US2001002314-A1.

XX XX 31-MAY-2001.

XX XX 04-AUG-1998; 98US-00128732.

XX XX 30-OCT-1987; 87US-00115922.

PR XX 16-NOV-1990; 90US-00614205.

PR XX 12-NOV-1993; 93US-00152250.

XX XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.

XX XX Dervan PB, Moser HE;

PI XX WPI; 2001-342909/36.

DR XX

XX XX New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.

PT XX

XX XX Example 2; Fig 4B; 20pp; English.

PS XX

XX XX This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present sequence represents probe of the invention which is used in an example illustrating how it binds to and cleaves a double stranded fragment of CC plasmid pDMG10 given in AH20315

XX XX

SQ Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 733 GAGAAACAGAACACA 745

Db 14 GAGAAACAGAAACA 2

RESULT 177

AAF53455

ID AAF53455 standard; DNA; 15 BP.

XX AC

XX AAF53455;

XX AC

XX 30-MAR-2001 (first entry)

XX XX

DE IGF-I oligonucleotide #4415.

XX XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX XX 21-JUN-2000; 2000WO-AU000693.

XX XX 21-JUN-1999; 99US-0140345P.

XX XX (MURD-) MURDOCH CHILDRENS RES INST.

XX XX Wright CU, Werther GA, Edmondson SR;

PI XX WPI; 2001-041421/05.

DR XX

XX XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

PT XX

XX XX Example 8; Page 89; 201pp; English.

PS XX

XX XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX XX

SQ Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;

Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACACAGACAC 746

Db 1 AGAACACAGACAC 13

RESULT 178

AAF53453

ID AAF53453 standard; DNA; 15 BP.

XX AC

XX AAF53453;

XX AC

XX 30-MAR-2001 (first entry)

XX XX

DE IGF-I oligonucleotide #4413.

XX XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX XX 21-JUN-2000; 2000WO-AU000693.

XX XX 21-JUN-1999; 99US-0140345P.

XX PR

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DT 15-MAR-2000 (first entry)
XX Control polynucleotide sequence SEQ ID NO:2.
DE
XX Dendrimer; polynucleotide multimer; hybridisation assay; ss.
KW
XX Synthetic.
XX OS
XX WO9961662-A1.
XX PN
XX 02-DEC-1999.
PD
XX 27-MAY-1999; 99WO-GB001697.
XX PF
XX 27-MAY-1998; 98GB-00011403.
XX PR
XX (ISIS-) ISIS INNOVATION LTD.
XX PA
XX Shchepinov MS, Southern EM;
XX PI
XX WPI; 2000-072636/06.
XX DR
XX New dendrimer compositions, used in hybridization assays for the
XX PT detection of target nucleic acids.
XX PT
XX Example 1; Page 7; 25pp; English.
XX PS
XX The present invention describes a dendrimer having branches that
XX CC terminate with the same polynucleotide (PN) sequence. Also described are:
XX CC (1) use of a multimeric PN for hybridisation interaction; and (2) an
XX CC assay for a target PN by hybridisation with an immobilised PN, which
XX CC comprises the preliminary step of conjugating the target to a dendrimer
XX CC having reactive terminal groups. The dendrimers comprising PN multimers
XX CC can be used in hybridisation assays for the detection of target nucleic
XX CC acids. The use of multimeric PNs allows multiple hybridisation reactions
XX CC to occur with a resulting increase in the stability of the hybridised
XX CC components compared to a duplex formed between PN monomers. This increase
XX CC in stability is characterised by higher melting temperatures and higher
XX CC temperatures of reassociation exhibited by the multimeric PNs in
XX CC comparative tests with PN monomers. The present sequence represents a
XX CC control polynucleotide sequence, which is used in an example from the
XX CC present invention
XX SQ Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. NO. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
Db 14 AAGAGAAAGAGAA 2
| | | | | | | | | |
| | | | | | | | | |

RESULT 176
AAH20313/C
ID AAH20313 standard; DNA; 15 BP.
XX
AC AAH20313;
XX
DT 31-JUL-2001 (first entry)
XX
DE DNA-EDTA-FE(II) probe 7.
XX
XX Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 5
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Thymidine has EDTA-FE(II) covalently attached at
XX FT

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RESULT 174
AAZ63819/C
ID AAZ63819 standard; RNA; 15 BP.
XX
AC AAZ63819;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 1866.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX Hepatitis C virus.
XX OS
XX WO9955847-A2.
XX PN
XX 04-NOV-1999.
XX PD
XX 26-APR-1999; 99WO-US009027.
XX PF
XX 27-APR-1998; 98US-0083217P.
XX PR
XX 18-SEP-1998; 98US-0100842P.
XX PR
XX 25-FEB-1999; 99US-00257608.
XX PR
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX Blatt L, Mcswiggen JA, Roberts E, Favco PA, Macejak D;
XX PI
XX WPI; 2000-062023/05.
XX DR
XX Novel ribozymes for the treatment of diseases and conditions related to
XX PT hepatitis C infection.
XX PT
XX Claim 1; Page 71; 123pp; English.
XX PS
XX The present sequence represents the preferred target sequence of an
XX CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
XX CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
XX CC the descriptor line. The HCV sequence was screened for optimal ribozyme
XX CC target sites using a computer folding algorithm and regions of the mRNA
XX CC which did not form secondary folding structures and contained potential
XX CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
XX CC target these sites and their activities optimised by either varying the
XX CC length of the binding arms or by modification to prevent degradation by
XX CC nucleases. The ribozymes of the invention inhibit gene expression and/or
XX CC viral replication, and are used to treat diseases associated with
XX CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
XX CC hepatocellular carcinoma. The ribozymes may be used in combination with
XX CC interferon to treat HCV infection, other infectious diseases, autoimmune
XX CC diseases, and cancer
XX
XX SQ Sequence 15 BP; 2 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. NO. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GGAGAAACAGAAC 744
Db 13 GGTGAACAGTAC 1
| | | | | | | | | |
| | | | | | | | | |

RESULT 175
AAZ48115/C
ID AAZ48115 standard; DNA; 15 BP.
XX
XX
AC AAZ48115;
XX
XX

```

CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

XX SQ Sequence 15 BP; 1 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACA 740
 DB 15 GCGAGGAGAAACA 3

RESULT 172
 AAX61194
 ID AAX61194 standard; DNA; 15 BP.

XX AC AAX61194;

XX DT 28-JUL-1999 (first entry)

XX DE Human chromosome alpha-satellite region.

XX KW Probe; human; chromosome 17 triple-helix forming oligonucleotide;
 XX genetic disorder; missing chromosome; aneuploidy; chromosome 21;
 XX infectious disease; diagnosis; alpha-satellite region; ss.

XX OS Homo sapiens.

XX PN WO9924623-A1.

XX PD 20-MAY-1999.

XX PF 10-NOV-1998; 98WO-US023765.

XX PR 10-NOV-1997; 97US-0064997P.

XX PA (UYPR-) UNIV PRINCETON.

XX PI Johnson MD, Fresco JR;

XX DR WPI; 1998-327425/27.

XX PT Novel use of triple helix forming oligonucleotides, useful for in situ
 XX detection of double stranded target sequence.

XX PS Claim 19; Page 13; 45pp; English.

XX CC This sequence represents a human chromosome alpha-satellite region. The
 CC invention relates to the use of a triple-helix forming oligonucleotide
 CC for in situ detection of a double-stranded target nucleic acid sequence.
 CC The method can be used to detect a genetic disorder e.g. to detect an
 CC extra or missing chromosome or fragment or aneuploidy, especially for
 CC detecting an extra or missing chromosome 17 or 21. The method can be also
 CC be used to screen for individuals at risk of developing a disease or for
 CC diagnosing an infectious disease. The use of triple helix forming
 CC oligonucleotides allows in situ detection of double stranded target
 CC sequence as opposed to prior art uses of developing potential anti-gene
 CC therapeutic agents or artificial restriction endonucleases

XX SQ Sequence 15 BP; 10 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAA 743
 DB 2 AGGTGAAAAGAA 14

RESULT 173

AAX33140/c

ID AAX33140 standard; DNA; 15 BP.

XX AC AAX33140;

XX DT 24-JUN-1999 (first entry)

XX DE Beta-galactosidase targeting peptide nucleic acid SEQ ID NO:11.

XX KW Beta-galactosidase; peptide nucleic acid; PNA; antibacterial;
 XX growth inhibition; antibiotic; bacteria; infection; disinfectant; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..15 /tag= a

FT modified_base 15 /note= "N-acetyl (2-aminoethyl) glycine backbone"

FT /tag= b

FT /note= "t is attached to an amidated lysine residue e.g.
 FT -t-Lys-NH2"

XX PN WO9913893-A1.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-US019199.

XX PR 16-SEP-1997; 97US-00932140.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Nielsen PE, Good L;

XX DR WPI; 1999-254325/21.

XX PT Killing or inhibiting bacterial growth by using a peptide nucleic acid.

XX PS Example 5; Page 21; 97pp; English.

XX CC A method has been developed for killing or inhibiting the growth of
 XX bacteria by contacting the bacteria with a peptide nucleic acid (PNA).
 XX The PNA is targeted to messenger or ribosomal RNA. The antibacterial
 XX composition has bacteriostatic and bactericidal properties. The PNA can
 XX be used to treat a mammal suffering from a bacterial infection where the
 XX PNA is complementary to a region of ribosomal RNA and of mRNA of the
 XX bacteria. Further treatment may include concurrent treatment with an
 XX antibiotic. The PNA can also be used as a method of disinfection by
 XX selecting an object to be disinfected, contacting the object with PNA (in
 XX solution) and rinsing the object with a sterile liquid to remove the PNA.
 XX The invention provides new ways of tackling bacterial infections which
 XX have become resistant to frequently used antibiotics. The present
 XX sequence represents a PNA from an example of the present invention

XX SQ Sequence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
 DB 15 AGGAGAAAGAGTA 3

OS Hepatitis C virus.
XX US2002082225-A1.
XX 27-JUN-2002.
XX 23-MAR-1999; 99US-00274553.
XX 23-MAR-1999; 99US-00274553.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS B.
XX (PAVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX Blatt L, Meswigen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX Claim 2; Page 59; 80pp; English.
XX The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsDIDEntry.html
XX Sequence 14 BP; 2 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 44.5%; Score 9.8; DB 1; Length 14;
XX Best Local Similarity 84.6%; Pred.No. 3.7e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 732 GGAGAACACGAC 744
XX |||||||
XX 13 GGTGAACACGTAC 1
XX
XX RESULT 170
XX ABQ81011
XX ID ABQ81011 standard; DNA; 14 BP.
XX AC ABQ81011;
XX XX
XX 10-JAN-2003 (first entry)
XX Human alpha foetal protein gene oligonucleotide.
XX Human; triple helix; alpha foetal protein; ds.
XX Homo sapiens.
XX WO200272724-A2.
XX PN
XX PD 03-OCT-2002.
XX 25-MAR-2002; 2002WO-FR001034.

XX 23-MAR-2001; 2001FR-00003953.
XX 23-APR-2001; 2001US-0285272P.
XX (AVET) AVENTIS PHARMA SA.
XX Blanche F, Cameron B;
XX WPI; 2003-018943/01.
XX Purifying double-stranded DNA, useful e.g. for isolating plasmids or
XX therapeutic genes, by triple helix formation with oligonucleotide
XX directed to a specific target sequence.
XX Claim 16; Page 10; 49pp; French.
XX The present invention relates to novel double stranded (ds) DNA sequences
XX which can interact with a third strand to form a stable triple helix. The
XX invention also relates to a method for purifying a ds DNA molecule,
XX comprising contact with a third DNA strand that interacts with a target
XX sequence (TS) in the ds DNA to form a triple helix. The present sequence
XX is an oligonucleotide from human alpha foetal protein gene, used as the
XX ds DNA sequence in the method of the invention
XX Sequence 14 BP; 9 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 44.5%; Score 9.8; DB 1; Length 14;
XX Best Local Similarity 84.6%; Pred.No. 3.7e+02;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 731 AGGAGAACACGAA 743
XX |||||||
XX 2 AGGAGAACAGAA 14
XX
XX RESULT 171
XX AAX31405/C
XX ID AAX31405 standard; DNA; 15 BP.
XX AC AAX31405;
XX XX
XX 21-MAY-1999 (first entry)
XX Tag sequence of a transcript decreased in colorectal cancer.
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX Claim 1; Page 49; 120pp; English.
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the

RESULT 167
 AAX14799/C
 ID AAX14799 standard; DNA; 14 BP.
 XX AC AAX14799;
 XX DT 24-MAR-1999 (first entry)
 XX DE Triple helix third strand of Hepatitis B virus nucleotides 1810-1823.
 XX KW Triplex formation; DNA detection; triple helix; identification; bacteria;
 XX KW oncogene; virus; ss.
 XX OS Synthetic.
 XX OS Hepatitis B virus.
 XX PN US5861244-A.
 XX PD 19-JAN-1999.
 XX PF 22-DEC-1993; 93US-00173489.
 XX PR 29-OCT-1992; 92US-00968436.
 XX PA (PROP-) PROFILE DIAGNOSTIC SCI INC.
 XX PI Hepburn AG, Wang C;
 XX WI; 1999-130384/11.
 XX PT Assay of genetic sequences based on triplex formation from double
 PT stranded analyte - and hybrid of anchor and reporter sequences, with
 PT reporter released if triplex formation occurs, used e.g. to identify
 PT bacteria.
 XX PS Disclosure; Col 19-20; 166pp; English.
 XX CC The present sequence represents a polynucleotide that is able to form a
 CC triple helix with a double stranded sequence. Cytosine bases in the
 CC present can be replaced with 5-methylcytosine for increased triplex
 CC stability. The present sequence is used in the assay of the invention,
 CC where it can be part of the anchor DNA or reporter DNA sequence. The
 CC assay comprises adding a sample containing double-stranded DNA test
 CC sequences to an aqueous medium containing at least one complex of anchor
 CC DNA, attached to a solid support, and reporter DNA, where either a part
 CC of the anchor DNA or reporter DNA is designed to form a triple-strand
 CC structure with part of the test sequence. Triplex formation results in
 CC the displacement of the reporter DNA which is detected as an indication of
 CC the presence of the DNA test sequence. The method is used to detect DNA
 CC sequences, particularly for identification of bacteria (by detecting
 CC genes for ribosomal RNA) in clinical samples, but also detection of
 CC oncogenes and Hepatitis B virus
 XX SQ Sequence 14 BP; 0 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.7e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAACAGAA 743
 Db 13 AGGAGAACAGAA 1
 RESULT 168
 AA264722/C
 ID AA264722 standard; RNA; 14 BP.
 XX AC AA264722;
 XX DT 28-MAR-2000 (first entry)
 XX DE Substrate for hairpin ribozyme which cleaves HCV at nt. 1863.

XX KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX OS Hepatitis C virus.
 XX PN WO9955847-A2.
 XX PD 04-NOV-1999.
 XX PF 26-APR-1999; 99WO-US009027.
 XX PR 27-APR-1998; 98US-0083217P.
 XX PR 18-SEP-1998; 98US-0100842P.
 XX PR 25-FEB-1999; 99US-00257608.
 XX PR 23-MAR-1999; 99US-00274553.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 XX WI; 2000-062023/05.
 XX PT Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 XX PS Claim 2; Page 95; 123pp; English.
 XX CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the
 CC Hepatitis C virus (HCV) RNA sequence at the base position given in the
 CC descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation and/or
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX SQ Sequence 14 BP; 2 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.7e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 732 GGAGAACAGAAC 744
 Db 13 GGTGAACAGTAC 1
 RESULT 169
 ABX01559/C
 ID ABX01559 standard; RNA; 14 BP.
 XX AC ABX01559;
 XX DT 23-DEC-2002 (first entry)
 XX DE Hepatitis C virus substrate #44 for HCV hairpin ribozyme #44.
 XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cyostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hairpin ribozyme; HP ribozyme; ss.
 XX

CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 14 BP; 7 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 728 GCAGGAGAACCA 740
DB 2 GCAAGGAGAGCA 14

RESULT 165
AAV48481
ID AAV48481 standard; DNA; 14 BP.
XX
AC AAV48481;
XX
DT 15-OCT-1998 (first entry)
XX
DE TGF-beta-1 antisense oligonucleotide TGF-beta1-30.
XX
KW Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
KW modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-00101531.
XX
PR 31-JAN-1997; 97EP-00101531.
XX
PA (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen K, Brysch W;
XX
DR WPI; 1998-400910/35.
XX

PT Preparation of antisense oligonucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of residues
PT able to form two or three hydrogen bonds, have greater activity and
PT reduced toxicity, used therapeutically or to modulate growth of cells in
PT culture.
XX
PS Claim 10; Fig 3b; 286pp; English.
XX
CC AAV48412-84 represent antisense oligonucleotides directed against
CC transforming growth factor beta-1 (TGF beta-1). The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in cases
CC of cancer or (targeting TGF) for stimulating the immune system
XX
SQ Sequence 14 BP; 5 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 729 CCAGGAGAACAG 741
DB 1 CCATGAGAGCAG 13

RESULT 166
AAX14811/C
ID AAX14811 standard; DNA; 14 BP.
XX
AC AAX14811;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix third strand of Hepatitis B virus nucleotides 274-287.
XX
KW Triplex formation; DNA detection; triple helix; identification; bacteria;
KW oncogene; virus; ss.
XX
OS Synthetic.
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROP-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX

PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 19-20; 168pp; English.
XX

CC The present sequence represents a polynucleotide that is able to form a
CC triple helix with a double stranded sequence. Cytosine bases in the
CC present can be replaced with 5-methylcytosine for increased triplex
CC stability. The present sequence is used in the assay of the invention,
CC where it can be part of the anchor DNA or reporter DNA sequence. The
CC assay comprises adding a sample containing double-stranded DNA test
CC sequences to an aqueous medium containing at least one complex of anchor
CC DNA, attached to a solid support, and reporter DNA, where either a part
CC of the anchor DNA or reporter DNA is designed to form a triple-strand
CC structure with part of the test sequence. Triplex formation results in
CC displacement of the reporter DNA which is detected as an indication of
CC the presence of the DNA test sequence. The method is used to detect DNA
CC sequences, particularly for identification of bacteria (by detecting
CC genes for ribosomal RNA) in clinical samples, but also detection of
CC oncogenes and Hepatitis B virus
XX
SQ Sequence 14 BP; 0 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAA 743
DB 13 AGGAGAACAGGA 1

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PF 06-APR-2001; 2001WO-IB000713.
XX
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WFI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 28052; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pcr_sequences
XX
XX Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 734 AGAACAAGACAC 746
DB 1 AAAAAACAACAC 13

RESULT 163
AAQ40599
ID AAQ40599 standard; DNA; 14 BP.
XX
XX AAQ40599;
XX
XX 25-MAR-2003 (revised)
XX 10-AUG-1993 (first entry)
XX
XX Hypervariable region detection probe 14C5.
XX
XX HVR; human; animal; forensic science; paternity testing; diagnosis;
XX animal breeding; hereditary diseases; tumours; allele; loss;
XX chromosomal regions; tumour region identification; ss.
XX
XX Synthetic.
XX
XX FR2680520-A1.
XX
XX 26-FEB-1993.
XX
XX 22-AUG-1991; 91FR-00010516.
XX
XX 22-AUG-1991; 91FR-00010516.
XX
XX (ETFR ) ETAT FRANCAIS.
XX
XX Vergnaud G;
XX
XX WFI; 1993-136548/17.
XX
XX Detecting the hypervariable regions of DNA for diagnosing hereditary
PT illnesses and tumours - by hybridising labelled polynucleotides and

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PT analysing genomic DNA of individuals which react with restriction
PT fragments.
XX
XX Example; Page 13; 46pp; French.
XX
XX The sequence is that of a polynucleotide probe which may be used in the
XX detection of new hypervariable regions (HVR) in a DNA sequence. HVR
XX represent a fingerprint useful in e.g. forensic science, paternity
XX testing, animal breeding, etc. The probe may be used as part of a method
XX for the efficient detection in humans or other animals, without the use
XX of mini-satellites or primary enrichment. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 14 BP; 8 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 733 GAGAAACAGAC 745
DB 1 GACAAACAGAC 13

RESULT 164
AAQ78477
ID AAQ78477 standard; DNA; 14 BP.
XX
XX AAQ78477;
XX
XX 25-MAR-2003 (revised)
XX 27-JUN-1995 (first entry)
XX
XX TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
XX angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
XX carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
XX immunosuppression; oligonucleotide; ss.
XX
XX Synthetic.
XX
XX WO9425588-A2.
XX
XX 10-NOV-1994.
XX
XX 29-APR-1994; 94WO-EP001362.
XX
XX 30-APR-1993; 93EP-00107089.
XX
XX 13-MAY-1993; 93EP-00107849.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
XX Bogdahn U;
XX
XX WFI; 1994-358266/44.
XX
XX New transforming growth factor beta anti-sense oligonucleotide(s) - for
PT treating immunosuppression, tumours, etc.
XX
XX Claim 6; Page 60; 74pp; English.
XX
XX The antisense oligonucleotides are useful in the treatment of tumours in
XX which expression of TGF-beta is of relevance for pathogenicity and/or
XX inhibition of pathological angiogenesis. They are used especially for the
XX treatment of the immunosuppressive effect of TGF-beta, augmentation of
XX the proliferation of cytotoxic lymphocytes, treatment of endogenous
XX hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
XX and malignant gliomas, including glioblastomas, treatment and prophylaxis
XX of skin carcinogenesis, and treatment of oesophageal and gastric
XX carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
XX AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-

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XX	Oligonucleotide SEQ ID NO 263069 for detecting SNP TSC0063918.
DE	
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
FN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	Olek A, Piepenbrock C, Berlin K;
PI	
XX	WFI; 2001-657177/75.
DR	
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
PS	Claim 1; SEQ ID NO 263069; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation. ABC00010
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
Query Match	44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity	84.6%; Pred. No. 3.6e+02;
Matches	11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	734 AGAACAGACAC 746
Dd	
	13 ATAAACCGAACC 1 .
RESULT 162	
ABC28035	
ID	ABC28035 standard; DNA; 13 BP.
XX	
AC	ABC28035;
XX	
DT	20-FEB-2002 (first entry)
XX	
DE	Oligonucleotide SEQ ID NO 28052 for detecting SNP TSC0007919.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
FN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	

DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 88771; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
 Db 1 AAGAGAAAAAGAA 13

RESULT 159

ABH35192
 ID ABH35192 standard; DNA; 13 BP.

AC ABH35192;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 235169 for detecting SNP TSC0057429.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 235169; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
 Db 1 AAGAGAAAAAGAA 13

RESULT 159

ABC52235/c
 ID ABC52235 standard; DNA; 13 BP.

XX ABC52235;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 52252 for detecting SNP TSC0014524.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 52252; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 0 A; 4 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 0 A; 3 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
DB 13 AGGAGAAACAGAA 1
|||||

RESULT 153
ABF97936
ID ABF97936 standard; DNA; 13 BP.
XX AC ABF97936;
XX 22-FEB-2002 (first entry)
DE DE Oligonucleotide SEQ ID NO 197933 for detecting SNP TSC0005346.
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX Claim 1; SEQ ID NO 197933; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
DB 1 AGTAGAAATAGAA 13
|||||

RESULT 154
ABC52234
ID ABC52234 standard; DNA; 13 BP.
XX AC ABC52234;
XX 21-FEB-2002 (first entry)
DE DE Oligonucleotide SEQ ID NO 52251 for detecting SNP TSC0014524.
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX Claim 1; SEQ ID NO 52251; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
DB 1 AGGAGAAATAGAA 13
|||||

RESULT 155
ABC39719


```

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 88772; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 3 C; 0 G; 10 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGAA 743
Db 13 AAGAGAAAAGAA 1
RESULT 151
ABH63093
ID ABH63093 standard; DNA; 13 BP.
XX
XX ABH63093;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 263070 for detecting SNP TSC0063818.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Oligonucleotide SEQ ID NO 263070 for detecting SNP TSC0063818.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
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XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 263070; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 734 AGAAGACAGACAC 746
Db 1 ATAAACCGAAGAC 13
RESULT 152
ABH35193/C
ID ABH35193 standard; DNA; 13 BP.
XX
XX ABH35193;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 235170 for detecting SNP TSC0057429.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 235170; 29pp + Sequence Listing; German.
XX
```

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
 Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 734 AGAACAACAGAAC 746
 | | | | | | | | | |
 Db 13 AAAAAACAAACAC 1

RESULT 148
 ABF97937/C
 ID ABF97937 standard; DNA; 13 BP.
 XX AC ABF97937;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 197934 for detecting SNP TSC0005346.
 XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WIPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 197934; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGAA 743
 | | | | | | | | | |
 Db 13 AAAAAACAAACAC 1

RESULT 150
 ABC8755/C
 ID ABC8755 standard; DNA; 13 BP.
 XX AC ABC8755;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 88772 for detecting SNP TSC0022307.

QY 731 AGGAGAAACAGAA 743
 | | | | | | | | | |

Db 13 AGTAGAAATAGAA 1
 RESULT 149
 ABH32900
 ID ABH32900 standard; DNA; 13 BP.
 XX AC ABH32900;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 232877 for detecting SNP TSC0056815.

XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WIPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 232877; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 44.5%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 743
 | | | | | | | | | |
 Db 1 AGGAGAAATAGAA 13

RESULT 150
 ABC8755/C
 ID ABC8755 standard; DNA; 13 BP.
 XX AC ABC8755;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 88772 for detecting SNP TSC0022307.

XX (UYJO) UNIV JOHNS HOPKINS.
 PA Vogelstein B, Kinzler KW, Zhang L, Zhou W;
 PI WPI; 2002-153821/20.
 XX
 XX New human nucleic acid containing specific SAGE tags, useful as
 PT diagnostic markers for cancer, also derived probes.
 PT
 XX Disclosure; Col 52; 161pp; English.
 XX
 XX The invention relates to an isolated, purified human nucleic acid (I)
 CC that has the same sequence as a mRNA found in humans and is a SAGE
 CC (serial analysis of gene expression) tag comprising a single stranded
 CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
 CC diagnostic and prognostic markers of cancer, especially of the colon and
 CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
 CC SAGE tags of the invention
 XX
 XX Sequence 15 BP; 6 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 732 GGAGAAACAG 741
 DB 5 GGAGAAACAG 14
 RESULT 146
 ABX00935/C
 ID ABX00935 standard; RNA; 15 BP.
 XX
 AC ABX00935;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #717 for HCV hammerhead ribozyme #717.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 XX US2002082225-A1.
 PN
 XX 27-JUN-2002.
 PD
 XX 23-MAR-1999; 99US-00274553.
 PF
 XX 23-MAR-1999; 99US-00274553.
 PR
 XX (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS B.
 PA (PVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
 PI WPI; 2002-617759/66.
 XX
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 PT replication and are useful to treat hepatitis C virus infections and
 PT cirrhosis, liver failure or hepatocellular carcinoma.
 XX
 PS Claim 1; Page 42; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 XX seqdata.uspto.gov/psidsDIDEntry.html
 XX
 SQ Sequence 15 BP; 0 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 45.5%; Score 10; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 728 GCCAGGAGAA 737
 DB 13 GCCAGGAGAA 4
 RESULT 147
 ABC28034/C
 ID ABC28034 standard; DNA; 13 BP.
 XX
 AC ABC28034;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 28051 for detecting SNP TSC0007919.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 28051; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

```

XX DT 13-AUG-2002 (first entry)
XX DE Human FOS gene allele-specific oligonucleotide sequencing primer #19.
XX KW Human; v-fos FBJ murine osteosarcoma viral oncogene homologue; FOS;
XX KW cytostatic; gene therapy; single nucleotide polymorphism; haplotyping;
XX KW haplotype pair; developmental bone disorder; cancer; tumour; ss; primer;
XX KW chromosome 14q21-q31; sequencing.
XX OS Homo sapiens.
XX PN WO200232931-A2.
XX PD 25-APR-2002.
XX PF 19-OCT-2001; 2001WO-US046142.
XX PR 19-OCT-2000; 2000US-0241620P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Anastasio AE, Kliem SE, Koshy B, Lee HH;
XX PI WPI; 2002-435529/46.
XX DR Novel genetic variants of V-Fos FBJ Murine Osteosarcoma Viral Oncogene
XX PT Homolog (FOS) isogenes, useful for improving efficiency and reliability
XX PT in drug development for treating developmental bone disorders.
XX PS Claim 15; Page 14; 73pp; English.
XX CC The invention relates to single nucleotide polymorphisms in the gene
XX CC encoding the human v-fos FBJ murine osteosarcoma viral oncogene homologue
XX CC (FOS) polypeptide. A method for haplotyping the FOS gene in an individual
XX CC comprises identifying the nucleotide at one or more polymorphic sites and
XX CC determining whether one of the copies of the gene is defined by one of
XX CC the FOS haplotypes given in the specification or whether both copies are
XX CC defined by a haplotype pair. This method is useful in genotyping, whereby
XX CC all possible haplotype pairs can be assigned to specific genotypes. An
XX CC association between a trait and a haplotype or haplotype pair of the FOS
XX CC gene can be identified by comparing the frequency of the haplotype or
XX CC haplotype pair in a population exhibiting the trait with the frequency of
XX CC the haplotype or haplotype pair in a reference population, where a higher
XX CC haplotype frequency in the trait population indicates the trait is
XX CC associated with the haplotype or haplotype pair. FOS and its
XX CC corresponding DNA are used for studying the expression and function of
XX CC FOS, for use in screening for candidate drugs to treat diseases related
XX CC to FOS activity, such as developmental bone disorders and tumours. The
XX CC sequences are also useful for studying the effect of variation on the
XX CC biological activity of FOS as well as on the binding affinity of
XX CC candidate drugs targeting FOS. Sequences ABK81338-ABK81357 represent
XX CC allele-specific oligonucleotide sequencing primers used for detecting FOS
XX CC gene polymorphisms
XX SQ Sequence 15 BP; 7 A; 2 C; 4 G; 1 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
DB 3 AGGAGAAACA 12
|||||
RESULT 144
ABL91826/c
ID ABL91826 standard; DNA; 15 BP.
XX AC ABL91826;
XX DT 11-JUL-2002 (first entry)

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 AGGAGAAACA 740
DB 3 AGGAGAAACA 12
|||||
RESULT 144
ABL91826/c
ID ABL91826 standard; DNA; 15 BP.
XX AC ABL91826;
XX DT 11-JUL-2002 (first entry)

```

```

XX DE Human LIPG gene allele specific oligonucleotide primer 5.
XX KW Human; ss; allele specific oligonucleotide; primer;
XX KW single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
XX KW drug screening; atherosclerosis; cardiovascular disorder;
XX KW LIPG haplotyping; LIPG genotyping.
XX OS Homo sapiens.
XX PN WO200216397-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US026639.
XX PR 25-AUG-2000; 2000US-0227825P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Duda A, Kazemi A, Kliem SE, Messer C;
XX PI WPI; 2002-292055/33.
XX DR Novel genetic variants of Lipase, Endothelial isogenes, useful for
XX PT improving efficiency and reliability in drug development for treating
XX PT diseases associated with LIPG activity, e.g. atherosclerosis.
XX PS Claim 16; Page 14; 134pp; English.
XX CC The invention comprises the DNA and amino acid sequence of the human
XX CC lipase, endothelial (LIPG) isogene. Specifically, the invention relates
XX CC to the discovery of 20 novel polymorphic sites within the LIPG gene. The
XX CC LIPG coding sequence and protein are useful for screening drugs that can
XX CC be used to treat atherosclerosis and other cardiovascular disorders. The
XX CC LIPG coding sequence can also be used to haplotype and genotype the LIPG
XX CC gene of an individual. The DNA sequences ABL91822 - ABL91861 represent
XX CC LIPG gene allele specific oligonucleotide primers
XX SQ Sequence 15 BP; 2 A; 3 C; 2 G; 7 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AGAAACAGAA 743
DB 13 AGAAACAGAA 4
|||||
RESULT 145
ABK32355
ID ABK32355 standard; DNA; 15 BP.
XX AC ABK32355;
XX DT 23-APR-2002 (first entry)
XX DE Human colon cancer SAGE tag #456.
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX KW serial analysis of gene expression; diagnostic; prognostic; probe;
XX KW cancer marker; ss.
XX OS Homo sapiens.
XX PN US6333152-B1.
XX PD 25-DEC-2001.
XX PF 20-MAY-1998; 98US-00081646.
XX PR 20-MAY-1998; 98US-00081646.

```

CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

SQ Sequence 15 BP; 6 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 45.5%; Score 10; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Indels 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741

Db 5 GGAGAAACAG 14

RESULT 141

AAZ63882/C

ID AAZ63882 standard; RNA; 15 BP.

XX AAZ63882;

XX AAZ63882;

XX 28-MAR-2000 (first entry)

DT

XX Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2516.

XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;

XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;

XX autoimmune disease; SS.

XX Hepatitis C virus.

XX WO955847-A2.

XX 04-NOV-1999.

XX 26-APR-1999; 99WO-US009027.

XX 27-APR-1998; 98US-0083217P.

XX 18-SEP-1998; 98US-0100842P.

XX 25-FEB-1999; 99US-00257608.

XX 23-MAR-1999; 99US-00274553.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;

XX WPI; 2000-062023/05.

XX Novel ribozymes for the treatment of diseases and conditions related to

PT Hepatitis C infection.

XX Claim 1; Page 73; 123pp; English.

PS The present sequence represents the preferred target sequence of an

XX enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves

XX the Hepatitis C virus (HCV) RNA sequence at the base position given in

XX the descriptor line. The HCV sequence was screened for optimal ribozyme

XX target sites using a computer folding algorithm and regions of the mRNA

XX which did not form secondary folding structures and contained potential

XX ribozyme cleavage sites were identified. Ribozymes were synthesized to

XX target these sites and their activities optimised by either varying the

XX length of the binding arms or by modification to prevent degradation by

XX nucleases. The ribozymes of the invention inhibit gene expression and/or

XX viral replication, and are used to treat diseases associated with

XX Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and

XX hepatocellular carcinoma. The ribozymes may be used in combination with

XX interferon to treat HCV infection, other infectious diseases, autoimmune

XX diseases, and cancer

XX Sequence 15 BP; 0 A; 6 C; 4 G; 0 T; 5 U; 0 Other;

SQ

Query Match 45.5%; Score 10; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Indels 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741

Db 5 GGAGAAACAG 14

RESULT 143

ABK81356

ID ABK81356 standard; DNA; 15 BP.

XX ABK81356;

XX

AC

Query Match 45.5%; Score 10; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Indels 0; Indels 0; Gaps 0;

QY 737 AACAGAACCCG 748

Db 4 AACAGAACCCG 15

RESULT 143

ABK81356

ID ABK81356 standard; DNA; 15 BP.

XX ABK81356;

XX

AC

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Indels 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAA 737

Db 13 GCCAGGAGAA 4

RESULT 142

AAS14448

ID AAS14448 standard; DNA; 15 BP.

XX AAS14448;

XX AAS14448;

XX 23-APR-2002 (first entry)

DT

XX ASO primer #11 to detect human SCY1 gene polymorphisms.

XX Human; single nucleotide polymorphism; SNP; SCY1; chromosome 17;

XX small inducible cytokine A1-I-309; haplotyping; genotyping; gene;

XX atherosclerosis; human immunodeficiency virus; HIV infection;

XX allele-specific oligonucleotide; ASO; primer; ss.

XX Homo sapiens.

XX WO200179236-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US012305.

XX 14-APR-2000; 2000US-0197119P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Choi JY, Kiem SE, Koshi B, Sausker EA, Stephens JC;

XX WPI; 2002-075066/10.

XX Genotyping human small inducible cytokine A1-I-309, homologous to mouse

XX Tca-3 gene of individual, involves determining identity of nucleotide

XX pair at specific polymorphic sites for two copies of the gene.

XX Claim 15; Page 13; 58pp; English.

XX The present invention relates to novel single nucleotide polymorphisms

XX (SNPs) in the human small inducible cytokine A1-I-309 (SCY1) gene

XX located on chromosome 17, and methods for haplotyping and/or genotyping

XX the SCY1 gene. The methods of the invention make use of allele-specific

XX oligonucleotides (ASOs) as probes and primers and/or primer-extension

XX oligonucleotides for detecting the SCY1 gene polymorphisms. The

XX polynucleotides and screened compounds are useful for the treatment of

XX diseases associated with SCY1 activity, such as atherosclerosis, human

XX immunodeficiency virus (HIV) infection, and other inflammatory disorders.

XX AAS14438-AAS14455 represent ASO primers for detecting human SCY1 gene

XX polymorphisms

XX Sequence 15 BP; 6 A; 4 C; 4 G; 0 T; 0 U; 1 Other;

SQ

Query Match 45.5%; Score 10; DB 1; Length 15;

Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 737 AACAGAACCCG 748

Db 4 AACAGAACCCG 15

RESULT 143

ABK81356

ID ABK81356 standard; DNA; 15 BP.

XX ABK81356;

XX

AC

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9988, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI92073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pt_sequences

XX Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
 Query Match 45.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 736 AATCAGACACACC 747

Db 13 AATCAGACACACC 2

RESULT 139

AAV93779/C

ID AAV93779 standard; RNA; 14 BP.

XX AC AAV93779;

18-FEB-1999 (first entry)

Human B-raf target sequence nucleotide position 388.

Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 screening; identification; synthesis; deprotection; purification; cancer;
 inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 stenosis; rheumatoid arthritis; ss.

XX Homo sapiens.

XX WO9850530-A2.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US009249.

XX 09-MAY-1997; 97US-0046059P.

XX 09-JUN-1997; 97US-0049002P.

XX 03-JUL-1997; 97US-0051718P.

XX 22-AUG-1997; 97US-0056808P.

XX 02-OCT-1997; 97US-0061321P.

XX 02-OCT-1997; 97US-0061324P.

XX 05-NOV-1997; 97US-0064866P.

XX 19-DEC-1997; 97US-0068212P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Katulic-Adamic J, Reynolds M, Kisich K, Bellon L;

XX Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;

XX Thompson J, Workman CT, Beaudry A, Sweedler D;

XX WPI; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected processes

XX - especially ribozymes that cleave Raf RNA for treating cancer,

XX stenosis, and also new ribozymes and modified nucleoside triphosphates

XX used as antiviral agents and synthons.

XX Claim 179; Page 174; 259pp; English.

XX A method has been developed for the identification of a nucleic acid

XX capable of modulating a process in a biological system. The method

CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, stenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene

XX Sequence 14 BP; 1 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 45.5%; Score 10; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 734 AGAAACAGAA 743

Db 11 AGAAACAGAA 2

RESULT 140

AAAX31401

ID AAX31401 standard; DNA; 15 BP.

XX AC AAX31401;

XX 21-MAY-1999 (first entry)

XX Tag sequence of a transcript decreased in colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;

XX diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

XX WO9853319-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US010277.

XX 21-MAY-1997; 97US-0047352P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Vogelstein B, Kinzler KW;

XX WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the

XX diagnosis, prognosis and treatment of cancers, particularly colon and

XX pancreatic cancer.

XX Claim 1; Page 48; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are

XX differentially expressed in colorectal cancer, in pancreatic cancer, or

XX in both. The tag sequences can be used to identify genes by matching the

XX tag to a gen data base member, or by using the tag sequences as probes to

XX isolate unidentified genes from cDNA libraries. The tag sequences can

XX also be used in a method for diagnosing colon or pancreatic cancer in a

XX sample suspected of being neoplastic. The method comprises comparing the

XX level of at least one transcript in a first sample of a tissue to a

XX second sample, where the first sample is a colonic tissue suspected of

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 264229; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
CC
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
CC
Query Match 45.5%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 736 AACACAGACACC 747
DB 13 RAACATACACC 2
RESULT 137
ABH64253
ID ABH64253 standard; DNA; 13 BP.
XX ABH64253;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 264230 for detecting SNP TSC0064030.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX

PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 264230; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 1 Other;
SQ
Query Match 45.5%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 736 AACACAGACACC 747
DB 1 RAACATACACC 12
RESULT 138
ABF80070/c
ID ABF80070 standard; DNA; 13 BP.
XX ABF80070;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 180067 for detecting SNP TSC0044584.
DE
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 180067; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC response to vaccination and/or therapy, in cancer immunoprophylaxis,
 CC immunotherapy and diagnosis, and monitoring of tumor progression or
 CC regression, and to produce large quantities of readily purified antigen
 XX

SQ Sequence 11 BP; 5 A; 2 C; 3 G; 0 T; 1 U; 0 Other;
 Query Match 45.5%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 CAGGAGAAAC 739

Db 2 CAGGAGAAAC 11

RESULT 134

ID ABV65653
 ID ABV65653 standard; cDNA; 11 BP.

AC ABV65653;

DT 21-OCT-2002 (first entry)

DE Human skin EST 3439.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Disclosure; Page 120; 1345pp; German.

XX The invention relates to in vitro identification (MI) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (MI) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 45.5%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GGAGAAACAG 741

Db 1 GGAGAAACAG 10

RESULT 135

ID ABF80071
 ID ABF80071 standard; DNA; 13 BP.

AC ABF80071;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 180068 for detecting SNP TSC0044584.

XX SNP; single nucleotide polymorphism; human; diagnosis; FNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 180068; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 45.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGAACACC 747

Db 1 AAACAGAACACC 12

RESULT 136

ID ABH64252/c
 ID ABH64252 standard; DNA; 13 BP.

AC ABH64252;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 264229 for detecting SNP TSC0064030.

XX SNP; single nucleotide polymorphism; human; diagnosis; FNA; cancer; CNS;


```

PN WO2003032898-A2.
XX
PD 24-APR-2003.
XX
XX 23-JUL-2002; 2002WO-US023475.
XX
XX 23-JUL-2001; 2001US-0307345P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Lyman SD, Van Ness KP, Paxton RJ;
XX
XX WPI; 2003-393470/37.
XX
XX P-PSDB; AA837156.
XX
XX New modified human thymic stromal lymphopoietin (TSLP) protein and
PT polynucleotide, useful for stimulating lymphocyte proliferation of
PT lymphopoiesis, particularly as a vaccine for treating e.g. AIDS or
PT autoimmune diseases.
XX
XX Disclosure; Page 41; 52pp; English.
XX
XX The invention relates to modified human thymic stromal lymphopoietin
CC (TSLP) protein and polynucleotide sequences. TSLP protein is useful for
CC stimulating lymphocyte proliferation of lymphopoiesis, or inducing STARS.
CC TSLP DNA is useful for producing a furin-resistant polypeptide having at
CC least one functional human TSLP activity. The invention is useful in the
CC manufacture of a medicament for stimulating lymphocyte proliferation, for
CC promoting lymphopoiesis, or for inducing phosphorylation of STARS. It is
CC also useful as a vaccine for treating AIDS, autoimmune diseases (e.g.
CC transplant rejection), or bacterial or viral infections. The present
CC sequence is human TSLP furin cleavage site peptide encoding DNA
XX
XX Sequence 15 BP; 10 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGACAA 745
DB 1 AGGAGAAAGGAA 15
RESULT 132
ABL91866/c
ID ABL91866 standard; DNA; 10 BP.
XX
XX ABL91866;
AC
XX
XX 11-JUL-2002 (first entry)
DE
XX
XX Human LIPG gene primer extension oligonucleotide 5.
XX
XX Human; ss; primer; extension oligonucleotide;
XX single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
XX drug screening; atherosclerosis; cardiovascular disorder;
XX LIPG haplotyping; LIPG genotyping.
XX
XX Homo sapiens.
OS
XX
XX WO200216397-A2.
PN
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US026639.
XX
XX 25-AUG-2000; 2000US-0227825P.
XX
XX (GENA-) GENAISANCE PHARM INC.
PA
XX Duda A, Kazemi A, Klien SE, Messer C;
PI
XX

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DR WPI; 2002-292055/33.
XX
XX Novel genetic variants of Lipase, Endothelial isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPG activity, e.g. atherosclerosis.
XX
XX Claim 18; Page 14; 134pp; English.
XX
XX The invention comprises the DNA and amino acid sequence of the human
CC lipase, endothelial (LIPG) isogene. Specifically, the invention relates
CC to the discovery of 20 novel polymorphic sites within the LIPG gene. The
CC LIPG coding sequence and protein are useful for screening drugs that can
CC be used to treat atherosclerosis and other cardiovascular disorders. The
CC LIPG coding sequence can also be used to haplotype and genotype the LIPG
CC gene of an individual. The DNA sequences ABL91862 - ABL91901 represent
CC LIPG gene primer extension oligonucleotides
XX
XX Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 45.5%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 734 AGAAACAGAA 743
DB 10 AGAAACAGAA 1
RESULT 133
AAF28124
ID AAF28124 standard; RNA; 11 BP.
XX
XX AAF28124;
AC
XX
XX 02-APR-2001 (first entry)
DT
XX
XX Vesicular stomatitis virus gene junction #1.
DE
XX
XX Vesiculovirus; vaccine; infection; cancer; ss.
KW
XX
XX Vesicular stomatitis virus.
OS
XX
XX US6169943-B1.
PN
XX
XX 02-JAN-2001.
PD
XX
XX 03-MAY-1996; 96US-00646695.
PF
XX
XX 04-MAY-1995; 95US-00435032.
PR
XX
XX (UYUA ) UNIV YALE.
PA
XX
XX Rose JK;
PI
XX
XX WPI; 2001-136716/14.
DR
XX
XX Producing recombinant replicable vesiculovirus, useful as vaccines for
PT treating or preventing microbial infections, comprises culturing a cell
PT containing a nucleic acid for the expression of vesiculovirus antigenomic
PT RNA.
XX
XX Disclosure; Fig 3; 119pp; English.
PS
XX
XX The present invention relates to producing a recombinant replicable
CC vesiculovirus. The method involves culturing a cell containing a first
CC recombinant nucleic acid that can be transcribed to produce an RNA
CC comprising a vesiculovirus antigenomic (+) RNA containing the
CC vesiculovirus promoter for replication and a ribozyme sequence
CC immediately downstream the antigenomic (+) RNA. The method is useful for
CC producing recombinant replicable vesiculoviruses, which can be used as
CC vaccines for the treatment or prevention of infections by a pathogenic
CC microorganism. The recombinant replicable vesiculoviruses are useful in
CC diagnosing and monitoring progression of infectious disorders, including

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XX PD 27-JUN-2002.
XX PF
XX PR 23-MAR-1999; 99US-00274553.
XX PR 23-MAR-1999; 99US-00274553.
XX PR (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX DR
XX PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX PT replication and are useful to treat hepatitis C virus infections and
XX PT cirrhosis, liver failure or hepatocellular carcinoma.
XX PS Claim 1; Page 42; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which
XX CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX CC (HP) motif where the binding arms comprise sequences complementary to one
XX CC of the substrate sequences defined in the specification. The HCV
XX CC of the substrate sequences defined in the specification. The HCV
XX CC ribozymes are useful for modulating the expression and/or replication of
XX CC HCV. They can be used to treat cirrhosis, liver failure and/or
XX CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX CC a condition associated with HCV infection in conjunction with one or more
XX CC other drug therapies, particularly type I interferon, especially
XX CC interferon alpha, beta or gamma or consensus interferon. The present
XX CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX CC Some of the sequence data for this patent did not form part of the
XX CC printed specification. The complete sequence data for this patent was
XX CC obtained in electronic format directly from the USPTO web site at
XX CC seqdata.uspto.gov/psipsDIEntry.html
XX CC
XX SQ Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 46.4%; Score 10.2; DB 1; Length 15;
XX Best Local Similarity 80.0%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 729 CCAGGAGAACAGAA 743
XX DB 15 CCAGGAGAACAGAA 1
XX
XX RESULT 130
XX ABX00934/C
XX ID ABX00934 standard; RNA; 15 BP.
XX AC ABX00934;
XX XX
XX DT 23-DEC-2002 (first entry)
XX DE
XX DE Hepatitis C virus substrate #716 for HCV hammerhead ribozyme #716.
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX KW type I interferon; interferon alpha; interferon beta; cytostatic;
XX KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX OS
XX XX Hepatitis C virus.
XX XX US2002082225-A1.
XX XX 27-JUN-2002.
XX PD

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XX XX 23-MAR-1999; 99US-00274553.
XX XX 23-MAR-1999; 99US-00274553.
XX XX (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX XX WPI; 2002-617759/66.
XX XX
XX XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX XX replication and are useful to treat hepatitis C virus infections and
XX XX PT cirrhosis, liver failure or hepatocellular carcinoma.
XX XX PS Claim 1; Page 42; 80pp; English.
XX XX CC The present invention relates to enzymatic nucleic acids which
XX XX CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX XX CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX XX CC (HP) motif where the binding arms comprise sequences complementary to one
XX XX CC of the substrate sequences defined in the specification. The HCV
XX XX CC ribozymes are useful for modulating the expression and/or replication of
XX XX CC HCV. They can be used to treat cirrhosis, liver failure and/or
XX XX CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX XX CC a condition associated with HCV infection in conjunction with one or more
XX XX CC other drug therapies, particularly type I interferon, especially
XX XX CC interferon alpha, beta or gamma or consensus interferon. The present
XX XX CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX XX CC Some of the sequence data for this patent did not form part of the
XX XX CC printed specification. The complete sequence data for this patent was
XX XX CC obtained in electronic format directly from the USPTO web site at
XX XX CC seqdata.uspto.gov/psipsDIEntry.html
XX XX
XX XX SQ Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
XX XX
XX XX Query Match 46.4%; Score 10.2; DB 1; Length 15;
XX XX Best Local Similarity 80.0%; Pred. No. 3.3e+02;
XX XX Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX QY 728 GCCAGGAGAACAGAA 742
XX DB 15 GCCAGGAGAACAGAA 1
XX
XX RESULT 131
XX AAD56173
XX ID AAD56173 standard; DNA; 15 BP.
XX XX
XX AC AAD56173;
XX XX
XX DT 07-AUG-2003 (first entry)
XX XX
XX XX Human TSLP furin cleavage site peptide encoding DNA.
XX DE
XX DE Thymic stromal lymphopoietin; TSLP; lymphopoiesis; STAT5; antibacterial;
XX KW furin-resistant protein; lymphocyte; vaccine; AIDS; autoimmune disease;
XX KW transplant rejection; infection; immunosuppressive; immunostimulant;
XX KW virucide; human; ds.
XX OS
XX OS Homo sapiens.
XX XX
XX XX Key
XX XX CDS
XX XX Location/Qualifiers
XX XX 1..15
XX XX /*tag= a
XX XX /product= "Human TSLP furin cleavage site peptide"
XX XX /note= "CDS does not include start and stop codon"
XX XX
XX XX

```

DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2513.
 XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX Hepatitis C virus.
 OS
 XX WO955847-A2.
 FN
 XX 04-NOV-1999.
 PD
 XX 26-APR-1999; 99KO-US009027.
 PF
 XX 27-APR-1998; 98US-0083217P.
 PR
 XX 18-SEP-1998; 98US-0100842P.
 PR
 XX 25-FEB-1999; 99US-00257608.
 PR
 XX 23-MAR-1999; 99US-00274553.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 PI WPI; 2000-062023/05.
 XX
 XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 PT
 XX Claim 1; Page 73; 123pp; English.
 PS
 XX The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
 Query Match 46.4%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 729 CCAGGAGAAACAGAA 743
 DB 15 CCAGGAGAGGAAAA 1
 RESULT 128
 AAF49128/c
 ID AAF49128 standard; DNA; 15 BP.
 XX
 XX AAF49128;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #88.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryiasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 FN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 61; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 46.4%; Score 10.2; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 733 GAGAACAGACACC 747
 DB 15 GAGAACAGAGGCC 1
 RESULT 129
 ABX00933/c
 ID ABX00933 standard; RNA; 15 BP.
 XX
 XX ABX00933;
 AC
 XX 23-DEC-2002 (first entry)
 DT
 XX Hepatitis C virus substrate #715 for HCV hammerhead ribozyme #715.
 DE
 XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 XX Hepatitis C virus.
 OS
 XX US2002082225-A1.
 FN

RESULT 125
AAQ74220
ID AAQ74220 standard; cDNA; 15 BP.
XX
AC AAQ74220;
XX
XX
DT 25-MAR-2003 (revised)
DT 02-JUN-1995 (first entry)
XX
DE Influenza virus strain B/Panama/45/90 NS and HA gene primer.
XX
KW Influenza virus; antigen; specific; immune response; nucleoprotein;
KW hemagglutinin; polymerase; matrix protein; non-structural protein; human;
KW vaccine; PCR; primer; polymerase chain reaction; amplify; ss.
XX
OS Synthetic.
XX
PN W09421797-A1.
XX
PD 29-SEP-1994.
XX
XX 14-MAR-1994; 94WO-US002751.
XX
XX 18-MAR-1993; 93US-00032383.
PR 08-JUL-1993; 93US-00089985.
XX
XX (MERI) MERCK & CO INC.
PA (VICA-) VICAL INC.
XX
XX Donnelly JJ, Dwariki VJ, Liu MA, Montgomery DL, Parker SE;
PI Shiver JW, Ulmer JB;
XX
XX WPI; 1994-317017/39.
XX
XX Polynucleotide vaccine comprising influenza virus genes - for vaccination
PT against more than one strain of influenza virus.
PT
XX
XX Example 5; Page 47; 171pp; English.
XX
XX The sequences given in AAQ74218-34 are primers which were used in the
CC extraction of viral RNA and cDNA synthesis of genes from type A and type
CC B influenza virus RNA. The first strand of cDNA from type A genes was
CC amplified using a primer which is complementary to a conserved region
CC located at the 3' terminus of the viral RNA for all A strain genes. A
CC separate set of primers was required for amplification of genes from
CC B/Panama/45/90 as it does not have common sequences at each end of viral
CC RNA. The amplified sequences were inserted into the expression plasmid
CC VJNs. VJNs is an expression vector which expresses influenza virus
CC genes. DNA constructs such as this, containing influenza virus genes, are
CC capable of inducing the expression of an antigenic influenza virus gene
CC product which induces a specific immune response upon introduction of the
CC DNA construct into animal tissue in vivo and resultant uptake of the DNA
CC construct by cells which express the encoded influenza gene. These
CC vectors act as polynucleotide vaccines, which induces neutralising
CC antibodies against human influenza virus. The encoded influenza virus
CC gene encodes nucleoprotein, hemagglutinin, polymerase, matrix or non-
CC structural human influenza virus gene products. The virus gene is
CC operably linked to one or more control sequences for incorporation in the
CC vaccine. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 7 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 731 AGGAGAAACAGACA 745
Db 1 AGCAGAAGCAGAGCA 15

RESULT 126
AAZ63881/C
ID AAZ63881 standard; RNA; 15 BP.
XX
AC AAZ63881;
XX
DT 28-MAR-2000 (first entry)
XX
XX Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2514.
DE
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN W09955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
PI WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 73; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
Query Match 46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 728 GCCAGGAGAACAGCA 742
Db 15 GCCAGGAGAACAGAAA 1

RESULT 127
AAZ63880/C
ID AAZ63880 standard; RNA; 15 BP.
XX
AC AAZ63880;
XX
DT 28-MAR-2000 (first entry)
XX


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XX 23-MAR-1999 (first entry)
DT PCR primer 1 used to amplify a 380 bp 5' UTR fragment.
DE RNA respiratory pathogen; common cold; multiple RNA pathogen infection;
XX single-stranded RNA virus; picornavirus; parainfluenza;
KW respiratory syncytial virus; pneumonia; EIB; asthma;
XX exercise induced bronchoconstriction; PCR primer; ss.
OS Synthetic.
OS Picornaviridae.
XX CA2231271-A.
XX 06-SEP-1998.
XX 05-MAR-1998; 98CA-02231271.
XX 06-MAR-1997; 97US-0040207P.
XX (UVR-) UNIV BRITISH COLUMBIA.
XX Hegele RG, Dakhama A;
XX WPI; 1999-071226/07.
XX Detection and diagnosis of multiple RNA respiratory pathogens - using
PT pooled random sequenced oligonucleotides as primers for reverse
PT transcription.
XX Example 1; Page 12; 30pp; English.
XX PCR primers AAX03274-75 were used in a RT-PCR to amplify a 380 bp
CC fragment of the 5' untranslated region (UTR) of Picornavirus, which can
CC detected using probe AAX03276. The primers are used in the method of the
CC invention. The specification describes a new method for obtaining cDNA
CC derived from multiple RNA respiratory pathogens present in cells from a
CC respiratory source. The method comprises extracting RNA from the cells,
CC producing cDNA by reverse transcribing the RNA using pooled short
CC oligonucleotide primers specific to two or more RNA respiratory
CC pathogens. The oligonucleotides are useful for obtaining and diagnosing
CC multiple RNA pathogen infections, especially single-stranded RNA viruses
CC including picornavirus, parainfluenza and respiratory syncytial viruses
CC which cause pneumonia, common cold, exercise induced bronchoconstriction
CC (EIB) and asthma
XX
XX Sequence 16 BP; 1 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
QY Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DQ 732 GGAGAACACAA 743
DB 16 GGGGAACAGAA 5
RESULT 121
AAS56811
ID AAS56811 standard; DNA; 16 BP.
AC AAS56811;
XX 16-JAN-2002 (first entry)
DT Target validation ribozyme TV30 DNA.
DE Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
XX cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
KW inhibitor dominant negative 4; breast basic conserved protein 1; BCL1;
XX BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.

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XX Homo sapiens.
OS WO200170982-A2;
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009559.
XX 23-MAR-2000; 2000US-00536058.
XX (IMMU-) IMMUSOL INC.
XX (BEGE/) BEGER C.
XX Beger C, Barber J, Wong-Staal F;
XX WPI; 2001-611503/70.
XX Novel polypeptides that are the regulators of BRCA-1, useful for treating
PT cancer and diagnosing the presence of neoplastic cells in biological
PT sample.
XX Example 6; Page 65; 97pp; English.
XX Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators,
CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA
CC and primers used in the methods of the invention. Hybridisation of
CC ribozymes to their targets results in cleavage of the RNA target. The
CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-
CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The
CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor
CC dominant negative 4 (ID4), breast basic conserved protein 1 (BCL1),
CC CHLR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and
CC diagnosing cancer and other proliferative disorders. The severity of an
CC incidence of cancer can be lessened by regulating tumour proliferation
CC through modulation of BRCA-1 expression. The sequences of the invention
CC are useful in the development of anti-cancer drugs
XX
XX Sequence 16 BP; 7 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
QY Query Match 47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DQ 736 AAACAGAACACC 747
DB 5 AAAGAGAACACC 16
RESULT 122
AAS56768
ID AAS56768 standard; RNA; 16 BP.
XX AAS56768;
XX 16-JAN-2002 (first entry)
DT BR2 protein ribozyme sequence tag RNA #3.
DE Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
XX cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
KW inhibitor dominant negative 4; breast basic conserved protein 1; BCL1;
XX BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.
XX Homo sapiens.
OS WO200170982-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009559.
XX 23-MAR-2000; 2000US-00536058.

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Db      3 TGCAGGAGGAA 14
|||||
RESULT 118
ABK32031
ID ABK32031 standard; DNA; 15 BP.
XX
XX AC ABK32031;
XX
XX
DT 23-APR-2002 (first entry)
XX
DE Human colon cancer SAGE tag #132.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
XX Homo sapiens.
OS
XX US6333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
PI WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 22; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 727 TGCAGGAGGAA 738
|||||
Db 3 TGCAGGAGGAA 14
|||||
RESULT 119
ACD56204/c
ID ACD56204 standard; RNA; 15 BP.
XX
XX ACD56204;
XX
XX
DT 24-SEP-2003 (first entry)
XX
XX HBV enzymatic nucleic acid substrate sequence #93.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
degenerative; disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis B virus.
OS
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX
XX 08-JUN-2001; 2001US-00877478.
XX
XX 08-JUN-2001; 2001US-0296876P.
XX
XX 24-OCT-2001; 2001US-0335059P.
XX
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (BLAT/) BLATT L.
XX
XX (MACE/) MACEJAK D.
XX
XX (MCSW/) MCSWIGGEN J.
XX
XX (MORR/) MORRISSEY D.
XX
XX (PAVC/) PAVCO P.
XX
XX (LEEP/) LEE P.
XX
XX (DRAP/) DRAPER K.
XX
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 214; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC enzymatic nucleic acid sequences disclosed in the present invention
XX
XX Sequence 15 BP; 1 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGGAAAC 739
|||||
Db 12 GCCAGGAGGAAAC 1
|||||
RESULT 120
AAX03274/c
ID AAX03274 standard; DNA; 16 BP.
XX
XX AAX03274;
AC
```

XX PS Claim 16; Page 13; 79pp; English.

CC The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAI4) gene located on chromosome 22q13.1, and methods for haplotyping and/or genotyping the DNAI4 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the DNAI4 gene polymorphisms. The polymorphisms and screened compounds are useful for the treatment of diseases associated with DNAI4 activity, such as neurological disorders. AAS19907-AAS19920 represent ASO probes for detecting human DNAI4 gene polymorphisms

XX SQ Sequence 15 BP; 1 A; 5 C; 2 G; 6 T; 0 U; 1 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 730 CAGGAGAAACAGAA 743
|||||: |||
15 CAGGAGATCAGGA 2

Db

RESULT 116
ABK09887/c
ID ABK09887 standard; DNA; 15 BP.
XX AC ABK09887;
XX DT 14-MAR-2002 (first entry)
XX DE P2RY1 gene allele-specific oligonucleotide #38.
XX KW Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant; coagulant; platelet aggregation; haplotyping; drug screening; transgenic animal; human; allele-specific oligonucleotide; ss.
XX KW Homo sapiens.
XX OS WO200190117-A2.
XX PN 29-NOV-2001.
XX PD 21-MAY-2001; 2001WO-US016432.
XX PF 19-MAY-2000; 2000US-0205996P.
XX PR (GENA-) GENAISSANCE PHARM INC.
XX PA Kazemi A, Koshiy B, Tanguay DA;
XX PI WPI; 2002-083074/11.
XX DR New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic variants, useful e.g. in studying the expression and function of P2RY1 and screening candidate drugs for treating diseases related to P2RY1 activity.

XX PS Claim 18; Page 13; 79pp; English.

CC The invention relates to a novel isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its fragment. The polymorphic variant comprises one or more variant amino acids selected from valine at a position 34 and glycine at a position 262. The polymorphic variants are useful in studying the expression and function of P2RY1, in expressing P2RY1 protein for use in screening for candidate drugs to treat diseases related to P2RY1 activity, in studying the effect of the variation on the biological activity of P2RY1, and the binding affinity of candidate drugs targeting P2RY1 for the treatment of disorders related to platelet aggregation. The haplotyping methods are

CC useful in validating P2RY1 as a candidate target for treating a specific condition or disease predicted to be associated with P2RY1 activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with P2RY1 activity. The transgenic animals are useful for studying expression of the P2RY1 isogenes in vivo, for in vivo screening and testing of drugs targeted against P2RY1 protein, and for testing the efficacy of therapeutic agents and compounds for disorders related to platelet aggregation in a biological system. ABK09887-ABK09924 represent human purinergic receptor P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of the invention

XX SQ Sequence 15 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 1 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAA 744
|||||: |||
14 RGGGACACAGAA 1

Db

RESULT 117
ABK32766
ID ABK32766 standard; DNA; 15 BP.
XX AC ABK32766;
XX DT 23-APR-2002 (first entry)
XX DE Human colorectal and pancreatic cancer SAGE tag #133.
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; serial analysis of gene expression; diagnostic; prognostic; probe; cancer marker; ss.
XX OS Homo sapiens.
XX OS US6333152-B1.
XX PN 25-DEC-2001.
XX PD 20-MAY-1998; 98US-00081646.
XX PF 20-MAY-1998; 98US-00081646.
XX PR (UJO) UNIV JOHNS HOPKINS.
XX PA Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX PI WPI; 2002-153821/20.
XX DR New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
XX PT Disclosure; Col 93; 161pp; English.
XX PS The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention

XX SQ Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCCAGGAGAAA 738


```

DE Human CFL1 ASO PCR primer #20.
XX
XX Human; cofilin 1; CFL1; gene therapy; antisense gene therapy; primer;
KW immunological disorder; ASO; allele-specific oligonucleotide; PCR; ss.
XX
XX Homo sapiens.
OS
XX WO200194376-A1.
PN
XX 13-DEC-2001.
PD
XX
XX 11-JUN-2001; 2001WO-US019815.
PF
XX
XX 09-JUN-2000; 2000US-0210884P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Anastasio AE, Duda A, Kliem SE, Koshy B, Sausker EA;
PI
XX WPI; 2002-566437/60.
DR
XX
XX Novel genetic variants of human cofilin 1, CFL1 gene for studying
PT expression, function of the gene and expressing CFL1 protein useful in
PT identifying drugs to treat immunological disorders.
PT
XX
XX Claim 17; Page 13; 84pp; English.
PS
XX
XX The invention relates to a novel polynucleotide sequence which is a
CC polymorphic variant of a reference sequence for the cofilin 1 (non-
CC muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
CC reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
CC the invention may have a use in gene therapy, and in antisense gene
CC therapy. The polynucleotide is useful for studying the expression and
CC function of CFL1 and expressing CFL1 protein for use in screening for
CC candidate drugs to treat diseases related to CFL1 activity. The
CC polymorphism and haplotype data are useful for validating whether CFL1 is
CC a suitable target for drugs to treat immunological disorders, screening
CC for such drugs and reducing bias in clinical trials of such drugs. The
CC present sequence represents one of a set of allele-specific
CC oligonucleotide (ASO) PCR primer used in the invention to detect
CC polymorphisms in the CFL1 Gene
XX
XX Sequence 15 BP; 6 A; 5 C; 3 G; 0 T; 0 U; 1 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 729 CCAGGAGCAACACA 742
DB 2 CCAGGAGCCACACA 15
|||||:|
|:|:|
RESULT 114
ABV99770
ID ABV99770 standard; DNA; 15 BP.
XX
XX
XX AC ABV99770;
XX
XX DT 24-FEB-2003 (first entry)
XX
XX DE Human PFKFB2 allele specific oligonucleotide probe #8.
XX
XX Human; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2; PFKFB2;
KW cytosolic; antidiabetic; gene therapy; cancer; diabetes; ss; ASO;
KW allele specific oligonucleotide; probe; polymorphism.
XX
XX Homo sapiens.
OS
XX WO200194363-A2.
PN
XX 13-DEC-2001.
PD
XX

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PF 07-JUN-2001; 2001WO-US018458.
XX
XX 07-JUN-2000; 2000US-0209935P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Duda A, Kazemi A, Koshy B;
XX
XX WPI; 2002-566434/60.
DR
XX
XX New 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene
PT variants, for improving efficiency and reliability in the development of
PT drugs for treating diseases associated with PFKFB2 activity e.g. cancer.
XX
XX Claim 16; Page 13; 95pp; English.
PS
XX
XX The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose
CC -2,6-bisphosphatase 2 (PFKFB2) isogene. The PFKFB2 of the invention has
CC cytosolic and antidiabetic activity. The polynucleotides may have a use
CC in gene therapy. The identified candidate agents targeting PFKFB2, are
CC useful for treating cancer and diabetes. The methods of the invention are
CC useful for improving the efficiency and reliability of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with PFKFB2 activity. The present sequence represents a allele specific
CC oligonucleotide (ASO) probe used in the invention to detect PFKFB2 Gene
CC polymorphisms
XX
XX Sequence 15 BP; 6 A; 4 C; 3 G; 1 T; 0 U; 1 Other;
SQ
Query Match 47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 733 GAGAAACAGAACAC 746
DB 1 GAGAAACRGTAACC 14
|||||:|
|:|:|
RESULT 115
AAS19913/C
ID AAS19913 standard; DNA; 15 BP.
XX
XX
XX AC AAS19913;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE ASO probe #7 to detect human DNAL4 gene polymorphisms.
XX
XX Human; single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;
KW dynein axonemal light polypeptide chain 4; haplotyping; genotyping;
KW neuroprotective; neurological disorder; allele-specific oligonucleotide;
KW ASO; probe; ss.
XX
XX Homo sapiens.
OS
XX WO200179235-A2.
PN
XX
XX PD 25-OCT-2001.
XX
XX PF 16-APR-2001; 2001WO-US012304.
XX
XX PR 17-APR-2000; 2000US-0197460P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bentivegna SC, Chew A, Choi JY, Koshy B;
XX
XX WPI; 2002-075065/10.
DR
XX
XX Genotyping human dynein, axonemal light polypeptide chain 4 gene of
PT individual, useful for determining haplotype of individual, comprises
PT determining identity of nucleotide pair at specific polymorphic sites for
PT two copies of gene.

```

CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

SQ Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGGAAA 738
 DB 3 TGCAGGAGGAAA 14
 |||||

RESULT 111

AAX31812
 ID AAX31812 standard; DNA; 15 BP.

XX AAX31812;

XX 21-MAY-1999 (first entry)

XX Transcript tag sequence increased in pancreatic and colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;

XX diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

XX WO9853319-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US010277.

XX 21-MAY-1997; 97US-0047352P.

XX (UJO) UNIV JOHNS HOPKINS.

XX Vogelstein B, Kinzler KW;

XX WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.

XX Disclosure; Page 80; 120pp; English.

CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the
 CC level of at least one transcript in a first sample of a tissue to a
 CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

SQ Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 727 TGCAGGAGGAAA 738
 DB 3 TGCAGGAGGAAA 14
 |||||

RESULT 112

AAS18254/C
 ID AAS18254 standard; DNA; 15 BP.

XX AAS18254;

XX 25-FEB-2002 (first entry)

XX ASO primer #1 to detect IMPDH2 gene polymorphisms.

XX Human; single nucleotide polymorphism; SNP; IMPDH2; chromosome 3p21.2;
 KW IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic;
 KW allele-specific oligonucleotide; ASO; primer; ss.

XX Homo sapiens.

XX WO200177363-A2.

XX 18-OCT-2001.

XX 11-APR-2001; 2001WO-US011851.

XX 11-APR-2000; 2000US-0196248P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Choi JY, Koshy B, Lee HH, Stephens JC;

XX WPI; 2002-041297/05.

XX New isolated polynucleotide having polymorphic variant of IMP2
 PT dehydrogenase gene, useful for studying expression of the gene in vivo,
 PT and for testing efficacy of therapeutic agents for cancer in biological
 PT system.

XX Claim 15; Page 13; 70pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human IMP dehydrogenase 2 (IMPDH2) gene located on
 CC chromosome 3p21.2, and methods for haplotyping and/or genotyping the
 CC IMPDH2 gene in an individual. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the IMPDH2 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC (developing) treatment of diseases associated with IMPDH2 activity, such
 CC as cancer. AAS18254-AAS18279 represent ASO primers for detecting IMPDH2
 CC gene polymorphisms

SQ Sequence 15 BP; 1 A; 3 C; 2 G; 8 T; 0 U; 1 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 15;

Best Local Similarity 91.7%; Pred. No. 3.1e+02;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAACACAGA 742
 DB 12 AAGAGAACACAGA 1
 |||||

RESULT 113

ABQ88673
 ID ABQ88673 standard; DNA; 15 BP.

XX ABQ88673;

XX 23-SEP-2002 (first entry)

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves rRNA mRNA at the
 CC nucleotide base position indicated in the DE line. The rRNA gene product
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
 CC specifically in the induction of inflammatory responses. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit rRNA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves rRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAACACAGA 742
 Db 13 AGGGAACACAGA 2
 RESULT 109
 AAT50236/c
 ID AAT50236 standard; RNA; 15 BP.
 XX
 AC AAT50236;
 XX
 XX 07-MAR-1997 (first entry)
 DT
 DE Rabbit CERP HH ribozyme target sequence #797.
 XX
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypobetalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
 KW LDL; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN WO9620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US016000.
 XX
 PR 23-DEC-1994; 94US-00363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Couture L, Stinchcomb D, Mcswiggen J, Bisgater C, Page M;
 XX
 DR WPI; 1996-321852/32.
 XX
 XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX
 PS Claim 4; Page 41; 72pp; English.
 XX
 XX AAT50138-T50359 represent target sequences for the rabbit cholesterol
 CC ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT50360-
 CC T50546). CERP is a 74 kD glycoprotein that facilitates neutral lipid

CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CERP. The ribozyme
 CC then binds to 5 nucleotides either side of this site. The ribozymes are
 CC able to cleave mRNA from the gene encoding CERP, thereby blocking
 CC synthesis and/or expression of the mRNA. By inhibiting CERP, the reverse
 CC cholesterol transport (RCT) pathway can be inhibited (or eliminated)
 CC thereby preventing the reduction in size density of the high density
 CC lipoproteins (HDL), prolonging HDL half life, and therefore increasing
 CC HDL levels. The ribozymes can be used to treat conditions associated with
 CC abnormal levels of CERP, specifically atherosclerosis, familial
 CC hypercholesterolaemia, peripheral vascular disease, dyslipidaemia,
 CC hyperbetalipoproteinaemia, hypobetalipoproteinaemia, vascular
 CC complications of diabetes, transplant, atherectomy and angioplastic
 CC restenosis. By inhibiting CERP, the levels of HDL and low density
 CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 CC decrease in LDL levels, and a corresponding increase in HDL levels). The
 CC HH ribozymes can also be used diagnostically to study genetic drift and
 CC mutations in diseased cells, and to detect CERP mRNA. As the HH ribozymes
 CC target specific regions of the CERP gene, they have low non-specific
 CC activity
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 732 GGAGAACACAGAA 743
 Db 12 GGAGAACACAGAA 1
 RESULT 110
 AAX31078
 ID AAX31078 standard; DNA; 15 BP.
 XX
 AC AAX31078;
 XX
 XX 21-MAY-1999 (first entry)
 DT
 XX Tag sequence of a transcript increased in colorectal cancer.
 DE
 XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO9853319-A2.
 PN
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US010277.
 PF
 XX 21-MAY-1997; 97US-0047352P.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Vogelstein B, Kinzler KW;
 PI
 XX WPI; 1999-070161/06.
 DR
 XX
 XX Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX
 PS Claim 2; Page 30; 120pp; English.
 XX
 CC AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a

XX AC ABZ72778;
 XX DT 09-APR-2003 (first entry)
 XX DE Rod opsin hairpin ribozyme target oligonucleotide SEQ ID NO:18.
 XX AC
 XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
 KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
 KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
 KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
 XX OS Homo sapiens.
 XX PN W0200288320-A2.
 XX PD 07-NOV-2002.
 XX PF 01-MAY-2002; 2002WO-US013679.
 XX PR 01-MAY-2001; 2001US-00847601.
 XX KW (UYFL) UNIV FLORIDA.
 XX PA
 XX PI Lewin AS, Shaw LC, Grant MB;
 XX DR WPI; 2003-111880/10.
 XX PT A recombinant adeno-associated virus-vectored ribozyme composition,
 PT useful for treating a disease or dysfunction of the mammalian eye e.g.
 PT retinal disease, e.g. diabetic retinopathy or age-related macular
 PT degeneration.
 XX PS Claim 1; Page 64; 115pp; English.
 XX CC The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
 CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (II) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (I) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
 CC exemplification of the present invention
 XX SQ Sequence 14 BP; 1 A; 4 C; 2 G; 0 T; 7 U; 0 Other;
 Query Match 47.3%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 91.7%; Pred. No. 3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 731 AGGAGAAACAGA 742
 DB 14 AGCAGAAACAGA 3

RESULT 108
 AAT54806/C
 ID AAT54806 standard; RNA; 15 BP.
 XX AC AAT54806;
 XX DT 25-MAR-2003 (revised)
 XX DT 07-APR-1997 (first entry)
 XX DE Mouse rela hammerhead ribozyme target sequence (nt. position 94).
 XX KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX OS Mus musculus.
 XX PN W09523225-A2.
 XX PD 31-AUG-1995.
 XX PF 23-FEB-1995; 95WO-IB000156.
 XX PR 23-FEB-1994; 94US-00201109.
 XX PR 29-MAR-1994; 94US-00218934.
 XX PR 04-APR-1994; 94US-00222795.
 XX PR 15-APR-1994; 94US-00224483.
 XX PR 15-APR-1994; 94US-00227958.
 XX PR 18-MAY-1994; 94US-00228041.
 XX PR 06-JUL-1994; 94US-00245736.
 XX PR 15-AUG-1994; 94US-00291932.
 XX PR 16-AUG-1994; 94US-00291433.
 XX PR 17-AUG-1994; 94US-00292620.
 XX PR 19-AUG-1994; 94US-00293520.
 XX PR 02-SEP-1994; 94US-00300000.
 XX PR 08-SEP-1994; 94US-00303039.
 XX PR 23-SEP-1994; 94US-00311486.
 XX PR 23-SEP-1994; 94US-00311749.
 XX PR 28-SEP-1994; 94US-00314397.
 XX PR 03-OCT-1994; 94US-00316771.
 XX PR 07-OCT-1994; 94US-00319492.
 XX PR 11-OCT-1994; 94US-00321993.
 XX PR 04-NOV-1994; 94US-00334847.
 XX PR 10-NOV-1994; 94US-00337608.
 XX PR 28-NOV-1994; 94US-00345516.
 XX PR 16-DEC-1994; 94US-00357577.
 XX PR 23-DEC-1994; 94US-00363233.
 XX PR 30-JAN-1995; 95US-00380734.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Gramm S, Karpelsky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott PE, Woolf T;
 XX WPI; 1995-351090/45.
 XX DR Ribozymes having modified bases and methods for producing them - for use
 XX PT in inhibiting disease related genes.
 XX PS Claim 2; Page 225; 407pp; English.

CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 736 AAACAGACACACC 747
DB 2 AAACACACACACC 13
|||||

RESULT 105

AAQ78476
ID AAQ78476 standard; DNA; 14 BP.

XX AC AAQ78476;

XX 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)

DE TGF-beta gene phosphorothioate antisense oligonucleotide.

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.

XX OS Synthetic.

XX PN WO9425588-A2.

XX PD 10-NOV-1994.

XX PF 29-APR-1994; 94WO-BP001362.

XX PR 30-APR-1993; 93EP-00107089.

XX PR 13-MAY-1993; 93EP-00107849.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;

XX DR WPI; 1994-358266/44.

XX PT New transforming growth factor beta anti-sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.

XX PS Claim 6; Page 60; 74pp; English.

XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESSEQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESSEQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 14 BP; 6 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGCA 742
DB 1 AGGAGAAACAGCA 12
|||||

RESULT 106

AAV70179
ID AAV70179 standard; DNA; 14 BP.

XX AC AAV70179;

XX 03-FEB-1999 (first entry)

DE Oligonucleotide SEQ ID NO:4 from Figure 14 of US5843661.

KW Universal DNA based molecular Turing machine; circular DNA molecule;
KW computation; algorithm; ds.

XX OS Synthetic.

XX PN US5843661-A.

XX PD 01-DEC-1998.

XX PF 24-APR-1996; 96US-00639080.

XX PR 24-APR-1996; 96US-00639080.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Rothmund PMK;

XX DR WPI; 1999-044569/04.

XX PT Universal molecular Turing machine - based on circular DNA molecule.

XX PS Disclosure; Fig 14; 90pp; English.

XX The present invention describes a universal molecular Turing machine
CC comprising a circular DNA molecule, having sites representing information
CC storage of the Turing machine, the DNA molecule including: an invariant
CC (Inv) restriction site inside the circular DNA molecule; a state
CC restriction site also inside the circular DNA molecule, and adjacent to
CC the Inv restriction site; a current symbol, encoded on the circular DNA
CC molecule at a distance from the state restriction site that represents a
CC state of the Turing machine; a sequence of intervening nucleotides
CC between the state restriction site and the current symbol; a set of
CC asymmetric restriction enzymes; and a set of transition oligonucleotides,
CC which are inserted into the circular DNA molecule as additional symbols,
CC to encode changes to the information storage caused by operation of the
CC Turing machine. The Turing machine is a model of computation. The
CC universal molecular Turing machine is capable of simulating any Turing
CC machine and hence any algorithm. AAV70176 to AAV70206 represent
CC oligonucleotides used to exemplify the present invention

XX SQ Sequence 14 BP; 6 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 GAAACAGAACAC 746
DB 2 GAAACACTACAC 13
|||||

RESULT 107

ABZ72778/C
ID ABZ72778 standard; RNA; 14 BP.

